

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 11:42:09 ; Search time 6528.21 Seconds  
(without alignments)  
6407.126 Million cell updates/sec

Title: US-09-864-680-2  
Perfect score: 3099  
Sequence: 1 caaatacttccttgagtgaa.....tttagttcaaaaaaaaaa 3099

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_estbun:\*  
3: em\_estcin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl1:\*  
10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145.2	4.7	663	10	B1433950 EST536711
2	135.4	4.4	535	10	BM109555 EST557091
3	135.4	4.4	691	10	B1406780 180E06 Ma
4	135.2	4.4	635	9	AW979731 EST341354
5	126.2	4.1	669	10	BM411546 EST585873
6	125.4	4.0	607	10	BE473157 EST418010
7	122.2	3.9	659	10	BE923412 EST427181
8	120.4	3.9	426	10	B1934806 EST554695
9	119.6	3.9	701	12	B1934083 EST53972
10	118	3.8	639	12	BH142383 TDGDO21TH
11	113	3.6	617	10	BE460726 EST412145
12	113	3.6	476	10	BM408141 EST582468
13	108.4	3.5	417	9	AM030063 EST295246
14	107.2	3.5	660	9	AM216532 EST295246
15	105.4	3.4	524	12	BH142479 TDGDP277H
16	104.8	3.4	576	9	A1772710 EST253810
17	103.4	3.3			

18	102.8	3.3	464	10	BF114223 EST441813
19	100.6	3.2	579	9	AM034628 EST278312
20	100.4	3.2	573	10	BM407382 EST581709
21	100.2	3.2	643	9	AM622905 EST306975
22	98.8	3.2	358	10	BF053416 EST438646
23	98	3.2	558	10	B1425924 EST574808
24	97.2	3.1	593	10	BM110993 EST558529
25	97	3.1	800	10	B1421945 EST532611
26	96.4	3.1	779	10	BG596578 EST495256
27	95.2	3.1	526	9	AM217536 EST296250
28	94.8	3.1	587	9	AM934420 EST360253
29	94.4	3.0	323	9	AM933105 EST358948
30	90.8	2.9	725	10	B1177939 EST517823
31	90	2.9	339	10	B1176878 EST38674
32	89.8	2.9	414	9	AW372477 EST38674
33	88.8	2.9	784	10	B1432945 EST535706
34	83.8	2.7	604	10	B1179578 EST518884
35	81.8	2.6	785	10	BM404923 EST579250
36	81.2	2.6	686	10	B1920482 EST540417
37	81.2	2.6	692	10	B1920471 EST540406
38	81.2	2.6	708	10	B1920408 EST540343
39	80.8	2.6	541	10	BM178803 EST580119
40	80.8	2.6	606	10	BM405792 EST516237
41	79.8	2.6	663	10	BG890386 EST516237
42	79	2.5	471	10	BF054511 EST439741
43	78.8	2.5	555	9	AW737464 EST338807
44	78.6	2.5	433	9	AM031596 EST275050
45	78.4	2.5	396	10	BM409153 EST583480

## ALIGNMENTS

RESULT 1  
LOCUS B1433950 663 bp mRNA linear EST 21-AUG-2001  
DEFINITION EST536711 P. infestans-challenged leaf Solanum tuberosum CDNA clone  
PPC8K40 5' sequence, mRNA sequence.  
VERSION B1433950  
SOURCE B1433950.1 GI:15258640  
KEYWORDS EST.  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 663)  
Restrepo, S., Griffiths, R.M., Smart, C.D., Cho, J., Chieningo, A., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B. Generation of ESTs from potato leaves Challenged with Phytophthora infestans, Compatible Interaction  
JOURNAL Unpublished (2000)  
COMMENT Contact: Cathy Ronning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: M13F-R.

FEATURES  
source location/Qualifiers  
1..663  
/organism="Solanum tuberosum"  
/cultivar="Kennedec"  
/db\_xref="taxon:4113"  
/clone="PPC8K40"  
/clone\_1lb="P. infestans-challenged leaf"  
/tissue\_type="leaf"  
/dev\_stage="6 week old"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-). Site\_1: EcoRI; Site\_2: XhoI; Whole plants were challenged with 450,000 sporangia/ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennedec plants showed



LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
BI406780	180E06 Mature tuber	BI406780	BI406780	EST.	potato.	Solanum tuberosum	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.	Nielsen, K.L., Crookshanks, M., Emmersen, J. and Welinder, K.G.	EST-sequencing of mature potato tuber (Var. Kuras)	Unpublished (2000)	Contact: Karen G. Welinder Institit for bioteknologi Aalborg Universitet Sohnsgaardsholmvej 49, 9000 Aalborg, Denmark Tel: +45 96358467 Fax: +45 98141808 Email: kwe@bio.auc.dk	Location/Qualifiers 1. .691
Query Match	Best Local Similarity	4.4%;	Score 135.4;	DB 10;	Length 691;							
Matches	266;	Conservative	0;	Mismatches	176;	Indels	15;	Gaps	1			
QY	2341	tttcaatgagcaaaagc	ttttccagcaagcgtcaagaagttgtaagttggaagaactatc	2400								
DB	120	tttccatgctgtgggtct	tttccacgcaacttcaagaagctgacaaattcaagaacatcacc	179								
QY	2401	taagatggtcatcactatg	gcacatacagctagctagttggtcctaaccttgtagtgcgcgaagctga	2460								
DB	180	ttatttggtcgaactgac	acatcatttagcgaattggcccaactcgaggtgcttcccaattga	239								
QY	2461	tgagtagcagctgtgtgt	gtgtaaga-----tggtcaccatgtgtatg	2505								
DB	240	acaaatttaaaagttgt	ttgttgatgagcttgagaaactgcctgggaagtacagaatag	299								
QY	2506	gatttaacatcgatgtag	cgttttgcctaataatatagttttctcaagttctggaagcca	2565								
DB	300	gatttttgcgtatttga	aaatttttgcctatgacagatgcatgtaattctggaagcga	359								
QY	2566	caaatgacaatttccgt	cctgcctgtagcgctcatgattgaagtccaataattgtaag	2625								
DB	360	ccaaagatcttctttt	cccatgcccttgagcggcgtattttataaaaactgtgttcttccaaag	419								
QY	2626	agataccatltgagttt	gcagatalatacacacactacagctgattgattgaagagagtg	2685								
DB	420	acatttccctaaagatt	tgacagattgatacactaaagcgaatttgagttatggagatga	479								
QY	2686	ctcccaaatctgggaat	ctgtgcgcgaattccagaagaacaagaagacctcgggaaca	2745								
DB	480	cttccttcccttggaat	tttgcctaaagcagatcccaaaagcagagactttgggaaca	539								

RESULT	4	635 bp	mRNA	linear	EST 18-MAY-2001
LOCUS	AM979731				
DEFINITION	EST341354 tomato root deficiency, Cornell University Lycopersicon esculentum cDNA clone CLEW8H19 5', mRNA sequence.				
ACCESSION	AM979731				
VERSION	AM979731.1	GI:8171253			
KEYWORDS	EST.				
SOURCE	tomato.				
ORGANISM	Lycopersicon esculentum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;				
REFERENCE	1 (bases 1 to 635)				
AUTHORS	Van der Hoeven,R.S., Garvin,D.F., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T.S., Romling,C.M., Craven,M.B., Bowman,C.L., Mierman,W., Frazer,C.M., Venter,J.C., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.				
TITLE	Generation of ESTs from tomato nutrient-deficient roots				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> 5 prime sequence.				
FEATURES	Location/Qualifiers				
source	1..635 /organism="Lycopersicon esculentum" /cultivar="T4496" /db_xref="taxon:4081" /clone="CLEW8H19" /clone_lib="tomato root deficiency, Cornell University" /tissue_type="roots" /dev_stage="5-6 weeks old" /note="Vector: pBluescript SK-; site_1: 5' EcoRI; Site_2: 3' XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850). Roots were harvested from plants grown under the following deficiencies/stresses: 10 mM Al, Zn, P, K, Fe, N), and mRNA was isolated from individual treatments. Proportional aliquots of mRNA of each treatment were mixed and used for library construction."				
BASE COUNT	200 a 99 c 163 g 173 t				
ORIGIN					
Query Match	4.4%; Score 135.2; DB 9; Length 635;				
Best Local Similarity	54.7%; Pred. No. 2.4e-19;				
Matches 338; Conservative	0; Mismatches 268; Indels 12; Gaps 3;				
544	atattgttggaagcgtatgatgataaagaacagttttgaagaatctgactgaagctact	603			
Db	30 ATATTGTTGGGTTTTGGGAATGACATAGAAAAAATGTTTCAGTATGTGATTAGAGC--TA	86			
604	ctggggaaccacaagatcattcccgatgttcgtggagtggagcctlaagtaaaacacttag	663			
Db	87 CAATAGATCTTAACACGTTGTCCTCAATTTGTAAGCATGGGTGGACAAAGGAAACAGCAGTTG	146			
664	caaaagaagattacaatgatgaatcaatctatgcgcgttttgatgttcaatgcctggccta	723			
Db	147 CTAGGAAGGTGTACATATAGTGACAACATGTTTTCATTTGATTTGATGTGAGCATGGTGCA	206			
724	catattctcaacagcaacacaaagaagaatttctggtgcctctgcattccacaatca	783			
Db	207 TCGTTTCCCAACATATATACCGGAGAAAGCTTTTACAGACATTTTGGATCAAGTTACC-	265			

```

/organism="Lycopersicon esculentum"
/cultivar="FA496"
/db_xref="taxon:4081"
/clone="cLEGS7123"
/clone_lib="tomato breaker fruit"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/notes="Vector: pBluescriptSKmCudaDp; Site.1: Corc1; Site.2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded

```

```
source
1. 00/
/organism="Solanum tuberosum"
/cultivar="Bintje"
/db_xref="taxon:4113"
/clone="cSTA3606"
/clone_id="potato stolon, Cornell University"
```









VERSION	BH142383.1	GI:15194909
KEYWORDS	GSS.	
SOURCE	tomato.	
ORGANISM	Lycopersicon esculentum	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae: eusterids I; Solanales; Solanaceae; Solanum;	
REFERENCE	1 (bases 1 to 639)	
AUTHORS	van der Hoeven, R., Sun, H., Cho, J., Utterback, T., Renning, C. and Tanksley, S.	
TITLE	Tomato Demethylated Genomic DNA Sequences	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> tomato demethylated genomic DNA Insert length: 1270 Std Error: 0.00 Seq primer: M13F-R Class: Shotgun.	
FEATURES	Location/Qualifiers	
source	1..639 /organism="Lycopersicon esculentum" /cultivar="E6203" /db_xref="taxon:4081" /clone="CTOG24C17" /clone_11b="CTOG" /issue_type="young leaves" /dev_stage="12-14 weeks post harvest" /lab_host="E. coli JM109" /note="vector: pBluescript SK(-). Site_1: EcoRI. Site_2: XhoI. This library was made from short EcoRI digested fragments of the genome of Lycopersicon esculentum ligated into pBS (SK-). The fragments were cloned into the methylation restrictive E.coli strain JM109 with the purpose of enriching the library for non-methylated DNA fragments. This procedure may enrich the pool of cloned fragments in JM109 cells for sequences representing expressed genes. Average insert size 1.27 kb." 	
BASE COUNT	188 a	104 c 150 g 197 t
ORIGIN		
Query Match	3.8%;	Score 118; DB 12; Length 639;
Best Local Similarity	52.0%;	Pred. NO. 1.5e-15;
Matches 319; Conservative	0;	Mismatches 285; Indels 10; Gaps 2.
OY 960	actaccggaatgataaagtagctgttatcggtgtagagaattttcttcgagatg 1019	
DB 9	ACTGGGCTCAAGATGTTTCTGATTATGCAATTGTCTCGTTTCCGCTCATATGAAG 68	
OY 1020	agcttcacgatcaagaatgagagctgttgatcggtgtagagaattttcttcgagatg 1079	
DB 69	TCTTTCTTAAGTCTAAGAAATAGTTGGAATCTATTCACCAAAAATTATTCAAAACAAAT 128	
OY 1080	gacttaccataatgaagtcgagagctgttgaaagaacacggaatgagatgcacgggta 1139	
DB 129	CCGTCCTCTCTCTTCAAAAAAAGGGGAGACATATTTGAANAACATATGCGAGATTA 188	
OY 1140	ccactaactatctcgttggttcagagcttcctcaattaaagaagaacataagaattgg 1199	
DB 189	CCCTCTCGGTTTGTGTTGTTGCTGAGACTGTGTGAAAAATGAGCCACACATGATTAAT 248	
OY 1200	aaaactctgtcctaagaatgtcaagtcattcgtcacaaatgacctgatgaagcatgtca 1259	
DB 249	TGCAGAGAGGTGAGAAATCTGAGCTCGTTCTTGGTACTGTGTGGAACGGTGCAAA 308	
OY 1260	cgtgtgcttggtggtgtagatcacttcgtaacagcgatcctcaaaacatgtcttcgcat 1319	
DB 309	TCAATTCCTCTCTGAGCTACAAATTAATTTGGCCCAATATTTTAAAGCGTTGTTCTCTAT 368	

QY	776	cacaatcaaatgatgacaggggttaagaatgatgtgtgtaagcagcagctagacagacatggtt	835
QY	1320	ttcggaattttccgaagaacagtgatattccagtgaaagatttgatgatgacatg	1379
Db	369	CTTGGAGGCTTTCCTGGAAGATATGAGCAATTCATCTTTCCAACTGTAGTTGGCTATGACATT	428
QY	1380	gctgaggggttccctcctgaagcttgaaaaatgat-----ttggaaggaagaggttgagaagtgt	1433
Db	429	GCTGAGCAATTCGTATAAGGCAAGAACAACATAAAGATATGAGAAGTGTGGCGAGGATAT	488
QY	1434	ttgcaagagcttgtcgatagatgtttagtctctgcgcacgaagagaagtcgcgatgaaaca	1493
Db	489	GTAGGAAGGCTTAATGTATGATGAGAAGTCTAAT-----TTTGGCTGGTGAACAAGGCTTAATGCA	544
QY	1494	aaattgatcatctgaaggttcattcatctaataatatactgacctgtgcgtgagagaattcaa	1553
Db	545	AGGATGAAAGATGTCGAAATATTCACATCTTCTTCCCAAAATGTGCTTAAGGSAACCTCA	604
QY	1554	aggagagaacatttt	1567
Db	605	ACTGAAATGTGTGT	618
RESULT	12		
LOCUS	BE460726/c	617 bp	mrna linear EST 18-MAY-2001
DEFINITION	BE460726	EST412145 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA	
ACCESSION	BE460726	clone CLE36A22, mRNA sequence.	
VERSION	BE460726.1	GI:9505028	
KEYWORDS	EST.		
SOURCE	tomato.		
ORGANISM	Lycopersicon esculentum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;		
	Lycopersicon.		
REFERENCE	1 (bases 1 to 617)		
AUTHORS	Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,		
	Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.D., Romling,C.M.,		
	Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley		
	,S.D.		
	Unpublished of ESTs from tomato fruit tissue, breaker stage		
TITLE	Unpublished (2000)		
JOURNAL	Contact: CUGI		
COMMENT	Clemson University Genomics Institute		
	Clemson University		
	100 Jordan Hall, Clemson, SC 29634, USA		
	Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>		
	5 prime sequence.		
FEATURES	Location/Qualifiers		
SOURCE	1. 617		
	/organism="Lycopersicon esculentum"		
	/cultivar="TA496"		
	/db_xref="taxon:4081"		
	/clone="CLEG36A22"		
	/clone_1ib="tomato breaker fruit, TIGR"		
	/tissue_type="Pericarp"		
	/dev_stage="breaker"		
	/lab_host="SOLR"		
	/note="vector: pBluescriptsmc2adap; Site_1: EcoRI;		
	Site_2: XhoI; Fruit were harvested at the breaker stage		
	(first sign of lycopene accumulation on the blossom end		
	of the fruit). Fruit were cut in half and the seeds and		
	locules were discarded prior to freezing the pericarp."		
BASE COUNT	162 a 148 c 100 g 207 t		
ORIGIN			
Query Match	3.6%; Score 113; DB 10; Length 617;		
Best Local Similarity	51.1%; Pred. No. 1.9e-14;		
Matches	291; Conservative 0; Mismatches 275; Indels 3; Gaps 1;		

```

Db 586 CACCATGGAGACTGATGATGTTGGAAAGATGATGAAGAGATCTAGAAAAACCACT 527
QY 836 acagaaagtttaagaagaagaggtacttaattctcttgatgatactcgtgagttgta 895
Db 526 TCGTGTATCTATTAAGAAAGCAAAATACCTTGTGTGGTGTGATGATGCTCGCAAAAGAGA 467
QY 896 agtggtagagaggtgtagagagatgcttccaaactgagaagaacagagagagtcgaact 955
Db 466 AGCATGGAGAGTTTGAAGAGACATTCGCCGATGACAAAGAT---GGCAGCAGAGTCAT 410
QY 956 gtgactaccgtaataatgataagtagctgtgtaagtgtgtagagaattttcttgcg 1015
Db 409 TATTACACGCGCAAGAGAGATATGCTGAAGCGAGCCGACGAGAGAGCTTTGTGTATTA 350
QY 1016 gatgagcttcaatgataagaatgagagttgagatcttcttaaaagtgacagctttcaag 1075
Db 349 ACTCTGTTCTCTAAGTCAAGAAAGAAAGTGGATCTCTTCTTGAAGAACTACTGTATGT 290
QY 1076 tgaagcatcacatagatgagtagcagactgttggaaagcaatcgcaatgatagtcaag 1135
Db 289 TCGAGCAATGCTGCGCAAAATGGAAGCTTACCTAAGAGATATGCTGGAAGAGTGAAGG 230
QY 1136 gtaccactaactatgtcgtggttgcaagggtcttcaaatctaaagagacaatagaaga 1195
Db 229 TTTACCTCTGCAATGTTGTATTTAGCGGACTACTTTCGATTAAGAAAGATCTAGATGA 170
QY 1196 ttggaagaacgtgtgcaagaatgataatcgtcacaaatgatactcgtatgaagatg 1255
Db 169 ATGGCAAAAGGTAAAGATACCTTTGGAGAGACATTAAGAAATTAATCTGTGGAAT 110
QY 1256 ttcaatgtgcttggtgttgatgatacacttgacaagcagactaaagaactgtctc 1315
Db 109 CTCGCAACATCTATCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 50
QY 1316 gcaattcggaattttccagaagacagtg 1344
Db 49 CTACTTGTATGTTTCCAGAGATCGAG 21

```

```

RESULT 13
LOCUS BM408141 756 bp mRNA linear EST 22-JAN-2002
DEFINITION EST582468 potato roots Solanum tuberosum cDNA clone cPRO33620 5'
end, mRNA sequence.
ACCESSION BM408141
VERSION BM408141.1 GI:18259771
KEYWORDS EST.
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanales; Solanales; Solanum.
1 (bases 1 to 756)
van der Hoeven,R., Sun,H., Karameycheva,S.A., Tsai,J., Van Aken,S.,
Utterback,T., Chalmers,A., Bougri,O., Buell,C.R., Ronning,C.,
Tanksley,S. and Baker,B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info, please contact Research Genetics, Libraries
Division tel: 1-800-711-6195, email cdna@resgen.com
Seq primer: T3.

```

```

FEATURES
source
1..756
Location/Qualifiers
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cPRO33620"
/clone_lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"

```

```

/lab host="SOLR"
/Note="Vector: pBluescript SK(-); Site:1: EcoRI; Site:2:
XhoI; supplier: Cornell University, Tanksley lab,
sequencing; The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."
BASE COUNT 229 a 150 c 166 g 211 t
ORIGIN

```

```

Query Match 3.5%; Score 108.4; DB 10; Length 756;
Best Local Similarity 52.7%; Pred. No. 2e-13;
Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

QY 2353 aagctttccagcaagcgtcaagaagttggaagttggaagaacttaactgaagctgcat 2412
Db 260 ATGCACTTCCAGAGAAATTAAGAAAGTTAACTTGAACCTTCCACTTCCACTTCCACTTCC 319
QY 2413 acttgacatcatagctgagttgcttaaccttgaggtgctgaagctgataagcctt 2472
Db 320 GATGGCCCTCTCTTTGATGATTTACCGAATCTCGAGTACTTAACCTAAGAAATATGCTT 379
QY 2473 gtgtgtggaagaatgagatcccaatgttataaggttaactgaatggaagcttgctaa 2532
Db 380 TCACAGTCCCAAGATGGGAACCAAGTTGAAGAGGGGCTTGGTTCTTTAAACTATGCTGA 439
QY 2533 ttaataagtttctcaagttctggaagcacaatgaacatttccgtctgagc 2592
Db 440 TTGAGATATCTGATATTAACACACTGAGTGGAGTGGCTTCAATGATCATTTCTGCTGAC 499
QY 2593 gccctcagatgagaagttgcaaaaattgaaagagataccatgagttgcagataac 2652
Db 500 ATCTAGTTCTTAAGAGTTGCTTTCACCTTGACACAGATCCCTCAGAGTCTGGGAATATTC 559
QY 2653 acaactacacgtgattgagtttaagaagatgctccccaacttgagggaatcgtcac 2712
Db 560 CGACTTTGCAGATATATGAGCTGGAAATTCACCACTATGCAAGTCTTACACTTAAG 619
QY 2713 gaattcagaagaagaagaagacctggaagaacacctgtgagatgttcccaatc 2772
Db 620 AGATCCCAAGAGGACACCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 679
QY 2773 cattgaagagagatgattcattca 2798
Db 680 ATTTCGGAGATTAATGCTGTTCCA 705

```

```

RESULT 14
LOCUS AM030063 417 bp mRNA linear EST 18-MAY-2001
DEFINITION EST273318 tomato callus, TAMD Lycopersicon esculentum cDNA clone
cLEC12K21, mRNA sequence.
ACCESSION AM030063
VERSION AM030063.1 GI:5888819
KEYWORDS EST.
SOURCE Lycopersicon
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanales; Solanales; Solanum;
Lycopersicon.
1 (bases 1 to 417)
Alcala,V., Vredalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Craven,M.B., Bowman,C.D., Ahn,S., Ronning,
C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html

```









GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 11:42:09 ; Search time 156.24 Seconds  
(without alignments)  
4872.108 Million cell updates/sec

Title: US-09-864-680-2

Perfect score: 3099  
Sequence: 1 caaatattcttgtagtgagta.....tttagtttaaaaaaaaaa 3099

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA :  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3099	100.0	3099	4 US-09-360-186-2	Sequence 2, Appl
2	2725.6	88.0	31491	4 US-09-360-186-1	Sequence 1, Appl
3	2718	87.7	2718	4 US-09-360-186-4	Sequence 4, Appl
4	172.2	5.6	5475	2 US-08-680-327-1	Sequence 1, Appl
5	172.2	5.6	5475	4 US-09-228-246-3	Sequence 3, Appl
6	170	5.5	10968	2 US-08-680-327-2	Sequence 2, Appl
7	170	5.5	10968	4 US-09-228-246-1	Sequence 1, Appl
8	164.2	5.3	5134	2 US-08-310-912A-157	Sequence 157, App
9	164.2	5.3	5134	4 US-09-301-085-157	Sequence 157, App
10	164.2	5.3	5134	5 PCT-US95-04589-157	Sequence 157, App
11	149.2	4.8	3997	3 US-08-947-823-2	Sequence 2, Appl
12	149.2	4.8	51952	3 US-08-947-823-1	Sequence 1, Appl
13	147.6	4.8	3982	3 US-08-947-823-4	Sequence 4, Appl
14	83.6	2.7	4465	3 US-08-930-996A-3	Sequence 3, Appl
15	72.6	2.3	7218	1 US-08-232-463-14	Sequence 14, Appl
16	56	1.8	4946	3 US-08-930-996A-1	Sequence 1, Appl
17	47.2	1.5	3925	4 US-09-330-330-2	Sequence 2, Appl
18	42.8	1.4	289	4 US-09-007-005-17	Sequence 17, Appl
19	42.8	1.4	289	4 US-09-244-796-17	Sequence 17, Appl
20	42	1.4	10332	4 US-09-330-330-3	Sequence 3, Appl
21	41	1.3	2353	4 US-09-004-838-2	Sequence 2, Appl
22	39.4	1.3	503	4 US-09-004-838-134	Sequence 134, App
23	38.4	1.2	1036	4 US-09-004-838-3	Sequence 3, Appl
24	37.8	1.2	1426	4 US-08-858-207A-98	Sequence 98, Appl
25	36.6	1.2	1652	4 US-09-004-838-6	Sequence 6, Appl
26	36.6	1.2	4163	4 US-09-004-838-70	Sequence 70, Appl
27	36.6	1.2	4208	4 US-09-004-838-1	Sequence 1, Appl

28	36	1.2	1902	3 US-09-041-991A-7	Sequence 7, Appl
29	36	1.2	5720	4 US-09-442-100-1	Sequence 1, Appl
30	35.8	1.2	1038	4 US-09-004-838-128	Sequence 128, App
31	35.4	1.1	732	4 US-08-998-416-1036	Sequence 1036, App
32	35.2	1.1	1872	3 US-09-041-991A-5	Sequence 5, Appl
33	35.2	1.1	51259	3 US-08-781-891-209	Sequence 209, App
34	35	1.1	3147	4 US-09-066-046-1	Sequence 1, Appl
35	35	1.1	7218	1 US-08-232-463-14	Sequence 14, Appl
36	34.8	1.1	1739	3 US-08-714-918-1	Sequence 1, Appl
37	34.8	1.1	1739	4 US-09-265-315-1	Sequence 1, Appl
38	34.8	1.1	1739	4 US-09-265-315-1	Sequence 1, Appl
39	34.8	1.1	1739	4 US-09-266-417-1	Sequence 1, Appl
40	34.6	1.1	277	4 US-09-007-005-3	Sequence 3, Appl
41	34.6	1.1	277	4 US-09-244-796-3	Sequence 3, Appl
42	34.4	1.1	1902	3 US-09-041-991A-9	Sequence 9, Appl
43	34.4	1.1	6152	4 US-08-973-462-1	Sequence 1, Appl
44	34.4	1.1	51952	3 US-08-947-823-1	Sequence 1, Appl
45	34.2	1.1	1096	4 US-09-004-838-132	Sequence 132, App

## ALIGNMENTS

RESULT 1  
US-09-360-186-2  
; Sequence 2, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskavicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; CURRENT FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: 60/093,957  
; EARLIER FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 3099  
; TYPE: DNA  
; ORGANISM: Capsicum annuum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (93)..(2810)  
US-09-360-186-2

Query Match 100.0%; Score 3099; DB 4; Length 3099;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	caaatattcttgtagtgagtaatttgaagtgtatattatcgcgaattgaagtgtgtagcatag	60
DB	1	caaatattcttgtagtgagtaatttgaagtgtatattatcgcgaattgaagtgtgtagcatag	60
QY	61	tcgcaagaagaacaaacagagatacagatataatgagtcacgaagtgtggtcttcta	120
DB	61	tcgcaagaagaacaaacagagatacagatataatgagtcacgaagtgtggtcttcta	120
QY	121	tgaagaacatgaatctctcttgacatcaattcgcgcagatgaatctatctcttgatc	180
DB	121	tgaagaacatgaatctctcttgacatcaattcgcgcagatgaatctatctcttgatc	180
QY	181	acagagaagaacttgcgtctcttgtagaaagttagtccctggaattattgtcaaga	240
DB	181	acagagaagaacttgcgtctcttgtagaaagttagtccctggaattattgtcaaga	240
QY	241	acttgaagaacaaacatgttttttgaggaatgacgagatttgaagttaggttaagaag	300
DB	241	acttgaagaacaaacatgttttttgaggaatgacgagatttgaagttaggttaagaag	300
QY	301	ttgcaagtgcctgtgatacacaattcaactgagactaacgagaactgtactggagaa	360
DB	301	ttgcaagtgcctgtgatacacaattcaactgagactaacgagaactgtactggagaa	360

Db 301 ttgcaagtgcgtcgataacacaaatcaactgagactgaacaggaactgtactgtgagaa 360  
QY 361 ataaagccgaagaaaaaagcgcgctcgaaaggttctgtcaaacctcgcaacaaatgacg 420  
Db 361 ataaagccgaagaaaaaagcgcgctcgaaaggttctgtcaaacctcgcaacaaatgacg 420  
QY 421 aggaactgatactatcgtgaaagagtcgacaagaatccaaagataaggaagaaacagat 480  
Db 421 aggaactgatactatcgtgaaagagtcgacaagaatccaaagataaggaagaaacagat 480  
QY 481 caaaggaatcatgtgtcatgatatcttcaagtccaacaaacgaatttgaaggttaaga 540  
Db 481 caaaggaatcatgtgtcatgatatcttcaagtccaacaaacgaatttgaaggttaaga 540  
QY 541 acaatgtgttgacgtgtgatcaagaagaaagttgttagaagatctgactagaagct 600  
Db 541 acaatgtgttgacgtgtgatcaagaagaaagttgttagaagatctgactagaagct 600  
QY 601 actctgggaaccgaacgaatcccgatgtcggaatggagacataggttaaaacaaact 660  
Db 601 actctgggaaccgaacgaatcccgatgtcggaatggagacataggttaaaacaaact 660  
QY 661 tagcaaaagaagttcaaatgatgaatcaatctatgcccgttttgatgtcatgctgg 720  
Db 661 tagcaaaagaagttcaaatgatgaatcaatctatgcccgttttgatgtcatgctgg 720  
QY 721 ctacacatactcacagccacaacaaagaaatttgcgtggcgctcttcacatccaa 780  
Db 721 ctacacatactcacagccacaacaaagaaatttgcgtggcgctcttcacatccaa 780  
QY 781 tcaaaatgagatgacaggttaagaatgattgtgtgaagcagagcagacagacattacaga 840  
Db 781 tcaaaatgagatgacaggttaagaatgattgtgtgaagcagagcagacagacattacaga 840  
QY 841 aaagttaaagaagaagaagttacttaattgtcttgatgatcttgagattggaagttg 900  
Db 841 aaagttaaagaagaagaagttacttaattgtcttgatgatcttgagattggaagttg 900  
QY 901 ggagatgacgtgaagacgatcttccaaactgaagacaatcgagagatcgaaactcttga 960  
Db 901 ggagatgacgtgaagacgatcttccaaactgaagacaatcgagagatcgaaactcttga 960  
QY 961 ctacccgttaatgagatgagctgtgttaacgtgtgtagaagaatttctcttcgagatga 1020  
Db 961 ctacccgttaatgagatgagctgtgttaacgtgtgtagaagaatttctcttcgagatga 1020  
QY 1021 gcttcacgtataaagatgaggttgaggtcttccaaagtgcagacatttccaaagaa 1080  
Db 1021 gcttcacgtataaagatgaggttgaggtcttccaaagtgcagacatttccaaagaa 1080  
QY 1081 catcaacataatgagtcgagactgtgtgaagacaatcgacagatgagtcgaaggttac 1140  
Db 1081 catcaacataatgagtcgagactgtgtgaagacaatcgacagatgagtcgaaggttac 1140  
QY 1141 caactaactattgtcgtgttcgagaggtcttcaaatctaaagagacaatagaagattga 1200  
Db 1141 caactaactattgtcgtgttcgagaggtcttcaaatctaaagagacaatagaagattga 1200  
QY 1201 aaactgttciaaagatgacgaatcttcgtcaaaatgatatgacttgtagagatgttc 1260  
Db 1201 aaactgttciaaagatgacgaatcttcgtcaaaatgatatgacttgtagagatgttc 1260  
QY 1261 ggtgtgcttggtgagttcgaatcgaatcgaacgacatcaaaacatgtctctcatt 1320  
Db 1261 ggtgtgcttggtgagttcgaatcgaatcgaacgacatcaaaacatgtctctcatt 1320  
QY 1321 tcggaattttccagaagaacagtgatataccagtgagaagatttgatgagatcatgagatg 1380  
Db 1321 tcggaattttccagaagaacagtgatataccagtgagaagatttgatgagatcatgagatg 1380  
QY 1381 ctgagaggtctcctgaaggttggaataatgatttggaagagaggttggaaggtgttcgaag 1440  
Db 1381 ctgagaggtctcctgaaggttggaataatgatttggaagagaggttggaaggtgttcgaag 1440

QY 1441 agcttgcgataagatgttagtctcgtcgcaagaagaatcgagatgagacaacaaat 1500  
Db 1441 agcttgcgataagatgttagtctcgtcgcaagaagaatcgagatgagacaacaaat 1500  
QY 1501 gatcagaatgagttcagatcagataatataacgttcgagagagagttccaagagaga 1560  
Db 1501 gatcagaatgagttcagatcagataatataacgttcgagagagagttccaagagaga 1560  
QY 1561 acaattttatcatgaaacgacatgtcttcgagatatacatccagaatgttcatactct 1620  
Db 1561 acaattttatcagaacgacatgtcttcgagatatacatccagaatgttcatactct 1620  
QY 1621 gtagtataaagtcagccctttaaagcgttcgagctgtgtagaataatattgtccct 1680  
Db 1621 gtagtataaagtcagccctttaaagcgttcgagctgtgtagaataatattgtccct 1680  
QY 1681 atgctctttaaagagctctcttaccctgttaaatcgtcaggttgagatcatgacaca 1740  
Db 1681 atgctctttaaagagctctcttaccctgttaaatcgtcaggttgagatcatgacaca 1740  
QY 1741 acaatctttgaaacgaacccatctgttctcctttcaactcttgagccttatatg 1800  
Db 1741 acaatctttgaaacgaacccatctgttctcctttcaactcttgagccttatatg 1800  
QY 1801 ttctcaaatcagaggtgtgtcatctcaaatctcaaatgaagcttgagctgagacagac 1860  
Db 1801 ttctcaaatcagaggtgtgtcatctcaaatctcaaatgaagcttgagctgagacagac 1860  
QY 1861 agattgagttctcctcgagagataactaagcctcatctgttgaagttaccctactgt 1920  
Db 1861 agattgagttctcctcgagagataactaagcctcatctgttgaagttaccctactgt 1920  
QY 1921 tcagctatgggaatttcgaatgaccccgaaatttgcaaggttaatgaaatctgcaagat 1980  
Db 1921 tcagctatgggaatttcgaatgaccccgaaatttgcaaggttaatgaaatctgcaagat 1980  
QY 1981 tcatgttcaacggttctcgatcagataataaatttttgctgagagaaatttggaactaa 2040  
Db 1981 tcatgttcaacggttctcgatcagataataaatttttgctgagagaaatttggaactaa 2040  
QY 2041 tgcgaattaaaggaacttaaacctgcccagatttatactgcccagattgcccagatgac 2100  
Db 2041 tgcgaattaaaggaacttaaacctgcccagatttatactgcccagattgcccagatgac 2100  
QY 2101 ttgacaagaagaagcactggattttcaaaccttaaacatttttactgtctccac 2160  
Db 2101 ttgacaagaagaagcactggattttcaaaccttaaacatttttactgtctccac 2160  
QY 2161 gttgttcgacgaagaggtatatactgagatcaagaatgccaacaaatagaacatgac 2220  
Db 2161 gttgttcgacgaagaggtatatactgagatcaagaatgccaacaaatagaacatgac 2220  
QY 2221 gaaataagagatgactataaagtttcgagacatgaggtctcccaacatctgtctac 2280  
Db 2221 gaaataagagatgactataaagtttcgagacatgaggtctcccaacatctgtctac 2280  
QY 2281 tgcagaacattggaatgaggtctatctctgtgattataagcctttgccaagatata 2340  
Db 2281 tgcagaacattggaatgaggtctatctctgtgattataagcctttgccaagatata 2340  
QY 2341 ttccaagtgcacaagaagcttttcgaacacgctcaagaagttgaagttgaaagaacatc 2400  
Db 2341 ttccaagtgcacaagaagcttttcgaacacgctcaagaagttgaagttgaaagaacatc 2400  
QY 2401 taagctgttcataacttggaacatcatagctgagttgcttaacacttgaggtgcgaagctga 2460  
Db 2401 taagctgttcataacttggaacatcatagctgagttgcttaacacttgaggtgcgaagctga 2460  
QY 2461 tggatgagcgtgtgtgttggaagaatggaatcccaattgttatgggaatttaacgtatga 2520  
Db 2461 tggatgagcgtgtgtgttggaagaatggaatcccaattgttatgggaatttaacgtatga 2520

QY 2521 agctttgctaataataagtttctcaagtcctggaagccacaatgacaatttc 2580  
|||||  
Db 2521 agctttgctaataataagtttctcaagtcctggaagccacaatgacaatttc 2580  
QY 2581 ctgctcttgagcgccatatttagaagttgcacaaattggaagaatcccttagt 2640  
|||||  
Db 2581 ctgctcttgagcgccatatttagaagttgcacaaattggaagaatcccttagt 2640  
QY 2641 ttgcagatacacacactcaagtcgtatgataagaagagtgctcccccacattggg 2700  
|||||  
Db 2641 ttgcagatacacacactcaagtcgtatgataagaagagtgctcccccacattggg 2700  
QY 2701 ttgcagatacacacactcaagtcgtatgataagaagagtgctcccccacattggg 2700  
|||||  
Db 2701 ttgcagatacacacactcaagtcgtatgataagaagagtgctcccccacattggg 2700  
QY 2701 aatctgctgcagaaatccagaagaagacccctgcgaaacaccccttgatgttc 2760  
|||||  
Db 2701 aatctgctgcagaaatccagaagaagacccctgcgaaacaccccttgatgttc 2760  
QY 2761 gttctcaaatccattgaaagagtgatctctgattcaagaagaacattaggaagatct 2820  
|||||  
Db 2761 gttctcaaatccattgaaagagtgatctctgattcaagaagaacattaggaagatct 2820  
QY 2821 caagcgcaagaagattgaactcttggaatttcattcgccctctatcacaaataccac 2880  
|||||  
Db 2821 caagcgcaagaagattgaactcttggaatttcattcgccctctatcacaaataccac 2880  
QY 2881 taattatcggttcaagcaatgtgtgactccaagagatgtatattcttctgtgt 2940  
|||||  
Db 2881 taattatcggttcaagcaatgtgtgactccaagagatgtatattcttctgtgt 2940  
QY 2941 aacataatttggattgtactgattccctctccctctcttcttcttgaacttacta 3000  
|||||  
Db 2941 aacataatttggattgtactgattccctctccctctcttcttcttgaacttacta 3000  
QY 3001 attcaacttcaagtaactagcagacacacattgattgattgattgattgattt 3060  
|||||  
Db 3001 attcaacttcaagtaactagcagacacacattgattgattgattgattgattt 3060  
QY 3061 tatacagatgagacaacacagtttagtttaaaaaaaa 3099  
|||||  
Db 3061 tatacagatgagacaacacagtttagtttaaaaaaaa 3099

RESULT 2  
US-09-360-186-1  
; Sequence 1, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskiewicz, et al.  
; TITLE OF INVENTION: Bst2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; CURRENT FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: 60/093,957  
; EARLIER FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 31491  
; TYPE: DNA  
; ORGANISM: Capsicum annuum  
US-09-360-186-1

Query Match 88.0%; Score 2725.6; DB 4; Length 31491;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2728; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 53 ggtcattatgcgcaaaagacaaacgagaaatagatatataggtcattgcaagtgtgac 112  
|||||  
Db 1440 ggtcattatgcgcaaaagacaaacgagaaatagatatataggtcattgcaagtgtgac 1499  
QY 113 ttctcttaagagaacaataatctctctgacattcaattgctcgatgtaactctatc 172  
|||||  
Db 1500 ttctcttaagagaacaataatctctctgacattcaattgctcgatgtaactctatc 1559

QY 173 ctgtgatcacagagaagaaacttgcgctcttcgtgaaaaagtagttccctggaagatt 232  
|||||  
Db 1560 ctgtgatcacagagaagaaacttgcgctcttcgtgaaaaagtagttccctggaagatt 1619  
QY 233 tgtcaagaacttgcagaaacaatgcttctgggaaatgacggaatttgaagtagagtc 292  
|||||  
Db 1620 tgtcaagaacttgcagaaacaatgcttctgggaaatgacggaatttgaagtagagtc 1679  
QY 293 aagaagaattgcagagttgctgtaatacacaaattcaactgagactaagaagaactgact 352  
|||||  
Db 1680 aagaagaattgcagagttgctgtaatacacaaattcaactgagactaagaagaactgact 1739  
QY 353 gggaagaataaaagccggaaaaaaagcgctcgaaagtttcgtcaaaagcttcaca 412  
|||||  
Db 1740 gggaagaataaaagccggaaaaaaagcgctcgaaagtttcgtcaaaagcttcaca 1799  
QY 413 agtagcagagacatgacatcattcgtgaaagagtcgacaaagatccaaagtaaagaaa 472  
|||||  
Db 1800 agtagcagagacatgacatcattcgtgaaagagtcgacaaagatccaaagtaaagaaa 1859  
QY 473 acaagatcaagaagatcattggttcatttctcaagttccaaacagatatttgaa 532  
|||||  
Db 1860 acaagatcaagaagatcattggttcatttctcaagttccaaacagatatttgaa 1919  
QY 533 gtttaagaacataatggttgcagtgatgacaaaggaacagttgttagaagatctgac 592  
|||||  
Db 1920 gtttaagaacataatggttgcagtgatgacaaaggaacagttgttagaagatctgac 1979  
QY 593 tagaagctactctgggaaacccaagatcccgatttgcggaatgggagacatagtaa 652  
|||||  
Db 1980 tagaagctactctgggaaacccaagatcccgatttgcggaatgggagacatagtaa 2039  
QY 653 aacaacttgcagaaagaatttacaatgataatcttatacgctgttgatgttca 712  
|||||  
Db 2040 aacaacttgcagaaagaatttacaatgataatcttatacgctgttgatgttca 2099  
QY 713 tgcctgggctacacatctcacacagcacaacaaagaaatttgcctgggctcttca 772  
|||||  
Db 2100 tgcctgggctacacatctcacacagcacaacaaagaaatttgcctgggctcttca 2159  
QY 773 ttccacaatcaaaatgagatgacaggttaagaatgtgtgaagcagatagacat 832  
|||||  
Db 2160 ttccacaatcaaaatgagatgacaggttaagaatgtgtgaagcagatagacat 2219  
QY 833 gttcaagaagaatttgaagaagaaggtacttaattgtcttgatgatactgaggttg 892  
|||||  
Db 2220 gttcaagaagaatttgaagaagaaggtacttaattgtcttgatgatactgaggttg 2279  
QY 893 tgaagttggagtgcgctgagacagatcttccaaacgaaagacatgcaaggtcgaat 952  
|||||  
Db 2280 tgaagttggagtgcgctgagacagatcttccaaacgaaagacatgcaaggtcgaat 2339  
QY 953 actgttgactaccctgaatgatgaaagtagctgttactgctgtgtgtagaatttctt 1012  
|||||  
Db 2340 actgttgactaccctgaatgatgaaagtagctgttactgctgtgtgtagaatttctt 2399  
QY 1013 gtcgagatgacttcaatgataagaatgaggttggagttcttcaaaagtgcagatttct 1072  
|||||  
Db 2400 gtcgagatgacttcaatgataagaatgaggttggagttcttcaaaagtgcagatttct 2459  
QY 1073 aagtgaagcattacacatgagttcgagactgttgcgaagaagaatcgacatgata 1132  
|||||  
Db 2460 aagtgaagcattacacatgagttcgagactgttgcgaagaagaatcgacatgata 2519  
QY 2520 cgggttaccactaactatgtcgtgtgttcgaaggtcttcaaatcctaagagacata 2579  
|||||  
QY 1193 agattggaagaactgttctaaagatgacagttcaattgtctacaaatgatactgaag 1252  
|||||  
Db 2580 agattggaagaactgttctaaagatgacagttcaattgtctacaaatgatactgaag 2639

QY 1253 atgttcaagtgcttggtggtgaattacagatcattgacaaagcagatctaaacatgtct 1312  
 |||  
 Db 2640 atgttcaagtgcttggtggtgaattacagatcattgacaaagcagatctaaacatgtct 2659  
 QY 1313 tctgatttcggaattttccagaagaacagatcattccagtgagaatttgaatgaatc 1372  
 |||  
 Db 2700 tctgatttcggaattttccagaagaacagatcattccagtgagaatttgaatgaatc 2759  
 QY 1373 atgtagtcgtaggggtctccgaagtggaattggaagagagaggttgaagagtg 1432  
 |||  
 Db 2760 atgtagtcgtaggggtctccgaagtggaattggaagagagaggttgaagagtg 2819  
 QY 1433 ttggaagaagcttgcagtagatgtctagctctccgaagaagaagctgagatggagc 1492  
 |||  
 Db 2820 ttggaagaagcttgcagtagatgtctagctctccgaagaagaagctgagatggagc 2879  
 QY 1493 aaaaattgagatcgtgaagtgatcagatcattatagaccgtgctgagagaagtcca 1552  
 |||  
 Db 2880 aaaaattgagatcgtgaagtgatcagatcattatagaccgtgctgagagaagtcca 2939  
 QY 1553 aagggagagaacattttatcagagaagacattgtcttgcagatcattatccagaatttc 1612  
 |||  
 Db 2940 aagggagagaacattttatcagagaagacattgtcttgcagatcattatccagaatttc 2999  
 QY 1613 atattctcgtatgataaaatgcagcccttaagcgctgagctgtagatgaattaaatca 1672  
 |||  
 Db 3000 atattctcgtatgataaaatgcagcccttaagcgctgagctgtagatgaattaaatca 3059  
 QY 1673 ttgtccctatggcttcttaagggctctcttaaccctgtaaatcgtcagttgagaatga 1732  
 |||  
 Db 3060 ttgtccctatggcttcttaagggctctcttaaccctgtaaatcgtcagttgagaatga 3119  
 QY 1733 tgacaacaacaattcttggaaacgaacacattctgttctcttcaactcttgagccttt 1792  
 |||  
 Db 3120 tgacaacaacaattcttggaaacgaacacattctgttctcttcaactcttgagccttt 3179  
 QY 1793 atattatgtctcaaacacagaggtgttcatcattcaaatcactcaagcttgagagtg 1852  
 |||  
 Db 3180 atattatgtctcaaacacagaggtgttcatcattcaaatcactcaagcttgagagtg 3239  
 QY 1853 aacacagacagattgatttccctccgagagataactaagcctcatctgttgaagtgctc 1912  
 |||  
 Db 3240 aacacagacagattgatttccctccgagagataactaagcctcatctgttgaagtgctc 3299  
 QY 1913 atcattgttcagctatgggaatttcgagatcccccagaagaatttgcagttatggaactc 1972  
 |||  
 Db 3300 atcattgttcagctatgggaatttcgagatcccccagaagaatttgcagttatggaactc 3359  
 QY 1973 gcagacatcattgttcaacaggttcgatacagataataattttgctgagagaatttg 2032  
 |||  
 Db 3360 gcagacatcattgttcaacaggttcgatacagataataattttgctgagagaatttg 3419  
 QY 2033 ggaactaatgcaattaaaggaattcttaaacgtccagatttatttggcagattggccag 2092  
 |||  
 Db 3420 ggaactaatgcaattaaaggaattcttaaacgtccagatttatttggcagattggccag 3479  
 QY 2093 tgagatctgttgcagaaggaagcacttgatttttcaaaactacaacatttcttactc 2152  
 |||  
 Db 3480 tgagatctgttgcagaaggaagcacttgatttttcaaaactacaacatttcttactc 3539  
 QY 2153 gttcccaagttgttcacaggaaggtattatagggagatcagaagtgcacaaaaattag 2212  
 |||  
 Db 3540 gttcccaagttgttcacaggaaggtattatagggagatcagaagtgcacaaaaattag 3599  
 QY 2213 aatcagtggaataagagtagactataaaagtttgggagcttggtctcccaaaactc 2272  
 |||  
 Db 3600 aatcagtggaataagagtagactataaaagtttgggagcttggtctcccaaaactc 3659  
 QY 2273 tctctatctgcagcaacttgaataattgagcttatactcgttgaattagccttttgc 2332  
 |||  
 Db 3660 tctctatctgcagcaacttgaataattgagcttatactcgttgaattagccttttgc 3719  
 QY 2333 agtgcatttcaagtgcacaaagcttttccagcaacgctcagaaggttgaagtggaaag 2392

Db 3720 agtgcatttcaagtgcacaaagcttttccagcaacgctcagaaggttgaagtggaaag 3779  
 |||  
 QY 2393 aactatctaaagcttgatcattacttggaactatagctgattgtgcttaacctgaagtgc 2452  
 |||  
 Db 3780 aactatctaaagcttgatcattacttggaactatagctgattgtgcttaacctgaagtgc 3839  
 QY 2453 gaagctgagatgagcgtgtgtgtgtgaagaatgacatcccaatgttatgtgattca 2512  
 |||  
 Db 3840 gaagctgagatgagcgtgtgtgtgtgaagaatgacatcccaatgttatgtgattca 3899  
 QY 2513 tctgattgaagctttgtctaatataatagtttctcaagttctggaagccacaatgta 2572  
 |||  
 Db 3900 tctgattgaagctttgtctaatataatagtttctcaagttctggaagccacaatgta 3959  
 QY 2573 caatttctgtctcttgagcgcctcatctgattgaagttgcaaaatttgaagagatacc 2632  
 |||  
 Db 3960 caatttctgtctcttgagcgcctcatctgattgaagttgcaaaatttgaagagatacc 4019  
 QY 2633 cattgagttgcagataac 2692  
 |||  
 Db 4020 cattgagttgcagataac 4079  
 QY 2693 acttggggaatctgtgcacgaattcagaagaacacagacccctgcgaacacacacgt 2752  
 |||  
 Db 4080 acttggggaatctgtgcacgaattcagaagaacacagacccctgcgaacacacacgt 4139  
 QY 2753 ggaatttcgattcattcaatccattgagaga 2784  
 |||  
 Db 4140 ggaatttcgattcattcaatccattgagagata 4171  
 |||  
 RESULT 3  
 US-09-360-186-4  
 ; Sequence 4, Application US/09360186  
 ; Patient No. 626343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Staskawicz, et al.  
 ; TITLE OF INVENTION: B2 Resistance Gene  
 ; FILE REFERENCE: 50687  
 ; CURRENT APPLICATION NUMBER: US/09/360,186  
 ; CURRENT FILING DATE: 1999-07-23  
 ; EARLIER APPLICATION NUMBER: 60/093,957  
 ; EARLIER FILING DATE: 1998-07-23  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: Patentln Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 2718  
 ; TYPE: DNA  
 ; ORGANISM: Capsicum annuum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(2718)  
 US-09-360-186-4  
 Query Match 87.7%; Score 2718; DB 4; Length 2718;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 atggtccatcagatgtgtgtcttctcttatagagaacaatagaatcttcttgacattcaat 152  
 |||  
 Db 1 atggtccatcagatgtgtgtcttctcttatagagaacaatagaatcttcttgacattcaat 60  
 |||  
 QY 153 tgcgcagatgcacatctcatctcgttgatcacaagagaagacattgctgctctcgtgaaaaa 212  
 |||  
 Db 61 tgcgcagatgcacatctcatctcgttgatcacaagagaagacattgctgctctcgtgaaaaa 120  
 |||  
 QY 213 gttagtccttcggaagattattgtcagaagacttgcagaacaaatgatttttggggaatg 272  
 |||  
 Db 121 gttagtccttcggaagattattgtcagaagacttgcagaacaaatgatttttggggaatg 180  
 |||  
 QY 273 aggaatttgaagtagagtagaagaagttgcagaagtgctgctgtaatacaacattcaatg 332

Db 181 acggaatttgagtagagtagaagtgcaagtctgctggaatacaaatccaactg 240  
QY 333 agactaacaggaactgtctacgtggagaaataaagccagaanaaaagcgctcgaaag 392  
Db 241 agactaacaggaactgtctacgtggagaaataaagccagaanaaaagcgctcgaaag 300  
QY 393 ttctgtaaaagccgcgaacaagtagcagagacatgcatctatctggaagaatcgaca 452  
Db 301 ttctgtaaaagccgcgaacaagtagcagagacatgcatctatctggaagaatcgaca 360  
QY 453 aagaatccaagaataaagaaacaagatccaagaatcatggtctcatgattttccaagt 512  
Db 361 aagatccaagaataaagaaacaagatccaagaatcatggtctcatgattttccaagt 420  
QY 513 tcaacaacagatatttgaaggttaagaacaatatggttggaagtgatgataaaggaaa 572  
Db 421 tcaacaacagatatttgaaggttaagaacaatatggttggaagtgatgataaaggaaa 480  
QY 573 caagtgttagaagaactctgactagaagactactctgggaacccaagatcccgattgtc 632  
Db 481 caagtgttagaagaactctgactagaagactactctgggaacccaagatcccgattgtc 540  
QY 633 gggaatggagagcataggtaaaacaaccttagcaaaagaagttaacaatgataatcaat 692  
Db 541 gggaatggagagcataggtaaaacaaccttagcaaaagaagttaacaatgataatcaat 600  
QY 693 ctatgcccgttttgatgtctcatgctgctgggtctaccatctcaacagcaacaanaaggaa 752  
Db 601 ctatgcccgttttgatgtctcatgctgctgggtctaccatctcaacagcaacaanaaggaa 660  
QY 753 atttgttgccctctgcacatccaacatgaatgatacagaggttaagatattggt 812  
Db 661 atttgttgccctctgcacatccaacatgaatgatacagaggttaagatattggt 720  
QY 813 gaagcagagcatagcagacatggttaacagaagaagtttaagagaagagttactaatgttc 872  
Db 721 gaagcagagcatagcagacatggttaacagaagaagtttaagagaagagttactaatgttc 780  
QY 873 ttggaatgatactcggaaatttgaaagtgtggagtggtgagacgaatgcttccaactgaa 932  
Db 781 ttggaatgatactcggaaatttgaaagtgtggagtggtgagacgaatgcttccaactgaa 840  
QY 933 gacaatcagaagagtcgaatactgttgacacccgtaagtatgaagtagctgttaagct 992  
Db 841 gacaatcagaagagtcgaatactgttgacacccgtaagtatgaagtagctgtgttaagct 900  
QY 993 ggtgttagagaattttcttgcgagatgagcttcatgatacaagaatggagttgagcttc 1052  
Db 901 ggtgttagagaattttcttgcgagatgagcttcatgatacaagaatggagttgagcttc 960  
QY 1053 ttcaaaaggtcacgatttttaagaatgaagcatttaccataatgattcgcgagactgttggaaag 1112  
Db 961 ttcaaaaggtcacgatttttaagaatgaagcatttaccataatgattcgcgagactgttggaaag 1020  
QY 1113 caaatcgagatgaatgttcaacgggttlaaccaactactatgtcgtgtgttcgagggctctc 1172  
Db 1021 caaatcgagatgaatgttcaacgggttlaaccaactactatgtcgtgtgttcgagggctctc 1080  
QY 1173 aaatctaaaaggacaataagaagatttgaaaacgtgtgtctaaagaatgtccaagtcatcgtc 1232  
Db 1081 aaatctaaaaggacaataagaagatttgaaaacgtgtgtctaaagaatgtccaagtcatcgtc 1140  
QY 1233 acaaatgatctcgtatgaacatgttcaacgtgtcgtctgtggttttcgatacacttgaca 1292  
Db 1141 acaaatgatctcgtatgaacatgttcaacgtgtcgtctgtggttttcgatacacttgaca 1200  
QY 1293 agcgatctaaaacaatgcttctgcacatcttcgaaattttccagaagaacagtgatatcca 1352  
Db 1201 agcgatctaaaacaatgcttctgcacatcttcgaaattttccagaagaacagtgatatcca 1260  
QY 1353 gttgaagaatttgatgatacattgagtgctcgaggggttccctgaaattggaanaatgatttg 1412

Db 1261 gttgaagaatttgatgatacattgagtgctgaggggttccctgaaattggaatgatttg 1320  
QY 1413 gaaggaaggtttggaagaattgtttgaaagacttgcgtatagatgtctatgctctgcacg 1472  
Db 1321 gaaggaaggtttggaagaattgtttgaaagacttgcgtatagatgtctatgctctgcacg 1380  
QY 1473 aagaagaatcgagatggaacaanaattagatcatatgaatgaatgattcatgataatagac 1532  
Db 1381 aagaagaatcgagatggaacaanaattagatcatatgaatgaatgattcatgataatagac 1440  
QY 1533 ctgtgcgtgagaagaagttcaaaaggagagacaattttatcatcagaagaacatgttcttac 1592  
Db 1441 ctgtgcgtgagaagaagttcaaaaggagagacaattttatcatcagaagaacatgttcttac 1500  
QY 1593 gttacataccagaatgttcatatctctgtatgtataaataatgcagcccttaagcggtg 1652  
Db 1501 gttacataccagaatgttcatatctctgtatgtataaataatgcagcccttaagcggtg 1560  
QY 1653 actgtgtgataaatttaatttgcctatgtcttactgttlaagggctctcttaacccctgta 1712  
Db 1561 actgtgtgataaatttaatttgcctatgtcttactgttlaagggctctcttaacccctgta 1620  
QY 1713 aatgcacgttgagaagatcagatgacaacaacaactctttgaaacgaaccatctgttttc 1772  
Db 1621 aatgcacgttgagaagatcagatgacaacaacaactctttgaaacgaaccatctgttttc 1680  
QY 1773 tctttatcttggacatttatattatgttctcaaatcaagaggtgttcatattcaata 1832  
Db 1681 tctttatcttggacatttatattatgttctcaaatcaagaggtgttcatattcaata 1740  
QY 1833 ctcaaaagctctggagctgagacacagacagattgattgttccctcgagagataaagc 1892  
Db 1741 ctcaaaagctctggagctgagacacagacagattgattgttccctcgagagataaagc 1800  
QY 1893 ctcatctggttgagagtaactcatgtgttcacgataaggaaatttcogatytaacctccagaa 1952  
Db 1801 ctcatctggttgagagtaactcatgtgttcacgataaggaaatttcogatytaacctccagaa 1860  
QY 1953 attgcaggttatggaatctgcagaacattcatgttccaacggtttcgaatcagataata 2012  
Db 1861 attgcaggttatggaatctgcagaacattcatgttccaacggtttcgaatcagataata 1920  
QY 2013 attttctgaggaattttggaactaagtcaattgaagcatttcaactcccaagatt 2072  
Db 1921 attttctgaggaattttggaactaagtcaattgaagcatttcaactcccaagatt 1980  
QY 2073 taattgcagaatgtcccaagtgtgaltcgttgacaagaaggagcaacttggattttccaac 2132  
Db 1981 taattgcagaatgtcccaagtgtgaltcgttgacaagaaggagcaacttggattttccaac 2040  
QY 2133 ttacaacattttcttactgtctccacagttgttgcacgaaggaggttatattgggaatt 2192  
Db 2041 ttacaacattttcttactgtctccacagttgttgcacgaaggaggttatattgggaatt 2100  
QY 2193 cagaatgttcaaaaataattaggaatcagtggaataaagatgactataaagtttccggagc 2252  
Db 2101 cagaatgttcaaaaataattaggaatcagtggaataaagatgactataaagtttccggagc 2160  
QY 2253 tcttggtctcccaacaactctgtctatctgcaggaacttgaataatgagcttatattct 2312  
Db 2161 tcttggtctcccaacaactctgtctatctgcaggaacttgaataatgagcttatattct 2220  
QY 2313 gttgattatagccctttgcccagtgataatttcaagtccaagaagcttttccaagaagctc 2372  
Db 2221 gttgattatagccctttgcccagtgataatttcaagtccaagaagcttttccaagaagctc 2280  
QY 2373 aagaagttgaagttggaagaactatctaaagctgtgtcatcacttgcagatcatatagctgag 2432  
Db 2281 aagaagttgaagttggaagaactatctaaagctgtgtcatcacttgcagatcatatagctgag 2340  
QY 2433 ttgcttaaccttgaggtgtcgtaagcttgatgatatgacgttgttgttgtaagaatggcat 2492  
Db 2341 ttgcttaaccttgaggtgtcgtaagcttgatgatatgacgttgttgttgtaagaatggcat 2400







```

; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,327
; FILING DATE: July 11, 1996
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/310,912
; FILING DATE: September 22, 1994
; CLASSIFICATION: 800
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 5151-45038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10968 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-680-327-2

```

```

Query Match      5.5%; Score 170; DB 2; Length 10968;
Best Local Similarity 50.6%; Pred. No. 5.2e-38;
Matches 547; Conservative 0; Mismatches 515; Indels 18; Gaps 5;

```

```

QY 508 caagttcaacaacagatatttgaaaggttaagacaatatggttgagctgagatcaca 567
   || || || || || || || || || || || || || || || || || || || || ||
DB 7120 CATCTTTTACAGTCTTACTCAAGAGCAAGCAAAATGCGAGGTTTTCAGATACAA 7179
QY 568 gaaacagttgttaagaagatctgactagaagctactctgaggaaacacagatccga 627
   || || || || || || || || || || || || || || || || || || || || ||
DB 7180 TGATGAATTAAGAGATTAAGTACTTGAGAGATCACTT--GAGCTTGATGTCATGCA 7236
QY 628 ttgtggagtgaggagcatagtaaaacaccttagcaaaagaagtttcaatgatgaat 687
   || || || || || || || || || || || || || || || || || || || || ||
DB 7237 TCGTGGCAGTCCAGGATGGGCAAGACTTACCTACCAAGAAAGATTTCATTAATGAC 7296
QY 688 caatctatgacgttttgatgttcatgctgagctgagctacatctcaacgacacaacaa 747
   || || || || || || || || || || || || || || || || || || || || ||
DB 7297 AAGTACCTCTGCTTCGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 7356
QY 748 aggaatcttgctgggacctctgcatctcaacaatcaaatgagtgacaggttaagaaga 807
   || || || || || || || || || || || || || || || || || || || || ||
DB 7357 GAGAGTGTGCTCCACCATTTGAAATGATGTCCTTGAGCCTTCTGATGCCAATGA 7415
QY 808 ttgggaaacagagcttaagacacatgttacagaaagtttaagaaagaaagtaactaa 867
   || || || || || || || || || || || || || || || || || || || || ||
DB 7416 --GAAGATGCTAATAGTGTGATGATGATGATGATGATGATGATGATGATGATG 7473
QY 868 ttgtcttgatgatatctggaagttgtaagttggaagtcgctgagacagatcttccaa 927
   || || || || || || || || || || || || || || || || || || || || ||
DB 7474 TTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7530
QY 928 ctgaagacacatgcaagggatggaatactgctgactacccgttaataatgagtaagctgtt 987
   || || || || || || || || || || || || || || || || || || || || ||
DB 7531 GTGATGTTTCAATAGGAGATGAATATTCCTTAACAACCCGCTTGATGATGTCGCG 7590
QY 988 atgcgtgtgtagagaattttcttgcgagatgagcttcaatgataagttgaggttga 1047
   || || || || || || || || || || || || || || || || || || || || ||
DB 7591 ATGTCAATATGTAAAGTGTATCCCATCATCTTCTGTTATTCAGAGATGACGAGATG 7650
QY 1048 gtctttcaaaaagtgacatcttcaagtgaaagcatlaccataatgagttcgagactgtt 1107
   || || || || || || || || || || || || || || || || || || || || ||
DB 7651 CATTAATTCAGAAAGAGTCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7710

```

```

QY 1108 gaaagcaatcgcagatgaaatgtaacaggttacaactaatatgtctgtgtgcaagac 1167
   || || || || || || || || || || || || || || || || || || || || ||
DB 7711 GATTGAAATATCAAAAAGTTGTAGAGGTTGGCTCTCCAGTTGTGTAGTACGCTG 7770
QY 1168 ttctcaatctaaagagacataagagatgtgaaactgtgtctaagatgtcaagtcac 1227
   || || || || || || || || || || || || || || || || || || || || ||
DB 7771 TTCTGAAACGAAAAGMAMACACTAGATTCAAGGAAAGTAGAACAAGTCTAAGTT 7830
QY 1228 tctgcacaatgtatccgtatgacagatgttcaagtgctgtgtgtgagatgacacac 1287
   || || || || || || || || || || || || || || || || || || || || ||
DB 7831 CCCAGAGAGATTGGCAGCTTGAAAGAGACGATATCTAATTTGATTTCAAGTTACAG 7890
QY 1288 tgaacagcagatctcaaaaacatgtcttctgcatctgaaatttccagaagacagata 1347
   || || || || || || || || || || || || || || || || || || || || ||
DB 7891 TACCACATATCTTAAGCCCTGTTTCTCTATTTTGGAGAGATTTTGGACGAAAGATA 7950
QY 1348 ttccagtgaaagatcttgatgatacatgagctgaggggttcct-----gaagttg 1401
   || || || || || || || || || || || || || || || || || || || || ||
DB 7951 TTCTATGCTCAAAAAGTACCAAGTTGTGGGTACTGTAAGGCTTTGTAACAACAAC 8010
QY 1402 aaatgatcttgagagagaggttgagagaggttgcagaagcttgcagatagatctag 1461
   || || || || || || || || || || || || || || || || || || || || ||
DB 8011 AAAAAGCACAAGAGATACCGCACAAAGTTCTTGGACGATCTTAATTTGTAAGATG 8070
QY 1462 tctctgcagcaagagagatcgagatgtaacaaatagatcatgtlaagttcatgacac 1521
   || || || || || || || || || || || || || || || || || || || || ||
DB 8071 TGATGGCCATGAGAGAGAGACCTAAT--ACCAAGTGAAAGCTGCCGATTCATGAT 8127
QY 1522 taatataagcctgtctgtgagagagagttcaaaagagagaacatttatcatgaagaca 1581
   || || || || || || || || || || || || || || || || || || || || ||
DB 8128 TGTTGATTAATTTCTCATGAGAAAGCCAAACAGAGAGATTTCTTCCAAATCAATA 8187

```

```

US-09-228-246-1

```

```

Query Match      5.5%; Score 170; DB 4; Length 10968;
Best Local Similarity 50.6%; Pred. No. 5.2e-38;
Matches 547; Conservative 0; Mismatches 515; Indels 18; Gaps 5;

```

```

QY 508 caagttcaacaacagatatttgaaaggttaagacaatatggttgagctgagatcaca 567
   || || || || || || || || || || || || || || || || || || || || ||
DB 7120 catcttttcaagctatactcaaaagacaaagaaagaaatggaaggttcttcaagataca 7179

```

QY 568 ggaacagttgttagaagatcctgactagaagctactctgtgggaacccaagatcccca 627  
 Db 7180 tagatgattaaagataaactactgtgagatcact--gagcttgatgtatccca 7236  
 QY 628 ttgtcgagatgggagcatgagtaaacacacttagacaaaagaagttatcatatgaat 687  
 Db 7237 tctgtgacagccagagattggcaagactacacagcaagaagatttaccatgatccag 7236  
 QY 688 caattctatgcgctttttagatgtatcgtggtggtaccatatactcaacagcaacaaa 747  
 Db 7297 aagtcacactctcgtctgcatgtatcgtatgtatgtgtgacatccatattatccatga 7356  
 QY 748 aggaatttgcgtggcctctgcatccacaatcaaatgagacaggtttatgaatga 807  
 Db 7357 gaggattgtgtctacacatttgaatgtatgtcttgagccttcgtatgcagatgaaaa- 7415  
 QY 808 ttgtggaagcagagctagacacatgtttacagaaaagttttaagagaagagctactaa 867  
 Db 7416 --gaaagatgtgaaatagctgtagatgaagccgacttttgttgcaagaagatcttga 7473  
 QY 868 ttgtcttgatgatalatcctgagatgtgagatgtgagatgagcgtgagacgtcttcca 927  
 Db 7474 ttccatgtatgagatgtgtgagactataagtggtgagacacatctatgtatgtgctt--ca 7530  
 QY 928 ctgaagacaatgacagagagtcgaatactgttgaactaccgttaagatgaatgaatgctt 987  
 Db 7531 gtgattgttcaaatagagtagaattatcccaaacacccgcttgatgtatgtctgcggaat 7590  
 QY 988 atgctgtgttagaagatttcttcttgagagatgagatgagatgagatgagatgagatgag 1047  
 Db 7591 atgcaaaatgtgaaagtgatcccatcctctgtcttcttcaagagatgagagagatgagatg 7650  
 QY 1048 gtcttcaaaaagtgacatcttcaagtgagatgagatgagatgagatgagatgagatgag 1107  
 Db 7651 cattatcagagaagaagatcttcaagagagagatgagatgagatgagatgagatgagatgag 7710  
 QY 1108 gaaagacaatgacagatgagatgagatgagatgagatgagatgagatgagatgagatgag 1167  
 Db 7711 gatttgaatatacaaaaagtgatgagatgagatgagatgagatgagatgagatgagatgag 7770  
 QY 1168 ttccaatactaaagagacaatagagaagtgagaaagtgagaaagtgagaaagtgagaaagtg 1227  
 Db 7771 ttctgaacagagaagaagacactagatctatgaaagtgagaaagtgagaaagtgagaaagtg 7830  
 QY 1228 tgcgtacaagaatgacatctgtagacagatgttcaagtgatgtgtgtgtgtgtgtgtgtgtgt 1287  
 Db 7831 cccagagagattgagcagcttgtagaagagacatataatgagatgagatgagatgagatgag 7890  
 QY 1288 tgaacagcagatctaaacacatgtctctgcatcttccgaaatttccagaagaagatgata 1347  
 Db 7891 taccaacatctttaaagctgtgttctctctatcttggagagatcttggcagagaaagata 7950  
 QY 1348 ttccaagtgagaaatttgaatgtgagatgagatgagatgagatgagatgagatgagatgag 1401  
 Db 7951 ttcatgtctcaaaaatgacacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8010  
 QY 1402 aaaaatgatttgagaagaggtttgagaagtttgcagaagcttgcagatagatgtctag 1461  
 Db 8011 aaaaagcagaagaagatataccgacacaggttcttgcagacatcttatttgtagaagtgtag 8070  
 QY 1462 tctctgcagcagaagagatgagatgagatgagatgagatgagatgagatgagatgagatgag 1521  
 Db 8071 tgaatgcagatgagagagacacta---accagaagtgaaaagcgtgcagcatctatgatt 8127  
 QY 1522 taatatagacactgt 1581  
 Db 8128 tgtgtcaataattctgcagatgagaaagcacaagaagagatttcttcccaacaata 8187

RESULT 8  
 US-08-310-912A-157  
 ; Sequence 157, Application US/08310912A  
 ; Patent No. 5981730

GENERAL INFORMATION:  
 APPLICANT: Ausubel, Frederick M.  
 APPLICANT: Staskawicz, Brian J.  
 APPLICANT: Brent, Andrew F.  
 APPLICANT: Dahlbeck, Douglas  
 APPLICANT: Katagiri, Fumiaki  
 APPLICANT: Kunkel, Barbara N.  
 APPLICANT: Mindrinos, Michael N.  
 APPLICANT: Yu, Guo-Liang  
 TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
 NUMBER OF SEQUENCES: 208  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2904  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30B  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/310,912A  
 FILING DATE: September 22, 1994  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/227,360  
 FILING DATE: April 13, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lech, Karen F.  
 REGISTRATION NUMBER: 35,238  
 REFERENCE/DOCKET NUMBER: 00786/254001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 100254  
 INFORMATION FOR SEQ ID NO: 157:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5134 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 US-08-310-912A-157

Query Match 5.3%; Score 164.2; DB 2; Length 5134;  
 Best Local Similarity 50.3%; Pred. No. 1.5e-36;  
 Matches 544; Conservative 0; Mismatches 518; Indels 19; Gaps 5;

QY 508 caagttcaacaagaatatttgaagtgagaaacataatggttgagcgtgatacaaa 567  
 Db 1196 CATCTTTTACCTTATCTCAAGAGCAAGAGAGAAATGAGGTTTTCAGATACAA 1255  
 QY 568 ggaacagttgttagaagatcctgactagaagctactctgtgggaacccaagatcccca 627  
 Db 1256 TAGATGAATTAAGATTAAGTACTGTGAGGATCACT--GAGCTTGATGTCAATCTCAA 1312  
 QY 628 ttgtcgagatgggagcatgagtaaacacacttagacaaaagaagttatcatatgaat 687  
 Db 1313 TCGTTGGCATGCGAGATGGGCAAGACACACTAGCAAAAGAGATTTCATGATCCAG 1372  
 QY 688 caattctatgcgctttttagatgtatcgtggtggtaccatatactcaacagcaacaaa 747  
 Db 1373 AAGTCACTCTGCTTCATGATGCTCATATGCTTGTGTGACTCAATATATTCATGGA 1432  
 QY 748 aggaatttgcgtggcctctgcatccacaatcaaatgagacaggtttatgaatga 807  
 Db 1433 GAGAGTGTGTGCTCAACCAATTTGAATGATGTGCTGAGCCTTCTGATCGCAATGAAGAAA- 1491











```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-07021005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3982 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 87..3860
OTHER INFORMATION: /note="Copy 2 cDNA for M1 nematode
OTHER INFORMATION: resistance gene of tomato"
US-08-947-823-4

```

```

Query Match          4.8%; Score 147.6; DB 3; Length 3982;
Best Local Similarity 49.4%; Pred. No. 6,9e-32;
Matches 511; Conservative 0; Mismatches 499; Indels 24; Gaps 4;

```

```

QY 541 acaatgtgttgacgtgatgatcaagaagaacagttgttagaagatctgactagaagct 600
DB 1642 ATTAATAATTTAGTGTGTTTGTGAGAGAGCAAACTTGATCTTAAGAAAGCTCACCAAGTG 1701
QY 601 actctgggaagcccaagatcatcccgattgctgggagtggaagcatagtgaaacaacct 660
DB 1702 GACCCGCAATTTAGATGTCATTTGCATTCACCCGGTATGCCGGGTTCAGGTAAGTAACCTT 1761
QY 661 tagcaaaagaagtttaaatgatgaatcaatctatcgcgcttgaatgttctgactgctgg 720
DB 1762 TGGCATATCAAAAGATATCAATGATTAAGTCTTCTAGACATTTTGACCTCGTCATGGT 1821
QY 721 ctaccatctcaacagcgcacaacaaagaatatttgcctggcctctgcacatccaca 780
DB 1822 GCACGGTTCATCAAGATATGACGACAGAAAGTTGTTGATACAAATTTTCAGTCAAGTTA 1881
QY 781 tcaaaatgatgacagaggttaaatgatgttggaagcagagctagacagatgttaca 840
DB 1882 GTGGCTCAAT-----TCAAAATTTGAGTGAATAATTTGATGTTGCTGATTAATTCGGA 1935
QY 841 aaagtlttaagaagaagagttacttaattgtcttggatatacttgaaagttgt 900
DB 1936 AACCACTGTTTGGAAAGAGTATCTTATGCTTAGATGATGTCGAGTACTACTACAT 1995
QY 901 gggatggcgttgagagatgtcttccacatgaaacatgacagggagtcgaataactgttga 960
DB 1996 TGGATGTAGTTGACAAAGACCTTTTC---CTGAAGCTTAAGAAAGAGTAGATGATTTTGA 2052
QY 961 ctaccgtaagtgtatgactgtttagctggtgtagaagaatttcttggcgaatga .1020
DB 2053 CAACCTGAGAAAGAGAGTGGCTTTGATGAGAAAGCTGACACTGATCTTTCAGCTTC 2112

```

```

QY 1021 gctcatgatacaagatgaggttgagctcttccaaagtgcagacttttcaagtgaag 1080
DB 2113 GATTGCTAAGACACAGATGAAGAGTGGGAACTTTAGATTAAGAGACATTTGCTATGAGA 2172
QY 1081 cattacatatagcttgcagactgttgaaagaacaatcgacagatgaatgttcaggttac 1140
DB 2173 GTTCCCTGATGAACATATGATGTCGTAAAGAAATAGCCGAAATTTGTAAAGGCTTC 2232
QY 1141 cactaatattgtcgttggttcgaggtcttccaatctaaagaacatgaagatttga 1200
DB 2233 CTTTGTCGCTGATCTATGCTATGCTGACTCATTTGCTGGAGGGAAGAAAGAGCTGT 2292
QY 1201 aaactgttctaagaatgataagtcacatctgcacaaatgatactgatacagatgttcac 1260
DB 2293 GCGTTGAAGTTTCAAGATTTTGAAGTCTTTATTTTGAACAGTGAAGTGAAGTGA 2352
QY 1261 gtgtgcttggttgagttacagatcaacttgcagaagcagactaaacatgtcttcacat 1320
DB 2353 AAGTTATAGATTAAGTTAGTACCATTTACCATCATCATCAAGCCATGCTTGTCTACT 2412
QY 1321 tcggaatttccagaagacagatgatacttcagtggaagatttgaatgataatgagtg 1380
DB 2413 TTGCACTTGGCCGAAAGACACTCTTTGACAAATCTATTTGTTTACTGTTTATTTGGCTG 2472
QY 1381 ctgaggggttccct-----gaagtltgaaatgatttgaagagaggttgcagaagtgtc 1434
DB 2473 CTGAGCATTTTGGGAAAGACGAGATGAAGGATTAAGAAAGAGTGTGTAAGCTTATA 2532
QY 1435 tgcagaagcttgcagatagatgtctagctcgtcagcaagaagaagtcgagatgagaca 1494
DB 2533 TGGATGATTTAAATTTCCAGTAGCTTGCTTAATTTGTTTCAATGAGATAGTGATATCTGA 2592
QY 1495 aaattgatactgttaaggttcagatcatatataatgaccgtgctgagagaagttcaca 1554
DB 2593 A-----TTTCCAATTCATGATCTTGTGATGATCCTTTGTTGATTAAGCAAGAA 2643
QY 1555 gggagaacatttt 1568
DB 2644 AGGAAATTTGTTT 2657

```

```

RESULT 14
US-08-930-996A-3
Sequence 3, Application US/08930996A
Patent No. 6100449
GENERAL INFORMATION:
APPLICANT: FLOHR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996

```



```

Oy 448 cgacaaagatccaagataaagsgaaacaagatccaagatcattgttcattgtttt 507
Db 1225 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1166
Oy 508 caagttcaacaagaatatttgaagttgaagacaatatgttgaacgtatgataa 567
Db 1105 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1106
Oy 568 ggaacagttgtgaagatctgactagaag 598
Db 1105 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1075

```

Search completed: September 11, 2002, 17:39:24  
Job time: 21435 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2002, 11:30:22 ; Search time 66.67 Seconds  
(without alignments)  
1507.751 Million cell updates/sec

Title: US-09-864-680-3

Perfect score: 4712  
Sequence: 1 MAHASVAMSLMRTIESLTFN.....PVDVRIINPLKESDSEER 905

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: A\_Geneseq\_032802.\*  
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4712	100.0	905	22	AA05409
2	4712	100.0	905	22	AA05409
3	1242.5	26.4	912	21	AA144818
4	1242.5	26.4	938	21	AA145004
5	1234.5	26.2	937	20	AA152152
6	1234.5	26.1	937	22	AA02143
7	1231.5	26.1	937	22	AA02145
8	1230.5	26.1	937	22	AA02148
9	1225.5	26.0	937	22	AA02144
10	1221.5	25.9	937	22	AA02146
11	1218.5	25.9	937	22	AA02149

12	1215.5	25.8	937	22	AA02147
13	980	20.8	1822	19	AA048360
14	852.5	18.1	1255	19	AA055974
15	834.5	17.7	1206	19	AA047080
16	834.5	17.7	1206	19	AA053583
17	834.5	17.7	1257	19	AA053582
18	828.5	17.6	1257	19	AA055975
19	711.5	15.1	309	22	AA02151
20	669	14.2	1266	18	AA025157
21	669	14.2	1266	21	AA007754
22	668	14.2	1240	17	AA003665
23	605.5	12.9	953	21	AA058854
24	604.5	12.8	1220	17	AA036664
25	554	11.8	901	20	AA01966
26	554	11.8	901	21	AA01926
27	553	11.7	901	19	AA080251
28	553	11.7	901	20	AA01965
29	553	11.7	901	21	AA01925
30	520	11.0	1205	21	AA049434
31	520	11.0	1251	21	AA03135
32	503.5	10.7	1969	19	AA072419
33	476	10.1	784	19	AA064151
34	451.5	9.6	1402	19	AA064150
35	447.5	9.5	1279	20	AA039634
36	439.5	9.3	1294	20	AA039633
37	428.5	9.1	917	16	AA080132
38	428.5	9.1	965	16	AA083440
39	428	9.1	342	21	AA009957
40	410.5	8.7	928	21	AA063308
41	408.5	8.7	928	21	AA063307
42	376.5	8.0	1292	20	AA039631
43	376.5	8.0	1292	20	AA039632
44	375	8.0	396	22	AA02152
45	366	7.8	1074	19	AA064186

# ALIGNMENTS

RESULT 1	AA05409	standard; Protein; 905 AA.
XX	AA05409;	
AC	24-SEP-2001	(first entry)
DT	Pepper Bst2 protein.	
XX		
DE	Bst2; pepper; resistance gene; plant pathogen; virulence gene;	
XX	bacterial spot disease; Xanthomonas campestris pv. vesicatoria;	
KW	AVRBS2; hypersensitive response; transgenic plant; tomato; tobacco;	
KW	rice; corn; wheat.	
XX		
OS	Capsicum annuum.	
XX	US6262343-B1.	
XX	17-JUL-2001.	
PD		
XX	23-JUL-1999;	99US-0360186.
PF	23-JUL-1998;	98US-0093957.
XX		
PR	23-JUL-1998;	98US-0093957.
XX		
XX	(RSCG ) UNIV CALIFORNIA.	
PA	Slaskawicz BJ, Dahlbeck D, Tai TH;	
XX		
PI	WPI: 2001-450496/48.	
XX	N-PSDB: AAD10203, AAD10204.	
DR		
XX		
XX		
PT	Nucleic acid molecules encoding Bst2 protein, useful for producing transgenic plants having resistance to the plant pathogen Xanthomonas	

Rx 193, modified r  
Tomato Prf protein  
Tomato pest resist  
Tomato MI resist  
Tomato MI resist  
Wild tomato Mi res  
Wild tomato Mi res  
Tomato pest resist  
Plant resistance p  
Tomato immunity 2  
Amino acid sequenc  
I2C-2 protein conf  
Sorghum resistance  
I2C-1 protein conf  
A protein giving a  
Rice probenazol re  
An antidiabetic gen  
A protein giving a  
Rice probenazol re  
Blast disease-resi  
Rice blast fungus-  
Rice bacterial lea  
Lettuce resistance  
Lettuce resistance  
Zea mays Rpg1-13 p  
Zea mays Rpg1-2 pr  
Rps2 disease resist  
A.thaliana RPS2 po  
Rice disease resist  
Protein encoded by  
Zea mays Rpg1-D pro  
Zea mays Rpg1-D pro  
Plant resistance p  
Lettuce resistance

PR campestris -  
 XX  
 PS Claim 1; Column 55-60; 37pp; English.  
 XX  
 CC The present sequence is Bs2 protein from pepper. The Bs2 gene is shown  
 CC to confer resistance to plant pathogen Xanthomonas campestris pv. vesicatoria which causes bacterial spot  
 CC disease. The Bs2 protein has Bs2 biological activity, i.e., when  
 CC co-expressed in a plant with a X. campestris AvrBs2 gene product,  
 CC it produces a localised hypersensitive response. The protein  
 CC includes a nucleotide binding motif and leucine rich repeats of the  
 CC type found in other plant resistance genes. The Bs2 nucleic acid  
 CC molecule is useful for producing transgenic plants such as pepper,  
 CC tomato, tobacco, broccoli, cauliflower, cabbage, cowpea, canola,  
 CC bean, soybean, rice, corn, wheat, barley, citrus, cotton, cassava and  
 CC walnut, that are resistant to plant pathogen Xanthomonas campestris.  
 CC The transgenic plants produced using Bs2 molecule develop a  
 CC hypersensitive response to the pathogen at the site of inoculation and  
 CC show an enhanced resistance to systemic infection. The Bs2 nucleic acid  
 CC molecule is also useful as polymerase chain reaction (PCR) primers for  
 CC amplifying portions of Bs2 nucleic acid molecule, as sequencing primers  
 CC to verify the authenticity of an amplified molecule, and as  
 CC hybridisation probes.  
 CC  
 XX  
 SQ Sequence 905 AA;  
 Query Match 100.0%; Score 4712; DB 22; Length 905;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 905; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAHASVASLMTTISLTSPKMSLSCDREELCALREKVSLEVFKNFKNVGEEM 60  
 DB 1 mahasvaslmttleslittfospmslscdhreelcalreksvlefknteknnvfem 60  
 QY 61 TDFEVEVREVASAEYITQLRLTGVYGENKSQKKARRRROSLQOYAEEMHIKWE 120  
 DB 61 tdfvevrevasaeyitqlrltgvgenksqkkarrirrgslqyaeemdhikwest 120  
 QY 121 KIDKGVKSVESLVHDFSSSTNDILKKNMNGRDOOROKLBDLFRSYSGEPKVPY 180  
 DB 121 kidkgvkvskeslvhdfssstndilvknmngvrdqgirkqldlfrsysgepkvpilv 180  
 QY 121 kidkgvkvskeslvhdfssstndilvknmngvrdqgirkqldlfrsysgepkvpilv 180  
 QY 181 GMSGIGTTLAKVEYNDESILCRPDVHAMATISQHNKKEILLGLHSTIKMDRVKMG 240  
 DB 181 gmsgigtltlakevyndesilcrfdvhamatisgqhnkkellglhstikmdrdvkmig 240  
 QY 241 EAEIADMLQSLKRRRLIYLDIWSCEWMDGVRRCPTEDNAGSRILLTTRNDVACYA 300  
 DB 241 eaeladmlqslkrrrliylldiwscewmdgvrircptednagsrillttrndevacya 300  
 QY 301 GVENFSLRMPFMDDESMSLFKSAFSSSEALPYEFETVGOIADEGHPLTIYVAVGL 360  
 DB 301 gvenfslrmpfmddesmslfksafsssealpyefetvgyqiadechnglptliyavagl 360  
 QY 361 KSKRTIEDMTKAVAKVSVYTNDEPDERCSRVLGSLYDHLTSDLTKLHLHFIPEDSDIP 420  
 DB 361 kskrtiedmtkavakvsvytndepdercsrvlgslsydhlsdtklhlhgfipedsdip 420  
 QY 421 VKNIMRSMWABGFLKLENDLEGVEKCLQELVRCILVYKRSRDKRKINSKVDLITD 480  
 DB 421 vknimrsmwabgflkclendlegveklqelvrcilvlykrsrdgkrlkrsckvhdliyd 480  
 QY 481 LCYREVORENFIINDIVLVSVPECSYLCMYKQOPKRYTSGDEINCPGIVRALLTPV 540  
 DB 481 lcveyoreneifimndivlvsvpecsyldcmymkpikrtyvgdeinpcpylrvalltpv 540  
 QY 541 NRQLRHDNNNLKRTSHVSEFHEPLLYLVKSEVHFLLKLVLELHROIDGPREILS 600  
 DB 541 nrqlrdhnnnlkrtshvsefhepllylvksevhfllkvllelhrqidgpreils 600  
 QY 601 LILWRYTSLFSGNFVPPETICRMNIQTITVORFNSDIIIFAEIWEMLQRLHKLPRF 660  
 DB 601 lilwrytslfsgnfvppeticrmniqtitvorfnsdiiifaeiweumlqrlhklprf 660

DB 601 liwrytstfsgynfdvppeticrlnlqtflvgrfrsdiilfaeiwelmqlrlhklprf 660  
 QY 661 YLPDPSGVKGRHLDNSNLQTTISYLSPPRCTKEVINGIQNVKKIGISGNDDVKSPRD 720  
 DB 661 ylpdpsgvkgrhldnsnlqttisylspprectkevinqnvkkigisgnddvksfrd 720  
 QY 721 SGLPNNLVYLOQLLETLSISVDYSELPIYISSAKAFPATLKKLIERLYLSMSYDIIAE 780  
 DB 721 sglpnnlvylqllletlsisvdsylpviysakafpatlkkliertylsywydiiae 780  
 QY 781 LPNLEVLKMDACCGEEMHPIVWGFNRKLKLLIYRSLFKRWKAKANDPVLIERMTSC 840  
 DB 781 lpnlevlkmddaccgeemhpiwngfinrlklllyksfltkwkatndhfpvlerimrsc 840  
 QY 841 KNLKEIPREFADHITLQLEIRECPKLGESAARIQKOEIDGNPVRISNPLKESDS 900  
 DB 841 knlkeiprefadhitlqlleirecpkrgesaariqkeedlgnpvdvrisnplkesds 900  
 QY 901 DSEEH 905  
 DB 901 dseeh 905  
 QY 901 dseeh 905  
 DB 901 dseeh 905  
 RESULT 2  
 AAB72198  
 ID AAB72198 standard; Protein: 905 AA.  
 XX  
 AC AAB72198;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Pepper Bs2 amino acid sequence.  
 XX  
 KW Bs2; pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;  
 KW xcv; bacterial spot disease; transgenic plant; crop: fruit; flower.  
 OS Capsicum annuum.  
 XX  
 PN WC200107635-A1.  
 XX  
 PD 01-FEB-2001.  
 XX  
 PF 23-DEC-1999; 99WC-US30891.  
 XX  
 PR 23-JUL-1999; 99US-0360186.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Staskawicz BJ, Dahlbeck D, Tai TH;  
 XX  
 DR WPI: 2001-168560/17.  
 DR N-PsDB; AAF63301, AAF63302, AAF63303.  
 XX  
 PT Novel Bs2 polypeptide from Capsicum annuum for producing transgenic  
 PT plants having resistance to bacterial spot disease caused by  
 PS Xanthomonas campestris pv vesicatoria (Xcv) -  
 XX  
 PS Claim 1; Page 61-64; 72pp; English.  
 XX  
 CC This invention relates to the amino acid sequence of the Bs2 protein  
 CC isolated from Capsicum annuum (pepper). The protein and DNA sequences of  
 CC Bs2 can be used to confer resistance to the plant pathogen Xanthomonas  
 CC campestris pv vesicatoria (Xcv) which causes bacterial spot disease. Bs2  
 CC DNA and protein sequences are useful for producing transgenic plants such  
 CC as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola,  
 CC cowpea, grape, bean, soybean, rice, corn, wheat, barley, citrus, cotton,  
 CC cassava and walnut, having resistance to X. campestris. The protein and  
 CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
 CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
 CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
 CC carnations and roses having resistance to X. campestris. The present  
 CC sequence represents the Bs2 protein of the invention.

SQ Sequence 905 AA:  
 Query Match 100.0%; Score 4712; DB 22; Length 905;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 905; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHASVASIMRTIESILTFNSPMQSLSCDHREELCALREKVSLEVPVKNFEKNVFGEM 60  
 DB 1 mahavasimrtiesilftfnspmqslscdhreelcalrekvaslevfvknfeknvfgem 60  
 QY 61 TDFEVEVREVASAEYTIQRLTGTVLGENKSOKKARREFRQSIQOVAEDMDHIMKEST 120  
 DB 61 tdfvevrevasaeytiqlrtlgtylgenksokkarrefrqsiqovaedmdhmwkest 120  
 QY 121 KIODKGQVSKESLWDESSSTNDILKVNKNVGRDDQKROLLEDLTRSYSGEPKVIPIV 180  
 DB 121 kiodkgqvskeslwdeessstndilkvnnvgrddqkrolledltrsygsgepkvipiv 180  
 QY 181 GNGIGKTTTLAKEVYNDESLICRPDYHAMATISQHNKKEILLGLHSTIKMDRKYKMG 240  
 DB 181 gngigktttlakevyndeslicrpdvhamatisqhnkkekllglhstikmdrkykmg 240  
 QY 241 EELADMLQKSLRRKRYLLVDIWSCEVWDVRRCPFEDNAGSRILLTTRNDEVACYA 300  
 DB 241 eeladmlqkslrrkryllvdiwscevwdrvrrcpfednagsrillttrndevacya 300  
 QY 301 GVENFSLRMSFMDQESMSLFRSAFSEALPYEEFTVGKQIADCHGLPLTIVVAGLL 360  
 DB 301 gvenfslrmsfmdqesmslfrsaafsealpyeefvvgkqiadchglpltivvagll 360  
 QY 361 KSKRTIEMKRYAKOVKSVTNDPDERCSRVLGLSYDHTLSOLKCLLHGJFPEPSDIP 420  
 DB 361 kskrtiemkryakovksvtndpdercsrvlglsydhtlsolkcllhgjfpesdip 420  
 QY 421 VKNLMRSMAEGFLKLENDLEGEVEKLOELVDRCLVLSKRSRDGKTIRSCVHDLIAD 480  
 DB 421 vknlmrsmaegflklenlelegeveklolvdrcvlvlskrsrdgktirscvhdliad 480  
 QY 481 LCVREVQRENITFMDVIDVSTPECCSYLCMKRMOPFKRYTGDEINVCYGLRALLTPY 540  
 DB 481 lcvrevorenitfmdvidvstpeccsyldcmkrmopfkrytgdeinvcyglralltpy 540  
 QY 541 NQOLRPHDNNILKRFHSVSEFPLEYVYLKSEVYHFKLKVLELRHQIDGFPREIIS 600  
 DB 541 nqolrphdnnilkrfhsvsefpleyylksevyhfkllvlelrhqidgfpreiis 600  
 QY 601 LILWRLSLFSYGNFDPVEICRLMNLQFTIVORFRSDIIFAEELIWEIMQLRHLKLPF 660  
 DB 601 lilwrlslfsygnfdpveicrlmnlqftivorfdsdiiifaeelwelmqlrhlklprf 660  
 QY 661 YLPDCSSGVYDKGRHDFNSLQRTISLSPCCCKEYIMQONWKIISGNKRDYSFRD 720  
 DB 661 ylpdcssgvdydkgrhdfnslqrtisylspccckeuyimqonwkiiisgnkrdysfrd 720  
 QY 721 SGPPNNLVYLOQLEITLSLVDVSLPVIISAKAPATLKLKLETTYLSMSYLIITAE 780  
 DB 721 sgppnnlvylqlelitslsvdyslplviisakapatlklklertylswyliitiae 780  
 QY 781 LPMLEVLKIMDDACGGEEMHPIVMGFNRLKLLIKYSFLKEWKATNDNPFVLERLMIRSC 840  
 DB 781 lpmlevlkimddacggeemhpivmgfnrlkllikysflkfwkatndnfpvlerlmirsc 840  
 QY 841 KNLKEPIREFADITHIQTILRECPKLGESARIOKEODLNNPDVINSPLKSSDS 900  
 DB 841 knlkepiorefadithiqlirecpklgesaariqkegedlgnpvdvinsplksds 900  
 QY 901 DSEEH 905  
 DB 901 dseeh 905

RESULT 3

AAY44818  
 ID AAY44818 standard: Protein; 912 AA.  
 AC AAY44818;  
 DT 18-MAY-2000 (first entry)  
 DE Potato Gpa2 resistance protein.  
 KW Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p;  
 marker; IPW4c; 11R; Potato Cyst Nematode; PCN; Globodera; nematode;  
 nucleotide binding site; NBS; nematode resistance; detection; diagnosis.  
 OS Solanum tuberosum.  
 FH Key Location/Qualifiers  
 FT Binding-site 172..178  
 FT /label="P-loop-motif  
 FT /note="Conserved motif within the Nucleotide Binding  
 FT Site (NBS)"  
 FT Binding-site 329..334  
 FT /note="Conserved motif within the Nucleotide Binding  
 FT Site (NBS)"  
 PN WO200006754-A2.  
 PD 10-FEB-2000.  
 PF 30-JUL-1999; 99WO-NL00491.  
 PR 31-JUL-1998; 98WO-NL00445.  
 PA (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.  
 PA (UYNA-) LANDBOUWUNIVERSITEIT WAGENINGEN.  
 PI Van Der Vossen EAG, Van Der Voort JNAMR, Lankhorst RMK, Bakker J;  
 PI Stiekema WJ;  
 DR MPI: 2000-183132/16.  
 DR N-PSDB; AA50262; AA50264.  
 PT New isolated Gpa2 nematode resistance gene from potato, useful for  
 PT producing plants which are resistant to nematodes and polypeptides for  
 PT use in nematocidal compositions  
 PS Claim 54; Fig 3a; 96pp; English.  
 CC The present amino acid sequence is the potato resistance protein Gpa2,  
 CC that confers resistance to infection by phytopathogenic nematode of the  
 CC Globodera genus. It has two conserved motifs within the nucleotide  
 CC binding site (NBS). The gene is mapped to the short arm of chromosome  
 CC 12 (12p), between the markers IPW4c and 11R. This locus is associated  
 CC with resistance to potato Cyst Nematodes (PCN) like G. pallida and  
 CC G. rostochiensis, that invade and damage the roots of Solanaceae. It has  
 CC nematocidal activity. A recombinant DNA sequence comprising the Gpa2 gene  
 CC sequence can be transformed or transfected into plants, to provide  
 CC increased resistance to nematodes. The polypeptides can also be used in  
 CC nematocidal compositions and for detection and diagnosis of nematode  
 CC infections.  
 SQ Sequence 912 AA:  
 Query Match 26.4%; Score 1242.5; DB 21; Length 912;  
 Best Local Similarity 35.1%; Pred. No. 1,6e-39;  
 Matches 340; Conservative 146; Mismatches 333; Indels 149; Gaps 29;

QY 1 MAHASVASIMRTIESILTFNSPMQSLSCDHREELCALREKVSLEVPVKNFEKNVNFGE 59  
 DB 1 mahavasimrtiesilftfnspmqslscdhreelcalrekvaslevfvknfeknvnfge 59  
 DB 1 mayasvslmrtl-----hqmeltgdc---lqpfyeklkslrall---ekscnimgd 47  
 QY 60 ---MTDFEVEVREVASAEYTIQRLTGTVLGENKSOKKARREFRQSIQOVAEDMDHIM 116  
 DB 60 ---MTDFEVEVREVASAEYTIQRLTGTVLGENKSOKKARREFRQSIQOVAEDMDHIM 116

```

Db      48 hegltllelevelleaytledmvsdesrnvlarnvgkrsramwgiffvlegalecldstcv 107
Qy      117 KESTKIODKGOVSKKE--SLVHDFSSSTNDILKVKNNMNGRDQROKQLEDLTRSYSGEP 174
      108 kymatsdsmkdikpqtsslv---slpendveqpenlmvgrenefemmdqldarg-grel 163
Qy      175 KVIPIVGMGIGKTTTLAKEVYNDESILCRPDVAMATISQOHKKEILGLHSTIKMD 234
      164 evsivgmgiqkltlaaklysdpylmrfdirakatsvgeqvcvrnvljgllsitsdepd 223
Qy      235 RKAMTEALADMLOKSLRKRYLYLDIMSCVWDVGRCPFTEDNAGSRILLTTRND 294
      224 -----ygladqlqkhlqgryl-vvldiwtteaaddiklcfpdcn-gsrilllttrnv 275
Qy      295 EVACVAGVNFSLRMSEFMODESMSLFKSAFSS--ALHYEPFTVVKOTADECHGLPLT 353
      276 evaeayassgkpphhmrlnmfdeswnllhkkifeegsyspelenjgkqalckgplp1a1 335
Qy      354 VVAVGLL-KSKRTIEDMKTVAADVKSFTVNDPDERCSRYLGLSYDHLTKTCLLHFGI 412
      336 tliagllskstkltdewgvaenrvsvsldleakcmrta1alsyhlphlpcfllyfa1 395
Qy      413 FPEDDSDIPYKNNMRSMAGFLKE--NDLEGEVEKCLQELVDRCIVLVSKRSRDTKTR 470
      396 faederylnkllvelwavegflneeegksleevaeclnelvdrlslshnvsfdg-etq 454
Qy      471 SKVHDLIYDLCVREVORENIFIMNDIYLDVSYPEC--SYLCMYKMKOPKRTGDEINC 528
      455 tcmgmhvtrelclrear-nmfvnlygksdqscagmgcsfksr----- 499
Qy      529 PYGLRYALLTPVNRQLRDHNNNL---KRTSHVSFSLPELRYLVKSEVHFLLKYL 584
      500 -----srslshneelwvcrnseahsiftlci---fkvcylstflvrv1 542
Qy      585 ELRHQIDGFPREITSLIMRLRYSL-----FSYGNFDPPELCRLMNQOT 629
      543 dglgtcplfbsgvslshlitylstrfnprrlqgyrsgkaavpslidlplslslslyqt 602
Qy      630 F-IVGRFRSDI-TIFAEIWEIMQLRHLKLPFYLPDCPSGSVDKGRHIDFSGNLQTSYL 687
      603 klylprfncypflipseilmpqlrklomgwnyl---rshpeptenr-lvlsiqclnel 658
Qy      688 SPROCTKEVINGIQVKKVLGSGNKDYSKPRDSGLPNNLYVLOOLETISLISVDS--- 744
      659 nprctgslflrlfplkkllevfyvkedfrnkd1---ydfrylyglekla-fstyssasa 714
Qy      745 -----LLPVIISAKAPATLKK 762
      715 cflkntaplgstqdpqlrfgmethlehsratatpplvtvfl1p---pdcifpqn1ks 770
Qy      763 LKLERT-YLSWSYLDIAELPNEVLKIMDACCGEEMHPIVMGFNRLLKLLIKYSFLKF 821
      771 ltfsgdflfawkdlisvqk1pkllevlqshnafkgeewevveegfphlkf1f1dslytry 830
Qy      822 WKANDNPFVLEIRLMISCKMLKEPIEFADITHLQLELRECPKLGESAR1OKEDD 881
      831 wraasdhfpylerlflsdofyldspfdadlttalidlfrcqsgynsak1qgd1qd 890
Qy      882 LGNNPVDV 889
      891 nysgsiev 898
Db

```

RESULT 4  
AAV45004  
ID AAV45004 standard; Protein; 938 AA.  
XX  
AC AAV45004;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Protein encoded by potato Gpa2 resistance gene.  
XX

```

KW      Resistance: Gpa2; potato; phytopathogenic nematode; chromosome 12p;
KW      marker; IPW4c; 11LR; Potato Cyst Nematode; PCN; Globodera; nematode;
KW      nematode resistance; Nucleotide Binding Site; NBS; detection; diagnosis;
KW      transgenic plant.
OS      Solanum tuberosum.
FH      Key
FT      Binding-site      Location/Qualifiers
FT      172..178
FT      /label= "P-loop_motif
FT      /note= "Conserved motif within the Nucleotide Binding
FT      Site (NBS). This region is specifically claimed"
FT      329..334
FT      /note= "Conserved motif within the Nucleotide Binding
FT      Site (NBS). This region is specifically claimed"
PN      WO200006753-A1.
PD      10-FEB-2000.
PR      31-JUL-1998; 98MO-NL00445.
PR      31-JUL-1998; 98WO-NL00445.
PR      31-JUL-1998; 98WO-NL00445.
PA      (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.
PA      (UYMA-) LANDBOUMUNIVERSITEIT WAGENINGEN.
PI      Van Der Vossen EAG, Van Der Voort JNAMR, Lankhorst RMK, Bakker J;
PI      Stiekema WJ;
DR      WPI: 2000-195310/17.
DR      N-PSDB: AA250652, AA250653.
PT      Recombinant Gpa2 polynucleotide from potato, Solanum tuberosum, useful
PT      to confer resistance to phytopathic nematodes of the genus Globodera in
PT      transgenic plants, e.g. resistance to potato cyst nematodes in potatoes
PT      .
PS      Claim 2: Page 50-54; 96pp; English.
XX      The present sequence is that of Gpa2 protein encoded by potato Gpa2
XX      resistance gene, that confers resistance to infection by phytopathogenic
XX      nematode of the Globodera genus. Gpa2 gene is mapped to short arm of
XX      chromosome 12 (12P), between the markers IPW4c and 11LR. This locus is
XX      associated with resistance to Potato Cyst Nematodes (PCN) like G. pallida
XX      and G. rostochiensis, that invade and damage the roots of Solanaceae. It
XX      has nematocidal activity. Recombinant DNA sequence comprising the Gpa2
XX      gene can be used to produce transgenic plants with increased resistance to
XX      nematodes. The polypeptides can also be used in nematocidal compositions
XX      and for detection and diagnosis of nematode infections.
XX      Sequence 938 AA;
Qy      Query Match      26.4%; Score 1242.5; DB 21; Length 938;
Qy      Best Local Similarity 34.9%; Pred. No. 1.6e-99;
Qy      Matches 344; Conservative 147; Mismatches 341; Indels 153; Gaps 30;
Db      1 MAHASVASLMTIESLTFNSPMOSLSCDHREELCALREKVSLEVFYKNEKN-NVFE 59
      1 mayavastlmtl-----hgsmltgc---lqpfyeklkslra1l---eksclngd 47
Qy      60 --MTDFEVEVVASAEYTIQRLRGTVLGEKKSQKKRRFRFROSLQOAVADMHIW 116
      48 hegltllelevelleaytledmvsdesrnvlarnvgkrsramwgiffvlegalecldstcv 107
Qy      117 KESTKIODKGOVSKKE--SLVHDFSSSTNDILKVKNNMNGRDQROKQLEDLTRSYSGEP 174
      108 kymatsdsmkdikpqtsslv---slpendveqpenlmvgrenefemmdqldarg-grel 163
Qy      175 KVIPIVGMGIGKTTTLAKEVYNDESILCRPDVAMATISQOHKKEILGLHSTIKMD 234
      164 evsivgmgiqkltlaaklysdpylmrfdirakatsvgeqvcvrnvljgllsitsdepd 223

```



```

QY 235 RVKMGAEALADMLQSLKRRRLIYLDIDWISCEVMDGVRCPPTEDNAGSRILLTTTRND 294
DB 224 -----YGLAQGLQHLLKGRYLVLDIWLCEAWDADKLCIPDCDN--GSRILLTTRV 275
QY 295 EVACVAGVNFSLRMSFMDQESWSLFFKSAFSS--ALPYEFETVQQTADCEHGLPLTI 353
DB 276 evaeayassgkprhmrlnmfcdeswnllhkkifeegsysefenfengqialkcgjplai 335
QY 354 VVVAGLL--KSKRTIEDKTVAKDVSVYTNDDPDRCSRYLGISYDHLTSDLTCLHFGI 412
DB 336 tlaagllskrlskldewgvaenvisvstleakcmrylalsyhlphlpcfllyfa 395
QY 413 FPEDSDIPYKNLMRSMGFLKLE--NDLEGEVEKCLQELDRCLVLSKRSRDOTKIR 470
DB 396 feedetiyknklyelkavagflneeegksievaetclnelvdrslshnsvfdg-eqg 454
QY 471 SCKVHDLIYDLGVREYQRENIFIMNDIVLDSYPEC--SYLCMYKMQPFRVTDGEINYC 528
DB 455 rcmghdvtrclcrear--nmnfvnrlrgksdqscagmqsfkar----- 499
QY 529 PYGLVALLTPVNRQLRDNNNL-----KRHSVFSFHLERLYLKESEVHFLLKLY 584
DB 500 -----srslhneelwvcrnseahsiltlcl--fkcvlelsfkivryl 542
QY 585 ELRHQIDGPREIISLIMRYLSTL-----FSYGNFDPPEICRLMNLQT 629
DB 543 dglgttcplfpgsvslshlyslfnpriqgyrskavpsalidrlslslcyt 602
QY 630 F-IVORFRSDI-IIFAEELIEMQLRHLKLPREFLPDPSGVSNGRHLDFSNLQTIYVL 687
DB 603 flklyhpfncypflpselltmpqlrkclcmgwnyl--tsheptenr-lvklsgclnel 658
QY 688 SRCCCKEYIMQVKKLGISGNKDDYKSFNDSGLPNNLVYIQQEILSLISVDYS---- 744
DB 659 nprycgsflirfplnkklvfgkedfrnhkdl---ydftrylyglekla-fslysssa 714
QY 745 -----LLPVTISAKFPATLKK 762
DB 715 cflkntapjgspqdpdlrfqmetlhetsratpdtptfllp-----ppdcfipnlks 770
QY 763 LKLEERT-VLSWSYLDIAELPNLEVLKLDMDACGGEHWPVIGFNRLLKLLIKYSFLKF 821
DB 771 lftsgdfllawkdlsivgklprlevlqishnatkgeewveegfphlflfidslyty 830
QY 822 WATNDNFYVLERLMRSCKNKLKEPIERADITHTLOLIELRECPKLGESANIQEQED 861
DB 831 wrasschfylerlflsdcfyidsprdfaditlaildiftcgsvgnsakqldqld 890
QY 882 LGNNPDVRI-----SNPLKESDSDS 902
DB 891 nygssieskwsifgsvttdeddds 915

```

RESULT 5  
AAV52152  
ID AAV52152 standard; protein; 937 AA.

```

XX AAV52152;
XX 01-FEB-2000 (first entry)
XX Potato resistance X protein sequence.
XX
XX Potato; Rx gene; resistance gene; potato virus X; PVX; transgenic plant;
XX broad spectrum extreme resistance; Narcissus mosaic virus; NMV; NVX; VNV;
XX Nandina virus X; Viola mosaic virus; Cymbidium mosaic virus; CYMV; PopMV;
XX Poplar mosaic virus; White clover mosaic virus; WCLMV; activate.
XX Solanum tuberosum.
XX
XX Key Location/Qualifiers
XX Region 168..180

```

```

FT FT /note= "Kinase motif 1a"
FT Region 237..247
FT /note= "Kinase motif 2"
FT Region 265..273
FT /note= "Kinase motif 3a"
FT Region 330..342
FT /note= "R gene signature"
FT Region 386..396
FT /note= "R gene signature 2"
FT Region 458..467
FT /note= "R gene signature 3"
PN WO954490-A2.
PD 28-OCT-1999.
XX 16-APR-1999; 99WO-GB01182.
XX 16-APR-1998; 98GB-0008083.
XX (PLAN-) PLANT BIOSCIENCE LTD.
PA Bendahmane A, Baulcombe DC, Kanyuka KV;
PI WPI; 1999-63406/54.
DR N-PSDB; AAZ37153, AAZ37154.
XX
PT New isolated plant virus resistance gene, used to produce transgenic
PT plants with resistance to virus infection
XX
XX Claim 5; Fig 1; 124pp; English.
XX
CC This is the amino acid sequence encoded by the potato Rx gene. The Rx
CC gene is a resistance gene which confers extreme resistance against
CC potato virus X (PVX). Sequence AAZ37154 is the Rx coding sequence free
CC from introns, while sequence AAZ37153 includes introns. The Rx gene can
CC be used to create a recombinant vector which encodes the Rx resistance
CC polypeptide AAV52152, this vector can be used to transform plant cells
CC to produce a transgenic plant with resistance to PVX. The Rx gene can be
CC used to engineer resistance traits, preferably broad spectrum extreme
CC resistance, into plants. The Rx gene can also be activated by non-PVX
CC viruses, e.g. Narcissus mosaic virus (NMV), Nandina virus X (NVX), Viola
CC mosaic virus (VMV), Cymbidium mosaic virus (CYMV), Poplar mosaic virus
CC (PopMV) and White clover mosaic virus (WCLMV). Rx can be used to offer
CC specific protection against this group. The Rx gene sequence can be used
CC to create antibodies specific for Rx. The antibodies can be used to
CC down-regulate Rx activity and also for the detection, identification or
CC isolation of Rx or homologues.
XX
SQ Sequence 937 AA;

```

Query Match 26.2%; Score 1234.5; DB 20; Length 937;  
Best Local Similarity 35.1%; Pred. No. 8.2e-99;  
Matches 345; Conservative 144; Mismatches 343; Indels 151; Gaps 32;

```

QY 1 MAHASVASIMRTTESLTFSPMQSLSCDHRELCLAREKVSLEVFYKFNK-NVFE 59
DB 1 mayaaavtslmrtl-----ngsmeltgdc---lqpfyeklkslrall---ekscnimgd 47
QY 60 ---MTDFEVEVRVASAETIQLRLTGVLGENKSOKKARRRFRROSLQOVEDMDHIW 116
DB 48 hegltlleveivaytcdmvsesnrnflaqlneerstrameiffvlqalecldst 107
QY 117 KESTKIQDKGQVSKS--SLVHDFSSSTNDILKVKNNMGRDQROKOLFEDLTRISGEP 174
DB 108 kymatscdsmkdlkpgtsslv---slpehveqpenlmvgyrenefemuldqqlary--gre 163
QY 175 KYVPIYGMGIGKTTLAKKEYNDESLICRFDVHAMATISQOHKKETILGLSTIKMD 234
DB 164 evsvivmgigltcltlakysdpcimstrdltakavsegyevrnv19llsltsdep 223
QY 235 RVKMGAEALADMLQSLKRRRLIYLDIDWISCEVMDGVRCPPTEDNAGSRILLTTTRND 294

```



```

QY 531 GLYRALLTPVNRQLRDHNNLL-----KRTHSVF---SFHLEPLYYLVKSEVHFELKLV 583
D 491 smqstfsks--rsrirlhkvleelawcrnseahsilmjgfevltl-----elsfklyrv 541
QY 584 LELNRHROIDGFPRELLSLIMWRYSL-----FSGYNEFVPEICRLMWLQ 628
D 542 ldlglntwplfpgsvlslhlrlyslirfncplqgygskavpsalldiprlslslcylq 601
QY 629 TFIYQ-RFRSDI-TIFAEIWEMLQRLHLKLPRIYLPDPCSGSDVKGHLDPSNLQTIYSY 686
D 602 tfklnlfpfpyfllpsealltmpqlrlcmgwnyl-----rsheptent-mwlknlqclng 657
QY 687 LSPRCREVIMGIQNVKLGISGNKDDYKSFSDSGLPNNLVYLOQLTISL-----738
D 658 lmpycctgsffrllfnlkkllqfvgvpedfinsgdl---ydftrylyqleelffrlyypya 714
QY 739 -----ISVDYS-----LLPVISSAKAFPATLKKLIER 767
D 715 cflknatpsgstqplrfqteilkeldfvgltapclllp-----ppdaifpnllskltfrg 770
QY 768 TY-LSWSYLDIIEALPNEVLEKLMDDACCGEEMHPIVNGFNRKLILIKYSFLKFWKATN 826
D 771 efsyavwkdslivgklpklevllswafiqkeweweeegfphlklflldvlylrvtrass 830
QY 827 DNPFVLERLIMRSCNLEKPIEFADIHITLQLELRECPPLKIGESAARIOKEODLGNNP 886
D 831 dhfyleravllrdcrnldsprdfaditlialldlycqvgsvnasqigqldqndyngss 890
QY 887 VDVR-----SNPLKESDSDS 902
D 891 levtlrhlflpksvltveddds 913

RESULT 7
ID AA002145 standard; Protein; 937 AA.
XX
AC AA002145;
XX
DT 29-AUG-2001 (first entry)
XX
DE Rx 72, modified resistance protein.
XX
KM Rx: modified resistance; NBS; LRR; cell death; autoactivator;
KW nucleotide binding site; leucine rich repeat; pathogen resistance;
XX
XX Solanum tuberosum.
OS synthetic.
XX
XX WO200129239-A2.
XX
XX 26-APR-2001.
XX
XX 12-OCT-2000; 2000WO-GB03930.
XX
XX 15-OCT-1999; 99GB-0024483.
XX
XX (PLAN-) PLANT BIOSCIENCE LTD.
XX
XX Bendahtmané A, Baulcombe DC;
XX
XX PI
XX
XX DR N-FSDB; AAS03715.
XX
XX WPI: 2001-290924/30.
XX
XX PT Producing activation characteristics of plant resistance proteins to
PT elictor, by introducing modifications in amino acid sequence of
PT protein -
XX
XX PS Disclosure; Page 61-65; 77pp; English.
XX

```

```

CC The sequence represents the amino acid sequence of Rx 72, a modified
CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a
CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which
CC mediates cellular response leading to pathogen resistance and/or cell
CC death or dysfunction in response to an elicitor. The Rx was modified by
CC introducing modification to the amino acid sequence to produce an
CC autoactivator polypeptide, capable of activation in absence of an
CC elicitor. Decoupling of resistance response from its natural elicitor is
CC useful for developing novel pathogen resistant plants. The modified
CC resistance proteins are useful for conferring resistance to non-natural
CC agents or stimuli and also for investigating resistance response pathways
CC and protein interactions e.g. with activators and repressors.
XX
SQ Sequence 937 AA;
XX
Query Match 26.1%; Score 1231.5; DB 22; Length 937;
Best Local Similarity 34.9%; Pred. No. 1.5e-98;
Matches 343; Conservative 143; Mismatches 346; Indels 151; Gaps 31;

QY 1 MAHASVASTMRTIESLTFNFSMOSLSCDHREELCALREKVSLEFVKNPEKN-NVFG 59
D 1 mayavuslmrtli-----hgsmltgc-----lqpfyeklkslraill-----ekscnimgd 47
QY 60 ---MTDFEVEVEVYASAEYTIQLRTGTVLGENKSQKKARRRROSLOQVAEEDMHIW 116
D 48 hegltllelvevayatytedcmwdsesrnvflagnleestrarnwelfflqaleledltv 107
QY 117 KESTKIQDKGROVSKS- -SLVHDESSSTNDILKYKNKNVGRDDQKLLLEDLTRSYSEP 174
D 108 kymatsdsmdklkptaslv---slpehdveqpenlmvgrnefemulldqarg- grel 163
QY 175 KVIPIVGMGIGKTTLAKEYNDESIICRPVHMATISQOHKNEILLGLHSIKMKDD 234
D 164 evvasivgmgiqkltlckllyscpmsrfdlratavsgcyvnnvllgllslsdsqpd 223
QY 235 RVKMIGEAELDMLOKSLKRRYLLVLDIWSCEVWDGVRRCFPTEDNAGSRILLTPRND 294
D 224 -----dqladrllqkhlkrryllvldidwtteawddiklcfpcyn-gsrilllttnv 275
QY 295 EVACYAGYENFSLKXSFMDODESWSLEKSAAPSE--ALPYEFYVGQIADCHGLPLTI 353
D 276 evaeyasgkphhmrlmndeswnllhkkllfegsypfemngkqalckgqlajai 335
QY 354 VYVAGIL-KSKRTIEDMTKTVAKDYKSFYTNPDDEKSCVILGSHYHLSDKTCLLHGI 412
D 336 tvlaqllskmgqrlidewqrlgenwsvvtcpeaqcmvlasylshlnphskpctlylai 395
QY 413 FPESDIIPVKMLMRSMWAEFLKLE--NDLEGEYEKLOELVDRCLVVSRSRSGTKIR 470
D 396 fteveqslvnelvelvpegflneeegskleavattcnelidsrlsfimhsfgrt-ie 454
QY 471 SCKVHDLIYDLCVREVORENIFIMNDIYLDVSYBCSYLCMKMOPFRVYTGDEINCPY 530
D 455 scgmhdytrelclrear--nmnfvnvl-----rgsdsq-nscsq 490
QY 531 GLYRALLTPVNRQLRDHNNLL-----KRTHSVF---SFHLEPLYYLVKSEVHFELKLV 583
D 491 smqstfsks--rsrirlhkvleelawcrnseahsilmjgfevltl-----elsfklyrv 541
QY 584 LELNRHROIDGFPRELLSLIMWRYSL-----FSGYNEFVPEICRLMWLQ 628
D 542 ldlglntwplfpgsvlslhlrlyslirfncplqgygskavpsalldiprlslslcylq 601
QY 629 TFIYQ-RFRSDI-TIFAEIWEMLQRLHLKLPRIYLPDPCSGSDVKGHLDPSNLQTIYSY 686
D 602 tfklnlfpfpyfllpsealltmpqlrlcmgwnyl-----rsheptent-mwlknlqclng 657
QY 687 LSPRCREVIMGIQNVKLGISGNKDDYKSFSDSGLPNNLVYLOQLTISL-----738
D 658 lmpycctgsffrllfnlkkllqfvgvpedfinsgdl---ydftrylyqleelffrlyypya 714
QY 739 -----ISVDYS-----LLPVISSAKAFPATLKKLIER 767

```

Db 715 cflktapsgrtdqlrfqtelnlkeidfgtaptlllp-----ppdaifpnllksltfrrg 770  
 Qy 768 ry-LSMSYDITAEIPNLEVLKMDACCCEHPIVAGFNRKLLIKYSFLKFWKATN 826  
 Db 771 etsvawkdslstvgkpklevlllswatlgkewevvegfnhkfllfdvlytyrass 830  
 Qy 827 DNEPVLERIMISCKNLKEIPREFDHTLQLEIRECPPLGESAARIQKQEDLGNRP 886  
 Db 831 dhfylyerlylrcnldslprdfadtltlalldycqgsvvnssakqldqndyass 890  
 Qy 887 VDVRI-----SNPLKESDSDS 902  
 Db 891 ievhtrhlfipksvtvteddds 913

RESULT 8  
 AAU02148  
 ID AAU02148 standard; Protein: 937 AA.  
 AC AAU02148;  
 DT 29-AUG-2001 (first entry)  
 DE Rx 7, modified resistance protein.  
 KW Rx; modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant.  
 OS Unidentified.  
 FH Key Location/Qualifiers  
 FT Misc-difference 162 /note= "Encoded by gac"  
 FT Misc-difference 177 /note= "Encoded by cca"  
 FT Misc-difference 178 /note= "Encoded by cca"  
 FT Misc-difference 218 /note= "Encoded by cct"  
 FT Misc-difference 218 /note= "Encoded by cca"  
 FT Misc-difference 221 /note= "Encoded by gac"  
 FT Misc-difference 430 /note= "Encoded by cca"  
 FT Misc-difference 585 /note= "Encoded by gac"  
 FT Region 1..786 /note= "Encoded by gt"  
 FT "Only amino acids 1-786 are encoded by the  
 FT cDNA sequence shown in the specification  
 FT and given in AAS03718"  
 PN WO200129239-A2.  
 PD 26-APR-2001.  
 PF 12-OCT-2000; 2000MO-GB03930.  
 PR 15-OCT-1999; 99GB-0024483.  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 PI Bendahmane A, Baulcombe DC;  
 DR WPI: 2001-290924/30.  
 DR N-PSDB; AAS03718.  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 PS Disclosure: Page 61-65; 77pp; English.

XX The sequence represents the amino acid sequence of Rx 7, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 XX Sequence 937 AA:  
 SQ  
 Query Match 26.1%; Score 1230.5; DB 22; Length 937;  
 Best Local Similarity 35.1%; Pred. No. 1.8e-98;  
 Matches 345; Conservative 145; Mismatches 342; Indels 151; Gaps 32;  
 Qy 1 MAHASVASLMKRTIESLTFNSPMQSLSCDRELCALREKVSLEFVFNFEKN-NVPE 59  
 Db 1 mayaaavslmrtl-----hpsmeltgqd---lqpfyeklxslrail---ekscnimgd 47  
 Qy 60 ---MTDFEVEVREYASAEYTIQLRLGTVLGENKSQKKARRRFRQSLQOVVEDMDHTW 116  
 Db 48 hegtlllelevelveaytiedmvsesrnvflaqlnestramwelfvlegalecdstcv 107  
 Qy 117 KESTIKDKGKQVSKR--SLVHDFSSTNDILKVNKNMGDQKROLLEDLTRSYSGEP 174  
 Db 108 kymatsdmkdlngpssiv---slpvhvgepdlmwygrenefemldqlarg-grsl 163  
 Qy 175 KVIPVGMGIGKTTAKKEYVNDSEILCRPDYAMATISQOHKKETLGLHSTIKMD 234  
 Db 164 evsaiygmgiqktclaktkysdpcmsrfditakavsgyevrnvlglstlsdpep 223  
 Qy 235 RVKMGAEALADMLQSLKRRRYLIVDDIWSCEVMDGVRCPTEDNKRILLTTTRND 294  
 Db 224 -----dqladrqkhkgrlylvavidltwteaawdklclpdcyn-grslllctrv 275  
 Qy 295 EVACYAGVENPFLRMSFMDQESWLFKSAFSSP-ALPYEFETVGQIADDECHGRLPI 353  
 Db 276 evaaeyassgkpphmrlmndideswnllhkrifeksgyspfeanlqqlalkcgsplal 335  
 Qy 354 VYVAGIL-KSKRTEDKKTVAQDKSPVTNDPBCSRVGLSYDHLTSDLKCTLHFGI 412  
 Db 336 tvagllskmgqridewqrigenvssvscpaeqcmrvlalsylhphkpcfllyfal 395  
 Qy 413 FPEDSDIPVKNLMKMSMAEGFLKLE--NDEGEYEKLOELVDRCLVLVSKRSRDGTR 470  
 Db 396 ftedeqslvnelvelwvveglneegksleevattcnelldstslfhnfsgt-le 454  
 Qy 471 SKVHDLIYDLCVREVORENIFIMNDIVDVSTPECSYLCMYKMQRPKRTGELINCP 530  
 Db 455 scgmhdytrelcltlear--nmnftvnyl-----yqksdq-nscq 490  
 Qy 531 GLYRALLLPVNRQLRDHNHNL-----KRTHSVF--SFHLPELVYVLKSEVNFKLK 583  
 Db 491 smgrstfs--rstirlhveelawcgrnseashlmjgfevcyl-----elsflvry 541  
 Qy 584 LELRHRQIDGFPEILSLIMLRYLST-----FSYGNEDVPEICRLMNO 628  
 Db 542 lelglnwplfsgvslslhlyslstfncpldqygskeavpslidlplsstsclyq 601  
 Qy 629 TFIYQ-RFRSDI-TTFEAEIWEIMQLNHLKLPREYLPDCSGSVYDGRNHDPSNLOTIS 666  
 Db 602 tfkinlfpysyflpseellmpqrltclcmgyny1---tshpctenr-lvlnknlid 657  
 Qy 687 LSPRCCKREYIMGIQNKKGISGNKDKYSPFRSGLPNNLVYLOOLELSTL----- 738  
 Db 658 lnprycgtsffrlpnklkqvfgvpedftrnsqdl---ydfrylyqleetfllypyaa 714

QY 739 -----ISVDYS-----LLPVIISSAKAPATLKKTLER 767  
 Db 725 cflknapsqsgtdplrtfqtellrkeidfggtappllp-----ppdafpqsikelttrg 770  
 QY 768 TY-LSWSTLDIAELPNLEVLKLMDDACCGEEMHPYVGNRLKLLIKYSFLKWKATN 826  
 Db 771 efswawklsivgkpklevllswnafigkeweevgefphkflfidvylrwrass 830  
 QY 827 DNFPVLERLMTIRSCNKLKEIPREFADITHLQELRECPRLGESAARIQKEDELGNRP 886  
 Db 831 dhfpylerlvtlrdcnldspirdaditltalldycqgsyvnasakqigddidnyss 890  
 QY 887 VDVR-----SNPLKESDSDS 902  
 Db 891 levhtlrhlfpksvttvedddd 913  
 RESULT 9  
 AA02144  
 ID AA02144 standard; Protein: 937 AA.  
 XX  
 AC AA02144;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE Rx 28, modified resistance protein.  
 XX  
 KW Rx: modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant.  
 XX  
 OS Solanum tuberosum.  
 OS Synthetic.  
 XX  
 PN MO200129239-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 12-OCT-2000; 2000MO-GB03930.  
 XX  
 PR 15-OCT-1999; 99GB-0024483.  
 XX  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 PI Bendahmane A, Baulcombe DC;  
 XX  
 DR WPI; 2001-290924/30.  
 XX  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 XX  
 PS Disclosure; Page 61-65; 77pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of Rx 28, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 CC  
 XX  
 XX Sequence 937 AA;

Query Match 26.0%; Score 1225.5; DB 22; Length 937;  
 Best Local Similarity 34.5%; Pred. No. 5e-98;

Matches 342; Conservative 146; Mismatches 336; Indels 167; Gaps 31;  
 QY 1 MAHAVASISMRIEISULFNSPMQSLCDHRELCARKEVSSLEFVYNFEKN-NVREE 59  
 Db 1 mayavtslmrtl-----hgsmeltgcd---lppfyeklsra1l--ekschingd 47  
 QY 60 ---MTDFEVEVESAAYTTLRLTGVLGECNSOKKARRRRROSLOQVAEDMDTH 116  
 Db 48 heglilleveivevaytedcmwdsesrvflaqnleesraimelffyelqaleidstcv 107  
 QY 117 KESTIKDQKQVSKNE--SLVHDFSSSTNDILKVNMMVGRDOKOLLEDTFRSYGEP 174  
 Db 108 kymatsdsmkdlkqtsislv---slpehdvqepnlmvgrenelemldqarg-grel 163  
 QY 175 KVPIVGMGGIGCTTLAKAEVYNDESILCRFDYHANAATISQNNKEIILGLHSTIKMD 234  
 Db 164 evsivgmgiqkltlcklysdpcimstrfdlrakatsvqeycvnvljglstlsdcpd 223  
 QY 235 RVKMGAEALDMLQSKLRKRYLLVLDIWSCEVWDGVRGCFPREDNAGSRILTTTRND 294  
 Db 224 -----dqladrqkhlkgyrrylvldidvteawdtkicfpocyn-gsrivlttnv 275  
 QY 295 EVACYAGVENFSLRMSFMDQESWSLFKSAFSSB-ALPYEFETGKQIADCHGLPLTI 353  
 Db 276 eaeyassgkpphmrlnmfmdeswnllhkklifekegyspelenigkqialkcgjlpai 335  
 QY 354 VYVAGLL-KSKRTIEDKRTVAKDVKSFTYNDPDEKCSRYLGSISTYHLSDKTCLLHGI 412  
 Db 336 tvlaqlskmqgrldewrigenvsvstpcqaacmvtlaistylhlpshkpcrlfyal 395  
 QY 413 FPEDSDIIVKMLNMRSMAGFELKE--NDLEGEVKECLOELVDRCILVYSKRSRGTKIR 470  
 Db 396 ftedeqisvnelvelwpegflneeegksieevatcnelidrliflfnfstfgt-le 454  
 QY 471 SKVHDLIYDLCVREVOENRFINMDIYDVSYPCSYLCKMOPFKRYGTDELINCPY 530  
 Db 455 scgmhvtrelclrear--nmfvnvl-----rgsdg-nscaq 490  
 QY 531 GLYVALILFPVKROLRDHNNMLKRTHSVFSFHEPLETYLVKSEV----- 575  
 Db 491 smgrsfks--rsrlrlh-----kveelawcnsaarslimjgfevcle 533  
 QY 576 VHFLLKLVLELRHQIDGPREILSLMLRYLST-----FSYGNFDPPE 620  
 Db 534 lsfklrvldglntwptfpgsvslhlyrlslrtpncldqygskeavpsidpils 593  
 QY 621 ICRLMNLOTFTVQ-RFNSDI-IIFAEETIWEIMQLRHLKLPRTYLPDCPSGVKGRHIDF 678  
 Db 594 lsslcylqtfklnlpfeyypfllpsealltmpqrlrlcmgwnyl---rshepteur-lvl 649  
 QY 679 SNLQITISLSPRCCTKEVIMQNVKIGISGNDDYKSPFSDSGLPNNLVYLOQLEITSL 738  
 Db 650 knlqclnqlnprycvgsffrlfpnlkklqvfgvpedfrnsqdl---ydftrylyqleelf 706  
 QY 739 -----ISVDYS-----LLPVIISSAKAPAT 759  
 Db 707 rlypyaacflknapsqsgtdplrtfqtellrkeidfggtappllp-----ppdafpqn 762  
 QY 760 LKRLKLETTY-LSMSYLDIAELPNLEVLKLMDDACCGEEMHPYVGNRLKLLIKYSF 818  
 Db 763 lksltifgefsvawklsivgkpklevllswnafigkeweevgefphkflfidvyl 822  
 QY 819 LKFKATNDNFPVLERLMTIRSCNKLKEIPREFADITHLQELRECPRLGESAARIQKE 878  
 Db 823 lryraasdhfpylerlvtlrdcnldspirdaditltalldycqgsyvnasakqigdd 882  
 QY 879 QEDLGNPVDVRI-----SNPLKESDSDS 902  
 Db 883 lqdnysgievhtlrhlfpksvttvedddd 913

RESULT 10  
 AA02146

ID AA002146 standard; Protein: 937 AA.  
 AC AA002146;  
 DT 29-AUG-2001 (first entry)  
 DE Rx 39, modified resistance protein.  
 RX Rx; modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 MW plant.  
 OS Solanum tuberosum.  
 OS Synthetic.  
 PN WO200129239-A2.  
 PD 26-APR-2001.  
 PF 12-OCT-2000; 2000WO-GB03930.  
 PR 15-OCT-1999; 99GB-0024483.  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 PI Bendahmane A, Baulcombe DC;  
 DR WPI; 2001-290924/30.  
 DR N-PSDB; AAS03716.  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein.  
 PS Disclosure: Page 61-65; 77pp; English.  
 XX The sequence represents the amino acid sequence of Rx 39, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 XX Sequence 937 AA:

Query Match 25.9%; Score 1221.5; DB 22; Length 937;  
 Best Local Similarity 35.0%; Pred. No. 1.1e-97;  
 Matches 344; Conservative 144; Mismatches 344; Indels 151; Gaps 33;

QY 1 MAHAASASLARTIESLTFNSPMOSLSDHRELALAEKXVSLEFVKNEKN NVNGE 59  
 DB 1 mayaaavtsimrli-----hgsmeltgcd---lqpfyeklksirail--eksonimgd 47  
 QY 60 ---MTDFEVEVEVSAAEYRQLRTGLTGVLGKNSQKKARRRROSLQOVAEDMDIIM 116  
 DB 48 heglitlleveivaytcedmdsdnsrnfiaqneestrimeffiflegalesidstv 107  
 QY 117 KESTRIQDKGKOVSKVE--SLVHDESSSTNDILIKVKNVNGDDQKQLLEDLTRSYSGEP 174  
 DB 108 kgmatsdemkdlkpqtsesivr---lpehdveqpenimvgrenefemldqfary-grel 163  
 QY 175 KYIPIVGMGIGITLAKVYNDESILCRPDVHAWATISQOHNKKEIILGLHSIKMDD 234  
 DB 164 evasivmgiglgkltlatklyscpimsrfditratavsgcyvznvllgllstlsddep 223

QY 235 RVKMGAEALADLMOKSLKRKRYLIYDDIMVCEVMDVGRVCFPEEDNAGSRILLTRND 294  
 DB 224 -----dqladrllqkhlqgrrylvividitwteawddklkfcpcdyn-gsrilllttrnv 275  
 QY 295 EVACYAGVENFSLRMSFMDQDESWSLFSKAAFSSE-ALPYEEYVGKQIADBCGHLPTI 353  
 DB 276 evaeayassgkprphmclmndeswnllhkkllfekegyspfeftenlgqialkcgslpial 335  
 QY 354 VVYAGLL-KSKRTIEMKTVAKDKVSFYVNDPDRCSRYLGSYDHRTSLDTCLLHFGI 412  
 DB 336 tviagllskmgqrlidewqrigenvssvstcdpaqcmrvtalsyhhplhlpfclyfai 395  
 QY 413 FPEDSDIPVKNLMRSMMAEGFKLE--NDLEGEVEKLOELVDRCLVLSKRSRDTKIR 470  
 DB 396 ftededqsvneivelpvpgflneegksieevattcnehlidrsllfhnstfgt-le 454  
 QY 471 SCRVDHLDLCVREVORENIFETANDIVLDVSTPECSYLCMKRMOPFKVGTDEINCY 530  
 DB 455 scgmhvtvrelclrear--nmfenvyl-----fgksdq-nscag 490  
 QY 531 GLXRALLTPVNRRLDRDNNNL-----KRTHSVF--SFHLEPLYVVLKSEVHFRLKV 583  
 DB 491 smgrstfs--tsrlrhkveelawcrnseahslimgfecvyl-----elsklytv 541  
 QY 584 LELRHRQIDGPREILSLIWLRYLSL-----FSYGNFDVPPETICRLMLQ 628  
 DB 542 ldlglntwplfpgsvslshlrylsrlfpcldqygyskeavpsliddplsisslcyiq 601  
 QY 629 TFIIVQ-RFRSDI-TIPEEILWELMQLRLKLPREYLPDCPSGSVDKGRHLDFSNDQTSY 686  
 DB 602 tfklnlpfpyrffllpselltmpqrlrlcmgyvyl---rshpenteur-lvlnhqlcng 657  
 QY 687 LSPRCCKEYIMKIOVWKIGISGNKDDYKSPFSDGLPNNVLYLOOLETSL----- 738  
 DB 658 lnpvctgsffrlfpnlkrlqvfgvpedrinsqdl---ydflylylqeeltfcllypyyaa 714  
 QY 739 -----ISVDYS-----LLPVIISSAKAPATLKLKLER 767  
 DB 715 cflknatpagsgtqdlprlftgellhkeidfggtapclllp---ppdafpqnllksitfgr 770  
 QY 768 TY-LSMSYLDIADLEPYLEVLAAMDACGEEHNPVYMGFNRLKLLIKYSLFKKAVN 826  
 DB 771 efesawkdslvqklkplevlllswnaflgkeweeveefpnlkllfldvlylrvass 830  
 QY 827 DNPVLERLMIRSCKNLKEPIEFADIIHTPLQLELRECPKLGESAAARIQEOEDLGNNP 886  
 DB 831 dhfpylevllircrnldspirfaditlaididyccqsvnsakqigqddqndygs 890  
 QY 887 VDV---RISNPLK---ESDSDS 902  
 DB 891 levhtrrllfpkavtveeddds 913

## RESULT 11

ID AA002149 standard; Protein: 937 AA.  
 AC AA002149;

QY 29-AUG-2001 (first entry)  
 DE Rx 32, modified resistance protein.  
 RX Rx; modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 MW plant.  
 OS Solanum tuberosum.  
 OS Synthetic.  
 PN WO200129239-A2.  
 PD 26-APR-2001.



xx The sequence represents the amino acid sequence of Rx 193, a modified resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a nucleotide binding site (NBS), leucine rich repeat (LRR), and which mediates cellular response leading to pathogen resistance and/or cell death or dysfunction in response to an elicitor. The Rx was modified by introducing modification to the amino acid sequence to produce an autoactivator polypeptide, capable of activation in absence of an elicitor. Decoupling of resistance response from its natural elicitor is useful for developing novel pathogen resistant plants. The modified resistance proteins are useful for conferring resistance to non-natural agents or stimuli and also for investigating resistance response pathways and protein interactions e.g. with activators and repressors.

xx Sequence 937 AA:

Query Match 25.8%; Score 1215.5; DB 22; Length 937;  
Best Local Similarity 34.9%; Pred. No. 3.8e-97;  
Matches 343; Conservative 143; Mismatches 346; Indels 151; Gaps 32;

QY 1 MAHASVASLAKTIESLTFNSPMOSLSCDHREELCALREKVSLEEVYKNEKN-NVPEGE 59  
DB 1 mayaaavtslmtl-----hgsmeitgcd---lqpfyeklkslraill---eksamngd 47  
QY 60 ---MTDFEVEVEVSAAEYTIQLRLTGTVLGENKSKOKKRRRRRQSLQGVADMDHIW 116  
DB 48 heglillevelevayvaytcdmvdseesrnfiaqlheesrtaamweifvlegaleclstlv 107  
QY 117 KESTIOPDKQVSKKE--SLVHDFSSSTNDILKNNVNGRDORQKOLEDLTFSYSGEP 174  
DB 108 kqmatasmdklkptsslv---slpehdveqpeninvgrenelemmldqarg-grel 163  
QY 175 KYIPIVGMGIGKTTTAAKEVYNDESILCRFVHAMATISQGHKKKELLGLHSTIKMD 234  
DB 164 evasivmgigigtclaklysdpcimsrfidrakatvsqgcyrnvlqllsitsdepd 223  
QY 223 RKVMIGEAELADMLQSLKRRKRYLVDIWSCEVWDVRCRPFEDAGSRILLTTRND 294  
DB 224 -----qiaaiairgkhlkgyrrylvlddwteawdtkicfpdcyn-gsrillttrnv 275  
QY 295 EVACYAGVENSRLRMSFMDODESMSLFSAAPSSB-ALPYEFETVKGQIADCHGLPLTI 353  
DB 276 eaevyassgkpphhmrlnmyfdeswnllhkkli feksygsyfpentlqgalkcgllprai 335  
QY 354 VVAVALL-KSKRTIEDKMTVAKDKSFYTNDEKSCSVLSLSDHLSDTKTOLLHGI 412  
DB 336 tvlaagllskmgqrldegwrlgenvssvscdpeaqcmvldlsyhhlpshlkpctfilyfat 395  
QY 413 FPEDEDIPIKNNLRMSMAEGFLKLE--NDLEGEVEKCLQELVDKCLVLSRKRSDGTKIR 470  
DB 396 fteedeqavneivewpveglneegksievaaltcnelidrsllfihfsfigrt-le 454  
QY 471 SKCVHDLIYDLCREVQREBNIFIMNDIYLVSYPCSTYLCMKQPKFRVYTGDELINCPY 530  
DB 455 scgmhvvtrtelclearear--mmfivnvl-----rgksdq-nscsq 490  
QY 531 GLYRALILPVNQLRDHDNNNL-----KRTHSVF--SFHLPIYVLAKSEVHPKILKY 583  
DB 491 smgrsfks--tsrlfihveelawcrnseashlmjgfeevtl-----elstfklyrv 541  
QY 584 LELRRQIDGPPREITSLMLRYLSL-----FSYGNFDPVPEICRLMWLQ 628  
DB 542 ldlgintwplfsgyslshlrylsirfncpqgyskeavpsldipstislsclq 601  
QY 629 TFIYO-REPSDI-IIFAEIWEIWLQRLHKLPRFYLPPCCPSGSDVKGHHDFSLOTISY 686  
DB 602 tfkllpfpfpyllpeelltmpqlrticmgwyl---rshpeent-lvklhqlcng 657  
QY 687 LSPRCCTKIVNGIONVKKLGISGNKDKYSFRDGLNNLVLQOQLTSL-----738  
DB 658 lmpyctgafifrlfnlkklygvpedfrnsqdl---ydftrylyqleelftrylypyaa 714

QY 739 -----ISVDYS-----LUPVIISAKAPATLKKLKER 767  
DB 715 cfikntapsstqdlrfrfqtellhkeidfgtceaplllp-----ppdaipnqlkaltfng 770  
QY 768 TV-LSMSYLDIAELPNEVLKMDACCCEWHPIVWGFNRKLLLYSFLAKWKATN 826  
DB 771 efavawkdslvgklpkplevlllswmafkgewevveegfpllkflfidgyvilyrass 830  
QY 827 DNPVLELRMRSCNKLKELPIEFADITHLOILEBCEPRLGESARIQEEDLGNP 886  
DB 831 dhpylerylvllrcrrldsptrfdadltclalldldycqgsvnsaklqgdqnyass 890  
QY 887 VDVI-----SNPLKESDSDS 902  
DB 891 ievthrlhfkpkvtvedddds 913

RESULT 13  
AAW48360  
ID AAW48360 standard; Protein; 1822 AA.  
XX  
AC AAW48360;  
XX  
DT 03-JUL-1998 (first entry)  
XX  
DE Tomato Prf protein.  
XX  
KW Prf; Pseudomonas syringae pv. tomato; PST; transgenic plant; fenthion;  
KW organophosphate insecticide; leucine zipper motif; immunoassay.  
XX  
Lycopersicon esculentum.  
FH  
FT Key Location/Qualifiers  
FT Misc-difference 569  
FT Domain /note="Encoded by gat"  
FT Domain 1120..1132 /label="p loop domain"  
FT Domain 1195..1205 /label="Kinase domain 2"  
FT Domain 1124..1231 /label="Kinase domain 3a"  
FT Domain 959..994 /label="Leucine zipper"  
FT Region 1398..1814 /label="Leucine-rich repeat motif"

W09802545-A2.  
XX  
PD 22-JAN-1998.  
XX  
PF 10-JUL-1997; 97WO-US12022.  
XX  
PR 11-JUL-1996; 96DS-0680327.  
XX  
PA (REGC) UNIV CALIFORNIA.  
XX  
PI Oldroyd GE, Rommens C, Salmerson JM, Staskawicz BS;  
XX WPI: 1998-110592/10.  
XX DR N-PDB; AAW17777.  
XX  
DR  
XX  
PT Isolated tomato Prf nucleic acid sequences - used to produce plants  
PT which are resistant to pathogens or to confer fenthion sensitivity  
XX to plants  
XX  
PS Examples: Fig 11; 63pp; English.  
XX  
XX The present sequence is of a tomato Prf protein which contains a  
XX leucine-rich repeat, nucleotide binding and leucine zipper motifs.  
XX Prf protein has been known to be required for resistance of tomatoes  
XX against Pseudomonas syringae pv. tomato (PST). Analysis of Prf mutant  
XX alleles suggest that in addition to its role in disease resistance, the  
XX Prf protein also functions in the response of tomato to the







Db 614 hqkintcpdlrlrpdewellekrtftgnespdelldvgkeiaenckgplrvadliag 673  
QY 359 LL---KSKRTIEDWKTVAVDVKSFTVNDPDERCSRVLGSLYDHLTSDKTCLHFGIPE 415  
Db 674 vlaagrektrsv--wlevgsslsfflinseve--ymkvteislchphlkpcclhfaswpk 730  
QY 416 DSDIPVKNLMRSMWMAEGFLKLENDLEG--EVEKC--LOELVDRCLVLYSKRSRDGTAKRSC 472  
Db 731 dcpitilylltvygaegfyve--ktemkgyeevvaixymddlissavicfneigd--llnf 786  
QY 473 KVDLLIYDLCVREVORENIFI-----MNDIVLDVSYPE 505  
Db 787 qthndlvhdfclikarckenlfdtrrsapedllprqitidydeeeenhfglnfwmfdankkr 846  
QY 506 CSTLCWYKKMQPFKRVWDEINCPYGLYRALLTPVNRQLRDHDNNMLKRTSHVSFHE 565  
Db 847 hsqkhlysl-----ringd-----qlddsvsd-----afhlr 873  
QY 566 PLYYVLKSEVVEHKLKVELRHROJ---DGPREILSLWLRVLSL-----FSYGN 614  
Db 874 -----hlrlrvldlepllmvnsllneicmnhlrylrvtqky]pfsfn 922  
QY 615 FDVPEICRLMNLQTFIVQFRSDIIFAEIWEMLQRLKLPFRYLPDCPSGSVDKGR 674  
Db 923 -----lwnleslfvsn--kgsllvllprldlvklyl-----svgacs 959  
QY 675 HLDPSNLQRTISYLSPPRCRKEVTMGIONVKLG--ISGNKDDYKSFSDSGLPNNLVYIQ 731  
Db 960 ffdmdadesllakd--tk-----lenlrllgelllsykctmnlfk--rfpn---lq 1005  
QY 732 QLEILSLISVDYS-----LLPYIISAKA-----FPAT 759  
Db 1006 vldqfelkeswdysteqhwpkldcleleleicvqfkssnlnhcgssvatnrpwwdfhfn 1065  
QY 760 LKKIKLEERTYLSWSYLDIAELPNLEVLKLMDDACCGEEMHPIVMG---FNRLKLLLIK 815  
Db 1066 lkelllydfpltsdstslarlpnlenlsydtliggeew--mgeedtfenlkfmlnr 1122  
QY 816 YSFLKFWKATNDNFPVYLERLMIRSCKNLKEIPFADIRTLQULIELRECPKLGESARI 875  
Db 1123 lltskweygeesfnpkfkqcgkleeippsfgdiyslkfikivk--spqledsalkl 1181  
QY 876 OKQEDL--GNNPVYDV 889  
Db 1182 kkyaedmrggneiqi 1196

Search completed: September 12, 2002, 13:59:50  
Job time: 8968 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2002, 11:30:22 ; Search time 27.22 Seconds  
(without alignments)  
812.093 Million cell updates/sec

Title: US-09-864-680-3

Perfect score: 4712  
Sequence: 1 MAHASVASIMRTIESLTFN.....PVDKRIISNPKESDSSEKH 905

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCNUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4712	100.0	905	US-09-360-186-3	Sequence 3, Appl1
2	980	20.8	1824	US-08-680-327-3	Sequence 3, Appl1
3	980	20.8	1824	US-09-228-246-2	Sequence 2, Appl1
4	852.5	18.1	1255	US-08-947-823-3	Sequence 3, Appl1
5	828.5	17.6	1257	US-08-947-823-5	Sequence 5, Appl1
6	667	14.2	1240	US-08-930-996A-4	Sequence 4, Appl1
7	617.5	13.1	1220	US-08-930-996A-2	Sequence 2, Appl1
8	565.5	12.0	429	US-08-310-912A-109	Sequence 109, App
9	565.5	12.0	429	US-09-301-085-109	Sequence 109, App
10	565.5	12.0	429	PCT-US95-04589-109	Sequence 109, App
11	530	11.2	920	US-08-930-996A-8	Sequence 8, Appl1
12	520	11.0	1205	US-09-330-330-1	Sequence 1, Appl1
13	476	10.1	784	US-09-004-838-12	Sequence 12, Appl1
14	447	9.5	1402	US-09-004-838-11	Sequence 11, Appl1
15	440	9.3	885	US-08-310-912A-2	Sequence 2, Appl1
16	440	9.3	885	US-08-841-089-2	Sequence 2, Appl1
17	440	9.3	885	US-09-301-085-2	Sequence 2, Appl1
18	440	9.3	885	PCT-US95-04570-2	Sequence 2, Appl1
19	440	9.3	885	PCT-US95-04589-2	Sequence 2, Appl1
20	429.5	9.1	909	US-08-310-912A-142	Sequence 142, App
21	429.5	9.1	909	US-09-301-085-142	Sequence 142, App
22	429.5	9.1	909	PCT-US95-04589-142	Sequence 142, App
23	420.5	8.9	907	US-08-930-996A-7	Sequence 7, Appl1
24	382.5	8.1	416	US-09-228-246-4	Sequence 4, Appl1
25	366	7.8	1074	US-09-004-838-111	Sequence 111, App
26	355	7.5	1323	US-09-004-838-90	Sequence 90, Appl1
27	351	7.4	1066	US-09-004-838-24	Sequence 24, Appl1

28	350	7.4	553	4	US-09-004-838-16	Sequence 16, Appl1
29	336	7.1	1817	4	US-09-004-838-125	Sequence 125, App
30	330.5	7.0	1854	4	US-09-004-838-108	Sequence 108, App
31	325.5	6.9	1890	4	US-09-004-838-88	Sequence 88, Appl1
32	323	6.9	1805	4	US-09-004-838-92	Sequence 92, Appl1
33	321.5	6.8	1143	2	US-08-310-912A-108	Sequence 108, App
34	321.5	6.8	1143	2	US-09-301-085-108	Sequence 108, App
35	321.5	6.8	1143	5	PCT-US95-04589-108	Sequence 108, App
36	321.5	6.8	1144	1	US-08-261-663A-2	Sequence 2, Appl1
37	321.5	6.8	1144	1	US-08-261-663A-4	Sequence 4, Appl1
38	321.5	6.8	1144	5	PCT-US95-07754A-2	Sequence 2, Appl1
39	321.5	6.8	1144	5	PCT-US95-07754A-4	Sequence 4, Appl1
40	320.5	6.8	1144	3	US-08-930-996A-9	Sequence 9, Appl1
41	320.5	6.8	1294	3	US-08-930-996A-10	Sequence 10, Appl1
42	316.5	6.7	1366	4	US-09-004-838-92	Sequence 22, Appl1
43	316	6.7	1604	4	US-09-004-838-95	Sequence 95, Appl1
44	314.5	6.7	1209	5	PCT-US95-04589-107	Sequence 107, App
45	314.5	6.7	1258	2	US-08-310-912A-107	Sequence 107, App

## ALIGNMENTS

RESULT 1						
US-09-360-186-3						
Sequence 3, Application US/09360186						
Patent No. 6262343						
GENERAL INFORMATION:						
APPLICANT: Staskawicz, et al.						
TITLE OF INVENTION: B2 Resistance Gene						
FILE REFERENCE: 50687						
CURRENT APPLICATION NUMBER: US/09/360,186						
EARLIER FILING DATE: 1999-07-23						
EARLIER APPLICATION NUMBER: 60/093,957						
EARLIER FILING DATE: 1998-07-23						
NUMBER OF SEQ ID NOS: 9						
SOFTWARE: PatentIn Ver. 2.0						
SEQ ID NO 3						
LENGTH: 905						
TYPE: PRT						
ORGANISM: Capsicum annuum						
US-09-360-186-3						
Query Match						
Best Local Similarity 100.0%; Score 4712; DB 4; Length 905;						
Matches 905; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MAHASVASIMRTIESLTFNPSMOSLSCDHRELCALREKVSLEVFYKNEKNNVFGEM	60			
DB	1	MAHASVASIMRTIESLTFNPSMOSLSCDHRELCALREKVSLEVFYKNEKNNVFGEM	60			
QY	61	TDVEYEVREVASAEYTTOLRLTGTVLGSKSQKKARRRFRQSLQOVAEDMDHTKEST	120			
DB	61	TDVEYEVREVASAEYTTOLRLTGTVLGSKSQKKARRRFRQSLQOVAEDMDHTKEST	120			
QY	121	KIODGKGVSKSLVHDESSSTNDILKYNNVGRDDOKLLEDLTRSYSEPKYIPYV	180			
DB	121	KIODGKGVSKSLVHDESSSTNDILKYNNVGRDDOKLLEDLTRSYSEPKYIPYV	180			
QY	181	GNGGIGKTTIAKEVYNDESILCRFDVHAWATISQHNKKEILGLLHSTIKMDRVMKG	240			
DB	181	GNGGIGKTTIAKEVYNDESILCRFDVHAWATISQHNKKEILGLLHSTIKMDRVMKG	240			
QY	241	EEELADMLOKSLKRRRYLVDDINSCFVWDCVRCFPEDNAGSRILTTNDEVACYA	300			
DB	241	EEELADMLOKSLKRRRYLVDDINSCFVWDCVRCFPEDNAGSRILTTNDEVACYA	300			
QY	301	GVENSFLRSPMDQESNLFKSAFSSBALYEFETVQKQIADBECHGLPLTIYVAGLL	360			
DB	301	GVENSFLRSPMDQESNLFKSAFSSBALYEFETVQKQIADBECHGLPLTIYVAGLL	360			
QY	361	KSKRTIEDKTYAKDVKSFTVNDPDCRSRVGLSTYDHLTSLDKTCLLHFGIFPEDSDIP	420			

```

Db 361 KSKRTIDMTVADVADVSFYTNDEPDERCSRVLGISTDHLSTDKTCLLHFGEIFPEDSDIP 420
QY 421 VKNLMRSMAEGFLKLNDEGEVEKCLQELVSDCLVLSKRSRSDGKIRSCKHDLIYD 480
Db 421 VKNLMRSMAEGFLKLNDEGEVEKCLQELVSDCLVLSKRSRSDGKIRSCKHDLIYD 480
QY 481 LCVREVORENIIFIMNDIVLDSVECSYLCMKQMPKRYTGDEINCPYGLYRALLTPV 540
Db 481 LCVREVORENIIFIMNDIVLDSVECSYLCMKQMPKRYTGDEINCPYGLYRALLTPV 540
QY 541 NRQLRDHDNNNLKRTHSVSFHLERPLYVLSKSEVHFLLKYLELRHROJDFPREILS 600
Db 541 NRQLRDHDNNNLKRTHSVSFHLERPLYVLSKSEVHFLLKYLELRHROJDFPREILS 600
QY 601 LHMRLVSLSTSGNEDVPEPICRLMNLQTFIVORERSDIIFAEIEMELMQLRLKLPF 660
Db 601 LHMRLVSLSTSGNEDVPEPICRLMNLQTFIVORERSDIIFAEIEMELMQLRLKLPF 660
QY 661 YLPDPSGSVDKGRHLDPSNLQITISYSPRCCTREVIIMGIONVKLGISGNKDDYKSF 720
Db 661 YLPDPSGSVDKGRHLDPSNLQITISYSPRCCTREVIIMGIONVKLGISGNKDDYKSF 720
QY 721 SGLPNNLVYLQLEIISLISVDYSLPVIISAKAPFATLKLKLERTYLSWSYLIIAE 780
Db 721 SGLPNNLVYLQLEIISLISVDYSLPVIISAKAPFATLKLKLERTYLSWSYLIIAE 780
QY 781 LPMLEVLKIMDDACCGBEMPIYMGFNRKLLIKYSFLKFMKATNPNFYLEMLRSC 840
Db 781 LPMLEVLKIMDDACCGBEMPIYMGFNRKLLIKYSFLKFMKATNPNFYLEMLRSC 840
QY 841 KNLKEIPFEFADHTIQLIELRECPKLGESAAIRQKQEDLGNPVDVATISNPKESDS 900
Db 841 KNLKEIPFEFADHTIQLIELRECPKLGESAAIRQKQEDLGNPVDVATISNPKESDS 900
QY 901 DSEEH 905
Db 901 DSEEH 905

```

```

RESULT 2
US-08-680-327-3
; Sequence 3, Application US/08680327
; Patent No. 5859321
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian S., Oldroyd, Gilles Edward,
; APPLICANT: Salmeron, John M., Rommens, Catus
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Winston
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,327
; FILING DATE: July 11, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/310,912
; FILING DATE: September 22, 1994
; CLASSIFICATION: 800

```

```

; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 5151-45038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1824 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-680-327-3

```

Query Match 20.8%; Score 980; DB 2; Length 1824;  
Best Local Similarity 30.9%; Pred. No. 8.7e-81;  
Matches 288; Conservative 167; Mismatches 342; Indels 136; Gaps 33;

```

QY 26 LSCDHREELCALREKVSLEVPYKNF-EKNNVGEWTDPEVEYREVASAAEYTI----- 78
Db 972 LIIDLKQHSVYKGLCLRSFIDHFESEYDEHDEACGLIARVSVMAKAEYVIDSLAY 1031
QY 79 -----QLRLGTVLGENKSOKKARRRFRQSLQOVAEDMDHIKKESTKI 122
Db 1032 SHPLMYKVLMISEYLENIKIVKNVGETCE-----RRNIEYVHEVAKTTTYV----- 1079
QY 123 QDKGQVSKESLYVDFSSFTNDILKVNKNVGRDDQKOLLEDTFRSYGEPK--VIPYV 180
Db 1080 -----APESFATYQ-----RANEBMGEODTIDELDKL-----LGSPELDVSTIV 1121
QY 181 GMSGIGKTTLAKEYYNDESILCRFDYHAMATISQHNKKEILLGLLHSTIKMDRYVMIG 240
Db 1122 GMPGLGKTTLAKKIYNDPEVTSRFDYHAQCVVYQVLSMRELLITLINDVLEPSDRNEK-E 1180
QY 241 EAEIADMLQSLKRRKRLIYLDIDWISCEVWDGYRRCPTEDNAGSRILLTTRDEVACYA 300
Db 1181 DGEIADLRFRFLTKRPLIYLDVWDYKVDNLCMCSVDVSNR-SRIILTTRINDVAEYV 1239
QY 301 GVENFSLRMSFMODEMSLFSKSAFESSEALPYEFTVGKQIADDECHGLPLTVIVVAGL 360
Db 1240 KCESDPHHLALFRDDESWITLQKEVFGESCPELEBVGREISKSGTSLSVIVAGYL 1299
QY 361 K-SKRTIEDMKYVAKDYKSVTNDPDERCSRVLGSLSDHILTSDKTCLLHFGEIFPEDSDI 419
Db 1300 KKKKKTLDSSWKVVEOSLSQISLESIS-IIGFSYKNLPHYLKPCLFLEGFGFLQKDI 1358
QY 420 PVKNLMRSMAEGFLKLNDE-LEGEVEKCLQELVSDCLVLSKRSRSDGKIRSCKHDL 477
Db 1359 HVSKNMRLMVAEGFVQANNKGGQEDTAQGLDILIGNVVMAMEK-RPNKVTVCIRHDL 1417
QY 478 IYDLCEVREVORENIIFIMNDIVLDSV-----YPCRSYLCMKQMPKRYTGDEINCPYGL 532
Db 1418 LHKFCWEKAKQE-----DPLLOINSGEVFPE--RLEBYRL--FVHYSYDEID-----L 1462
QY 533 YRALLPVNRQLRDH-DNNNLKRTHSVSFHLERPLYVLSKSEVHFLLKYLELRHROJ 591
Db 1463 WPSRSRNVSRSLFENAIIDPMLPRDISFIFE-----SFKLVKVLDESFN 1509
QY 592 DG-FPREIISLIMRLKLSLSTSGNEDVPEPICRLMNLQTFIVORERSDIIFAEIEMELM 650
Db 1510 GGFPEPEIOLYLQMKYFAQTDAN-SIPSSIAKLENLETFVVGAGLGEMLPC-SLTKMY 1567
QY 651 QLRLKLPREFYLPDPSGSVDKGRHLDPS-----NLQITSYSPRC-----TKEYI 697
Db 1568 KLRHIVY-----NDKRSGLHNMMDVLTGNSQLPNIETFS--TPRLTFYKDKAEKYL 1616
QY 698 MGIONVKKL-----GISGNKDDYKSFSDGLPNNLVYLQLEIISLISVDYSLPVIIS 752
Db 1617 RKMPLKRLKLSCTFSGTFGYSRLKG--RCVRF-P-RLDFLSHLESILKIVSNSY---PAKLPH 1671

```

QY 753 AKAPATLKKLLERTYLSYDIIAELPMLVYLKIMDDACGGEWHPIYMGFNRLKL 812  
 Db 1672 KFNPPSOARELTLSKFLPMTQISIIAELPMLVYLKILLRPFEDHWEKDFLELKYL 1731  
 QY 813 LKYSFLKFKATNDNPFVLERMIRSCNKLKEIPFADITHIQLIETLRCPRLGESA 872  
 Db 1732 KIDMLKVVQMSISDDAPFKLEHLVLTCKHLEKIPSRFEDAVCLNRYEVMNCNNVANS 1791  
 QY 873 ARIQEO-EDLGNPNVVRISNP--LKESDSDS 902  
 Db 1792 QDIQTMQHEVIANDSFVTYTIQPPDMSKEQPLDS 1824

RESULT 3  
 US-09-228-246-2  
 ; Sequence 2, Application US/09228246  
 ; Patent No. 6245510  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Staskawicz, B. S. et al.  
 ; TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences: Compositions  
 ; TIME OF INVENTION: and Methods for Plant Pathogen Resistance  
 ; FILE REFERENCE: 51700  
 ; CURRENT APPLICATION NUMBER: US/09/228,246  
 ; EARLIER FILING DATE: 1999-01-11  
 ; EARLIER APPLICATION NUMBER: 08/680,327  
 ; EARLIER FILING DATE: 1996-07-11  
 ; EARLIER APPLICATION NUMBER: 08/310,912  
 ; EARLIER FILING DATE: 1994-09-22  
 ; EARLIER APPLICATION NUMBER: 08/227,360  
 ; EARLIER FILING DATE: 1994-04-13  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1824  
 ; TYPE: PRF  
 ; ORGANISM: Lycopersicon esculentum  
 ; US-09-228-246-2

Query Match 20.8%; Score 980; DB 4; Length 1824;  
 Best Local Similarity 30.9%; Pred. No. 8.7e-81;  
 Matches 288; Conservative 167; Mismatches 342; Indels 136; Gaps 33;

QY 26 LSCDHRELCALREKVEVSELEFVKNF-EKNNVGEEMTDFEVEVEVSAAEYTT----- 78  
 Db 972 LIIDLKHQIESVKEGLCLCSFIDHSESYDEHDEACGLIARVSYMAKAEYVLDSCLAY 1031  
 QY 79 -----OLRLTGVVLGENKSQKKARRRFRQSLQOVAEDMDHIKKESTKI 122  
 Db 1032 SHPLWYVLMISEYLENIKILVKNVGETCE-----RNIEVYAEVAKTTTYV----- 1079  
 QY 123 QDKGKOVSKESLVHDESSSTNDILKYNANVGRDQKOLLEDTFRSYGEPK--VIPIV 180  
 Db 1080 -----APSFSAVYQ---RANEEMEGEDTIDEKDKL---LGSPEDIVISIV 1121  
 QY 181 GMGIGICTTAKAEVYNDESTLCREDYAHAMPTISQOHKKKELLGLHSTIKMDRYVMIG 240  
 Db 1122 GMFGGLGTTTAKKTIYNDPEYTSRFDVHACVYQIOLISWRELLITLMDVLEPSPDNK-E 1180  
 QY 241 EAEIADMLQSLKRRKRYLIVLDIWISCEVMDGVARCPPTEDNAGSRILLTTRNDEVACYA 300  
 Db 1181 DGEIADLBRFLTLTKRLLIIDDVMDKWMNLCMCFSDVSNR-SRIILITRLNDVAEYV 1239  
 QY 301 GVENFSLRMSFMDDEWSLFSKSAFSESLPYEFETVQKQIADCEHGLPLTVVAVGL 360  
 Db 1240 KCSDEPHHLTLFRDDESWTLLOKEVEFGESCPELEEDVGEFISKSGCLPLSVLVAGVL 1299  
 QY 361 K-SKRTEDKATYAKDVKSEVTDNPDRCGRVGLISYDHLTSDLKTGTLHGIPRESDI 419  
 Db 1300 KOKKTIIDSKKVVYEQSISORISLESIS-ITGFSTKKNLPHTLKPCFLTFGGGLQGDKI 1358  
 QY 420 PVNKLMSMAEGFLKLEND--LEGEVEKLOELVDRCLVLVSKRSHDGTKIRSCKVHDL 477

Db 1359 HVSMTKIMVAEGEVQANNEGQEDTACGFLDDLIGRNVAMER-RNRTKVKCRHIDL 1417  
 QY 478 IYDLCVREVORENTIFIMNDIVLVS-----YPCSYLCMYKMPKRVGTGEINTCPYGL 532  
 Db 1418 LHKCEMERAKOE-----DFLLQINSGEGVPE--RLEERYL--FVHSYODEID----- 1462  
 QY 533 YRALTLFPNRQLRDH-DNNNLTKRTHSVSFHLEPLRYVLAKSEVVPKLLVLELRHQI 591  
 Db 1463 WRPSRSNVRSLLFNALIDPNDLMPDISITFE-----SFKLVAVLDESTNI 1509  
 QY 592 DG-FPRELLSLIMRYLSLFSYGNFEDVPEICRLMNLQTFIVORRSDIILFAEIRIEML 650  
 Db 1510 GGFPEETEIQVLIQKKFYAQTGDAN-SIPSTAKLENLETFVVRGAGEMILPC-SLKMY 1567  
 QY 651 QLRHLKLPREFYLPDPCSGSVYKGRHLDS-----NLQITISLSRCC-----TKEVI 697  
 Db 1568 KLRIRIHV-----NDVRSFGLHENMDVLTGNSQLNLETFSS--TPRLYVGKDAERYL 1616  
 QY 698 MGIONVKKL-----GISGNKDQYKSPRDSGLPNNLVYLOOLEIISLVDSLSLPVITIS 752  
 Db 1617 RKMFKRLKLSCTFSGTGYSKRLKG-KCVRRP-RIDFLSHLESILKLVNSY---PAKLPH 1671  
 QY 753 AKAPATLKKLLERTYLSYDIIAELPMLVYLKIMDDACGGEWHPIYMGFNRLKL 812  
 Db 1672 KFNPPSOARELTLSKFLPMTQISIIAELPMLVYLKILLRPFEDHWEKDFLELKYL 1731  
 QY 813 LKYSFLKFKATNDNPFVLERMIRSCNKLKEIPFADITHIQLIETLRCPRLGESA 872  
 Db 1732 KIDMLKVVQMSISDDAPFKLEHLVLTCKHLEKIPSRFEDAVCLNRYEVMNCNNVANS 1791  
 QY 873 ARIQEO-EDLGNPNVVRISNP--LKESDSDS 902  
 Db 1792 QDIQTMQHEVIANDSFVTYTIQPPDMSKEQPLDS 1824

RESULT 4  
 ; Sequence 3, Application US/08947823  
 ; Patent No. 6114605  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Williamson, Valerie M.  
 ; APPLICANT: Kaloshian, Isagouhl  
 ; APPLICANT: Yaghoobi, Jafar  
 ; APPLICANT: Bodeau, John  
 ; APPLICANT: Milligan, Stephen  
 ; TITLE OF INVENTION: Procedures and Materials for Confering  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/947,823  
 ; FILING DATE: 09-OCT-1997  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCY/US97/18802  
 ; FILING DATE: 09-OCT-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/028,191  
 ; FILING DATE: 10-OCT-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 023070-0702100S  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1255 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-947-823-3

Query Match 18.1%; Score 852.5; DB 3; Length 1255;  
 Best Local Similarity 30.1%; Pred. No. 2,7e-69;  
 Matches 274; Conservative 156; Mismatches 336; Indels 145; Gaps 34;

QY 31 REELCALREKVSLEVFVKNEK---NNVFGEMTFEVEVREVASAEYTIOLRLTGV- 86  
 DB 413 KEIEIYVQDLKFIKFEVDAGQGLKRLMARVLDVAEADVID---SIIIVDNGILH 468  
 QY 87 ---LGENKSQKKARRRFRKSLQGVADMDHIMKESTKIDKQKVSLEVHDFSSST 142  
 DB 469 LIFSLPTITIKIKIKIEETISALDENIPKDRGLIIVNSPK---KPERKSLTDD--- 518  
 QY 143 NDLVKNMNVGDRDQKQLLEDLFRSYSGEKKVPIYMGIGIKTKTLAKEVYNDESTLC 202  
 DB 519 ---K1---TVGEETENLILKRLT-SSGADLDVISTMGSGTTLATVYNDKSVSS 570  
 QY 203 REDVHAMATISQHNKKEILLGLSTIKMDRVKIMGEALADLQKSLRKRRLYLVD 262  
 DB 571 REDLAWKVCVDCGCEK-LNLTIFSOYS-DSDSLSENIDVADKRLQKRLYLVD 628  
 QY 263 DIWSEVWDVRCRPTEDNAGSRILLTRNDEVACYGVENFSIRMSFMDQDSWSLFK 322  
 DB 629 DVMQTTTMDLTPPP-ESKKSRIILTRREKVALHGLKMTDPLRLPDESWEILLE 687  
 QY 323 SAAFSSEALPYEFETVGRKQIADCHGLPLTIYVAVGLL---KSKRTIDMTKVAADKSF 379  
 DB 688 KRAFNGESCPDELIVYKFIENCKGLVADLIVAGVIAKGRKSV--WLEVOSSLSF 745  
 QY 380 VTNDEPERSVGLSYDHLTSDLTCLHFGIFEDSDIPYKILMRSMAGFL-KLE- 437  
 DB 746 IINSEVE-VMKVIELSYDHLPHLKLPLFYAFSPKDFSLFIYELNVYFAGGFGVKTGM 804  
 QY 438 NDLGEVENCLOEIVDRCLVYKSRSGRTKRSCKVNDLYLDCVREVQRENFI---- 493  
 DB 805 NMEEVYKTYMDLITYSSLVIF--NEGVAL-NFQIHDLVHDFCLIKARENLEFDQIRS 861  
 QY 494 ---MNDIVLVSYPECSYKMKMPFKKVTGDEINVCYPG 531  
 DB 862 SAPSDDLPRQIITIDDEEHFGLNVFMDSNKRSKHIVSL---RIID----- 909  
 QY 532 LYRALITPVNROLRDHNNNLKRTHSVSRHLEPLYYLAKSEVYHFKLVLKRLHQI 591  
 DB 910 ---OLDSSVSP---AFHLR-----HLRLRLVLDLHTSFI 937  
 QY 592 ---DGPRLSLMLRYLSFSGNFDVPEICRLMLQPIYGRPSRSDIIIFAEELWE 648  
 DB 938 MKVDSLNLNLCMLNHRYSIDTQVKY-LPLFSNLMNDESLEFSTNRS-LIVLLPRLD 995  
 QY 649 LMLRLHLKLP--RFLYLPDPSGVDRGRHLDFSNLQITISYL--SPRCCCKEYIMQVAK 704  
 DB 996 LKRLVSLVADACSFDMADDE-SILLADTKLENRIITELLISVSKTKNFKRFPMLQ 1054  
 QY 705 KLGISGNKDYKSFSDSGLPNNLYVLQLELISLISVDYSLPLVISSAKA----- 755  
 DB 1055 LLSFE-LKESMDYSTEQHFSLELDFLETEL---SVGFKSSNTNDSSSVATNRPMDFH 1110  
 QY 756 PRATLAKKLKLEKTYLSWSLIDLIAPLPLNLEVLKMDDACCGEEMPIYMG-----FNRLK 811  
 DB 1111 FPSNKLITLRLREFPLTSDLSFIARLPNLEELSLYHTIIHGEWN--WGEDDFENLKE 1167

QY 812 LLIKSLFKWKAINDNPEVLERMIRSKNKEIPFIEADITLQLELRECPKLGES 871  
 DB 1168 LNFNVYSIKWEVEGSEFSFPLEKLRGCHKLEIPPSFEDIYSLSKSIYV-SPLEDS 1226  
 QY 872 AARIQKQEDL 882  
 DB 1227 ALKIKVEYEDM 1237

RESULT 5  
 US-08-947-823-5  
 ; Sequence 5, Application US/08947823  
 ; Patent No. 6114605

GENERAL INFORMATION:  
 APPLICANT: Williamson, Valerie M.  
 APPLICANT: Kaloshian, Isghoul  
 APPLICANT: yaghoubi, Jafar  
 APPLICANT: Bodeau, John  
 APPLICANT: Milligan, Stephen  
 TITLE OF INVENTION: Procedures and Materials for Confering  
 TITLE OF INVENTION: Pest Resistance in Plants  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/947, 823  
 FILING DATE: 09-OCT-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US97/18802  
 FILING DATE: 09-OCT-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/028,191  
 FILING DATE: 10-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bastian, Kevin L.  
 REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 023070-0702100S  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1257 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-947-823-5

Query Match 17.6%; Score 828.5; DB 3; Length 1257;  
 Best Local Similarity 29.5%; Pred. No. 4.3e-67;  
 Matches 288; Conservative 147; Mismatches 317; Indels 223; Gaps 41;

QY 13 IESLITNSPMQISCHREELCALREKVSLEVFVKNEKNNVFGEMT-----DFEVE 66  
 DB 398 LNDLDSNAYSISL---KEET---ELVSOELFTRSF---FDDAAEQGLKDIAR 445  
 QY 67 VREVASAEYTIQ---LRLTGV-----LGENKSQKKARRRFRKSLQGVADMDHIMRE 118  
 DB 446 VLDVAYAKVDYDSIIVRNGLHLIFSLPTITIKIKIKIEETISALDENIPKDRGLIIVN 505





```

Db      532 DGGFEKLPYLYKLEDR-----TLPTGSSVNF-----YNPLTKRVNLINILPTLSLRA 581
Qy      584 LELRHRQIDGFPREI-LSLIMLRVLSLFSYGNFNDVPEICRLMNLQTFIVORRSDIIF 642
Db      582 LSLSHKMEELPNDLFIKLKLRLFDISRTNIRKLDPDSICVLYNLETLLSSCKIEELP 641
Qy      643 ABEIMELMOLRLKLPFLPDCPSGVKGRHLPDSNLQTSISYSPROCTKEVINGION 702
Db      642 QME--KLIMLRHLDISNTHLMKP-----LHLSRLKSLQVL---VGAKFLVGNR 686
Qy      703 VKKLGISGN-----KDYKSPRDSGLPNNLYLQLEILSLSYDS----- 744
Db      687 MDLDEAGQALYGSLSVYKLENNVDREAVKPKRKRENNHVEQLSLESEISADNSQTERD 746
Qy      745 LIPVI-----ISSAK-----APATLKKLLEKRYLSMSY-LDIIAELPNE 785
Db      747 ILDELPRKNIQEVKIIIGRTNFPNMVADPLFLKLVKLSLNCDCYSLPALGQLPCLK 806
Qy      786 VLKL-----MODACGGEWHPIVNGFNKLKLLK 815
Db      807 FLVSGMGHGRVYVEEFYRLSSKKEPNCLEKLEFEDMTKQWALGIG----- 856
Qy      816 YSLFKWKATNDFPYLERLMIRSCNKLK-EIPIEFADIIHTLIQLRECP 865
Db      857 -----EPFLKLSIINCPELSLEIPIDPS---SLKRFVFGCP 892

```

RESULT 7  
US-08-930-996A-2  
Sequence 2, Application US/08930996A  
Patent No. 6100449

```

GENERAL INFORMATION:
APPLICANT: FIDHR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSPORTATION AND
TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1220 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-996A-2

```

Query Match 13.1%; Score 617.5; DB 3; Length 1220;

```

Best Local Similarity 23.9%; Pred. No. 1,le-47;
Matches 249; Conservative 165; Mismatches 277; Indels 353; Gaps 48;
Qy      42 SSLIEFVKNFEKN---NVFGEWTEDEVREVAEAETITQRLTGVLGENKSOKKA 97
Db      14 SALNVLFDRLAPNGDLLNFRKHTD-DVELEFKIGDILSLQVLSD---AEKKASNOF 69
Qy      98 RRRFROSLOQVAEDMHKE-----STKIDKGQVSKESLY--HDF-----SSST 142
Db      70 VSGWLKRLQTVADAENLELVYNEALRLKLVETSNOQVSDNLCLSDDFPLNKKLEDT 129
Qy      143 NDILKAKNNMVGK-----DDQ-----RKQLLEDLT--RSYSGEKP 175
Db      130 IKKLEVLKQIGRLGKLEHFIETKQETRPSPSLVDSGIFGKKNLEMLVGLSLMDRK 189
Qy      176 ----VIPIVGMGIGKTTLAKEVYNDESILCRFDVHANAATISQHNKKEILGLH--- 227
Db      190 RKNLAVPPIVGMGIMGKTLAKAVYNDEYOKHFGILTAMFCVSEAYDARIPKGLQETG 249
Qy      228 -STIKMD-----RYKMGIEAELADK---LOSLKRRFLIYLDIDISGEV--WDGVRG 276
Db      250 STDLRKADNMLNQLVAKADNINQLVAKLEKLNKRFVLVLDVWNNYPERMDLRNL 309
Qy      277 FPLEDNAGSRILLTTRNDEVACVGNFSLRSMFMDDESNLSLK--SAFSSSEALPYE 334
Db      310 F-LQDIGSKIIYVTRKESVALM--MDSGAIYWGILSDESNALFKRHSLEHDKPREHE 366
Qy      335 FEIVGKQIDEGHGLPILTVVAGLLSKRTIEDMTYAKDVKSFTYNDPDECSR----- 390
Db      367 FEIVGKQIDEGHGLPILTVVAGLLSKRTIEDMTYAKDVKSFTYNDPDECSR----- 421
Qy      391 VGLSYDHLTSDTKTLHFGIPEDSDIPVKNLMSMAEGFLKLENDLEGEVEKLOE 450
Db      422 ALMLSTNDLPALHKLQCLACATIPKDYORKBEVHIMLANG-----LYHOFHSGNOY 474
Qy      451 LVDRCLVLVSKNSRDGKTRSCKVNDLYDLVREYORENIFMNDIYLDVSTPECSTYC 510
Db      475 FLE-----LRSLFEMASEPSEEDVEE---FLMHLVLDLQDIASSNHC 516
Qy      511 MKMKQPFKVTGDEINVCYGLYRALLTPVNRQLRHDNNNLKR--THVSFSE---HLE 565
Db      517 I-----RLEDNKSSHMLEGRHMSYSTIGDGEFE 545
Qy      566 PLYVYLKSE-----VVA-----FKLKVLELRHRQIDGFPREI- 598
Db      546 KKLSEKSEQRLRLPTDIQFHYSKSKLRYLHNLPTLSLALSLSHQVLEPLNDL 605
Qy      599 LSLIMLRVLSLFSYGNFNDVPEICRLMNLQTFIVQ--RRRSIIIAEELMQL----- 652
Db      606 IKIKLRFPLDSETSITKLPDSIFVLYNLETLLSCEYLEELPLQMEKILINLRHLDISN 665
Qy      653 -RHLKLP-----RF-----YLPDCPS--GS-----VDK----- 672
Db      666 TRRLKIPHLRLSLKSLQVLVGAFLVGVGRMETIAGAPLWYSLSLLELNNVVDREAVK 725
Qy      673 -----GRHLDFSNLQT---ISYSPROCTKEVINGIONVKKLGISGNK 712
Db      726 AKMKRENNHVEQLSLESEISADNSQTERDILDELRLPH-----KNIKAVEITG-- 773
Qy      713 DDKSFRDSGLPN-----NLVYLQLEILSLISVD--YSLLEY 748
Db      774 ----YRGTFNPNWVADPLFVKLVHLNLRNCKDCYSLPALGQLPEFLSIRGMHGRV 828
Qy      749 I-----ISSAKAPATLKKLLEKRYLSMSYLDIIAELPNEVLKMDACGGEWHPI 802
Db      829 TEEYGRLLSSKPF--NSLVKLFE-----DMPE-----WKQWHTL 862
Qy      803 VMGFNRLKLLIKYSLKFWKATNDFPYLERLMIRSCNKLK-EIPIEFADIIH----- 854
Db      863 GIG-----EPFLKLSIINCPELSLEIPIDPS---SLKRFVFGCP 900
Qy      855 -----TLQLELRCP 865

```



```

0Y 301 GENESELRSPMDQDSWLSLFFKSAASSPALPYEFETVKGQIODECHGJPLTVVAVAGLL 360
Db 275 KESDPEHHRLRDRDESWLLLOKEVYQSGSCPELEDVGFELSKSCRGPLSVYVAVAGVL 334
0Y 361 K-SKRTIEDMKTVYADVKSFVTNDPDERCSRVLGLSYDHLTSDLTKTCLLHFGIFPEDSDI 419
Db 335 KKKTKTLDDSKMAYVEOSLSSORIGSLSEIS-IIGFSYKNLPHYLKPCFLYFGGFLQKDI 393
0Y 420 PVKNLMRSMAGGLKLEND 439
Db 394 HDSKMTKLWVAEEVOANNE 413

RESULT 10
PCT-US95-04589-109
Sequence 109, Application PC/TUS9504589
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Skaskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumiki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04589-109

Query Match 12.0%; Score 565.5; DB 5; Length 429;
Best Local Similarity 32.5%; Pred. NO. 1.3e-43;
Matches 143; Conservative 81; Mismatches 157; Indels 59; Gaps 12.

0Y 26 LSCDREELCALREKVSLEVFVNKNFERNNV-FGEMTDFEVEYREVASAAYTI----- 78
Db 7 LIIDLKHQIESVKEGLLCLRSPIDHFSSEYVHDEACGLIARVSMAYKAEVVIDSCLAY 66
0Y -----QRLRTGYLGEENKSQKKKRRRFRSLOQVADMDHIKKESTKI 122

```

```

Db      67  SHPLMYKYLWISVLENDLKLKLVKVVGECE-----RRNTEYTVAEVA-----KTTTNV 114
OY      123  ODKGQVSKESLIVHDEFSSTMDILKVKNNMYGRDDQKRLLEDITRISYSEBPK--VPIYV 180
Db      115  -----APFSAYTQ---RANDEMGCFDDTIDELDKL---LGGSPELDVISIV 156
OY      181  GMGIGGCTTLTKEVYNDLSICRFDYAHAMATISQHHKKETILGLHSTTKMDRVMIG 240
Db      157  GMPGIGKTTLLAKITYNDEPVSREFDVAQCVYVLYSMRELLITLIDVLEPSPDRNEK-E 215
OY      241  EAEIADMLQSLKRRKRYLIVLDIWCSEWMDVGRCPPTEDNAGSRILLTTRDEVAACYA 300
Db      216  DGEIADDELRRFLTKRFLITLIDVDYDKWMNLCCMCFSDSNR--SRITLTRLINDVAEYV 274
OY      301  GVENSTLMSMTDDQESMLFKSAFSEALPYEFENVGKQIADCEHGLTLTVVAAGLL 360
Db      275  KCESPHHRLRFRODESWTLQKVEFGQESCPPELEVGFEISGGLPLSVLVAGVL 334
OY      361  K-SKRTIEDWKTVAADKVSFVTNDPDERCKSVLGLSYDHLTSDLKTLHFGJFPEDSDI 419
Db      335  KKKKTLTDMKVVGVSSQRIQSLESIS-IIIGSYKNLPHYLKPFLYFGFGLGKDI 393
OY      420  PYKNLMSRWMAEGFLKLEND 439
Db      394  HDSKWTKLWVAEEFVQANNE 413

RESULT 11
US-08-930-996A-8
Sequence 8, Application US/08930996A
Patent No. 6100449
GENERAL INFORMATION:
APPLICANT: FLUHR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 920 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-996A-8

```



```

OY 470 RSCKVHLYLVCVREVORENI-----FIMNDI-----VLVY 501
| | | | | : : : : :
DB 700 DSCKVHLMMDIAISKSTEENLVREVEGSAVIGHAIRLAISSNMKGDKSEEGIVDL 759
OY 502 SYPECSYLCMYKQPKRYTGDENICPGY---LYRALLTPVRQRLDHDNNMLKRTHS 558
| | | | | : : : : :
DB 760 S--RIRSLSLF-----GDMKPFYVYGMKMFIRVLPECTRGLEYHHLDDIWKINHL 808
OY 559 VFSFHLPEPLYV--LKSEVYHFKLVLELRHNOIDGEPREILSLIWLRTLSFSYGNF 616
| | | | | : : : : :
DB 809 KF-LSRGCTRIDLPDLGNLRLOLMDIRGTIVYKALPRTIITKLOKLOTIHAGKRTDY- 866
OY 617 VPEICRLMNLQTFIVORERSIIIFA---EIIWELMOLRLKLPB-----FYLP 663
| | | | | : : : : :
DB 867 -----VWEKHSIMQRCRKVCATCCCLPLCEMYGPLHKLARQAWAFACCKVP 919
OY 664 DCSG-----SVKG-RHL-DFSNLOTISYSPRCCKEYIMGIONAKKLGISC-NKD 713
| | | | | : : : : :
DB 920 SMTGVHEEGAMVPSGIRKLDHRLNINVRGNALINDIGM-LTGLHKLGVAGINKK 978
OY 714 DYKSPDSDGLPNLVYLOOLEILISY-----DYSLLP-----VIISAKAP 757
| | | | | : : : : :
DB 979 NGRAPFLA-----ISNLKLESISVSSAGMPCGCCLDLISPENLOSLIKYSLKTL 1033
OY 758 ATLK-----KLEERTYLSWS--YLDIAELPNEVLKIMDACCGEWH--PIVMGFN 807
| | | | | : : : : :
DB 1034 EWIKELQHLVYKLVSTRLLEHDVAMEPLGELPKVEIIV--SPFKSEIHFEPQGTG 1091
OY 808 RLKLLIKISFL--KFKATNDNPFVLERLMTRS-----CNKLEPIER- 850
| | | | | : : : : :
DB 1092 FVSLRVKLKLAGIMGIVSEEGTMEPLERLOVGRILEMEIGFSGLEFONINEVOLSW 1151
OY 851 -----ADHITLOIELRECPKIGESARQKOEOLGNP 886
| | | | | : : : : :
DB 1152 FPHDHRIRAAAGADYETAMEEVOEARRKGELKKRI--REOLANP 1199

RESULT 13
US-09-004-838-12
Sequence 12, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmere, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

```

```

; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 784 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY:
; LOCATION: 1..784
; OTHER INFORMATION: /note= "RLG1B amino acids"
US-09-004-838-12

Query Match
Best Local Similarity 25.3%; Pred. No. 6.1e-35;
Matches 196; Conservativity 138; Mismatches 276; Indels 164; Gaps 37;

19 FNSP-MOSLSCDH-REELCALREKVSLEVFVKNEFK--NNVFGEHTDFEVEYEVASAA 74
| | | | | : : : : :
DB 73 FOPIIHTYCSHRSISLXMAEILGS-AFFAVFEKLASEALKRVAACSVIDKELEKN 131
OY 75 EYTIOLRLGTIVGENKSKQ--KKAARPROSLQOVAEDMDHMKRE-STKI-----QD 124
| | | | | : : : : :
DB 132 SSXINIK-----ALLNDASQKEISKEAVKEMWLNQHLPYOIDDLGLDGLATKAIHRKFS 187
OY 125 KGRQVSK-----ESLVHDFSSTINDILKVKNNM----- 152
| | | | | : : : : :
DB 188 YGATINKVRKRLIPSCFSSSSTMRNKKIHNTSKLOELLERNNNLICEIGESRKLNRK 247
OY 153 -----VGRDOORKOL-----EDLTRSYSGEPKVIPIYMGIGIKTTAKERYND 197
| | | | | : : : : :
DB 248 SETSXLDPSSTVGRTRDKKALLKLYEPCDRNFS-----IIPYMGKGLDKTTIGRLITDX 303
OY 198 ESILCRFDVAMATISQOHNKKEILLGLHSTIKMDRYKMGIEALADW-----LQKS 251
| | | | | : : : : :
DB 304 MQVKDHFELKAWCVSDEDF--IFGISKTIPESIEG--GNGEFKDLNLQVALKEK 355
OY 252 LKKRRLIYLDIDWSECV--WDGVRRCFPREDNAGSRILLTTNDEYACAGYENSLSM 309
| | | | | : : : : :
DB 356 ISKRRLVYLDVWSESSTYDTEILLERPF-LAGAPGSKVIITTRKLSLNLQGLDQ-POY 413
OY 310 SFMDODESWSLFKSAF-----SSSEALPYEFETVQKQADECHGLPIYVVAAGLKSRT 366
| | | | | : : : : :
DB 414 SDSLHNMALSLFQAHAFVYNSPDSHPRI-LKPHGEIVKCDGLPIALIALGRLLTRKRD 472
OY 367 EDKRTYAKDVKSFTNDPDERCSRVLGSLYDILTSKTCLLHFGIPEPDSDIIPVKLMR 426
| | | | | : : : : :
DB 473 EEWKELINS-ELIWLGRKDE-IIPXLRLSYNDLSASLKFAYCSLFPKDYFNKREKLI 530
OY 427 SMMABEFLKEN--DLGEVEKCLQELVDRCLVLYSKSRDQTKRSCVHDLIYDLCV 483
| | | | | : : : : :
DB 531 LWAABEGLFHNENTKSMERLXLEYFDLLSRSEF--QHALDKSL--FVVDHLMNDLAT 585
OY 484 REYORENIFIMNDIYLD-----VSYPECSYLC-----MYK-MQPKRYTGDENICPGLYR 534
| | | | | : : : : :
DB 586 SYA--GDYFLRLDIEKKKALEKRYHMSFVCSBYMYKKFPEPKGAK-----KLT 634
OY 535 ALITPVNRQLRDHDNNMLKRTHSVFSFHLPEPLYVYKAEVYHFKLVLELRHNOIDG 594
| | | | | : : : : :
DB 635 FLAMPV-----GMK-----SWTFYLS--NKVLDLDELRLPLRVLSYSLSIKEV 679
OY 595 PREIISLWLRKLSLFSYGNFVYPRICLMLNQTPI-----YQFRSDIIIFAEIWE 648
| | | | | : : : : :
DB 680 PETIGNLKRLRYLNSHISITHIPENVCNLYNQTLILCGCFITKFPNNFL-----K 732
OY 649 LMQLRLKLPREFYLDPCSGSYDKGRHLDPSNLOTISYSPRCCKEYIMGION 702
| | | | | : : : : :
DB 733 LNLRLHLD-----ISDTPOLKMKSSGIGELKNLHILTS-----KLIIIGEN 772

```

RESULT 14



CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2904  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent Release #1.0, Version #1.30B  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/310,912A  
 FILING DATE: September 22, 1994  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/227,360  
 FILING DATE: April 13, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Leach, Karen F.  
 REGISTRATION NUMBER: 35,238  
 REFERENCE/DOCKET NUMBER: 00786/254001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 100254  
 INFORMATION FOR SEQ. ID NO. 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 885 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-310-912A-2

Query Match 9.3%; Score 440; DB 2; Length 885;  
 Best Local Similarity 22.6%; Pred. No. 1.5e-31;  
 Matches 220; Conservative 171; Mismatches 357; Indels 226; Gaps 42;

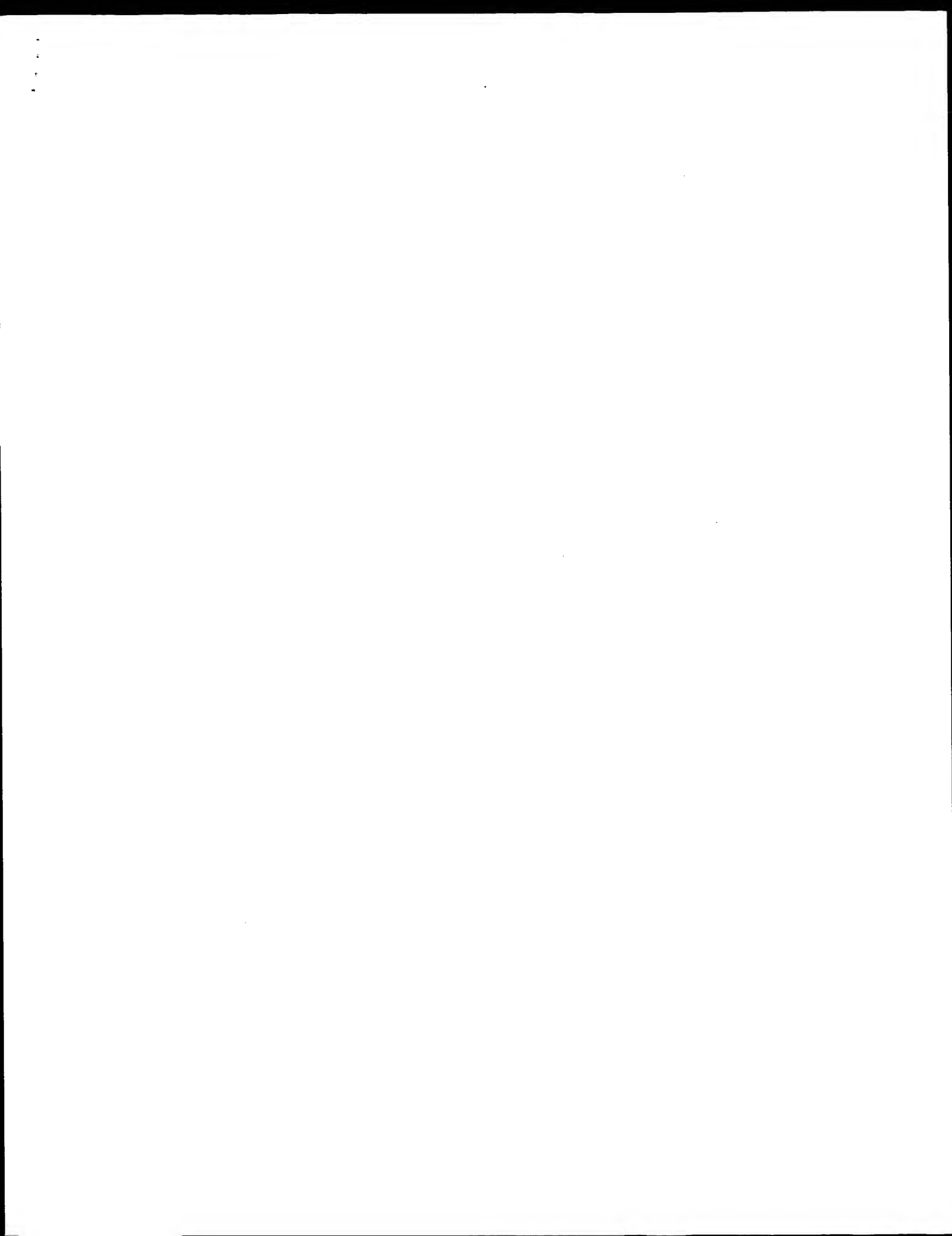
QY 23 MSLSCDHEEELCALREKVSLEVFVKNFEKNVFGEMTDFEVE-----VREV 70  
 DB 12 ISLLIVGCAQVLC-----ESMMAERGHKTDLRQAITDLRIQDDGLEGRSCSNRAREW 65  
 QY 71 ASAEYTIOLRLGIVLGENKSSQKKARRR-----RQSLQOVAEDM 112  
 DB 66 LSAVQYTERKTALLRFRRRRQRTMRRRRYLSCFCADYKLCKKVSATLKSIGELERS 125  
 QY 113 DHMKESTKIQDKGQVSKESLVHDFSSSTNDILKYNMNGRDQKQLEDLTRSYSG 172  
 DB 126 EAIKTGGSIQVYCRREIPKS-----VGNNTTMEQVLEFL--SEEE 165  
 QY 173 EPRVIVPGMGIGIKTTTAKVEYNDESIL--CRFDVHAMATISQOHKKEI-----LLG 224  
 DB 166 ERGIIVGPGVGKTTLMQST--NNELLITKGHOYDVLIVQVMSRREGECTIOAAGARIG 224  
 QY 225 LHSSTIKMDRVKMGIEAELADMLQSLKRRKRYLIVDDIMSCEVWD---GVRRCFPT 280  
 DB 225 L-----SMDE--KETGE--NRALKIYRALROKRPILLDDVM--EEIDLEKGTGPR--PDR 272  
 QY 281 DNAGSRILLTRNDEVACAGVNFSLRMSFMDQDESMSLFKSAAFSSAL--PYEFETYG 339  
 DB 273 ENK--CKVMFTTRISIALCNMNGAE--YKLRFVLEKKHAWELFCSKYWRKDLSSSITRLA 330  
 QY 340 KQIADCECHGLPLTIVVAGLTKSKRTIEDMKTVAKDKSVFVNDPDER-----CSRVLGL 394  
 DB 331 EIVVSKCGGLPLALITLIGGMAHRETEEMIHASE-----VLTFRPAEMGMNVFALLKF 386  
 QY 395 SYDHLTSD--LKTGLLHFGIFPEDSDIPVKNLMKSMABGFLKLENDLEGEVER---CLOE 450  
 DB 387 SYDNLESDDLRSQFLCALFPEEHSEIEQIIVEYVWGEGLTSSHG--NTIYKGYFLIGD 445  
 QY 451 LVDRCLVYSKRSDGTKIRSCVHDLIYDLCVREYQRENIFIMNDIYL---DVSYPECS 507  
 DB 446 LKAACLL-----ETGDEKTOVMKHNHVSFALMAASEQGY--KELLIVPSMGHTAP 497

QY 508 YLCMYKMQPEKRYVNGDELINCPYGLYRALLFPVNRQLRDHDNNNLKRTSHVSEFHEPL 567  
 DB 498 KAENMRQALVLSLDNKRIGTLPEKLCIPKLTLLMLQ-----QNSLKRITGF----- 545  
 QY 568 YVVLKSEVHERKLKVELLRHROIDGPPREILSLIMRLYSLFSYGNFDVPEICRLMNL 627  
 DB 546 -----FMHMPVLRVIDLSTSTETELPLSKIVELVYHLSMSGTKISVLPQELGNLRKL 598  
 QY 628 QTFIVQFRSDIIFAEIEMLMQLRHLKLPREYLP--DCPSGVYDKGRHLDPSNLQ----- 662  
 DB 599 KHLDLQRTQFLQTIIPRDALICWLSKLEVLNLYSYAGWELQSFGEDEAEELGFADLEYLEN 658  
 QY 683 -----TISYSPRCCTGEVIMGI-----QNYKKLGISG 710  
 DB 659 LTTGIGIVLSELTIKTLPERGALHKKHQHLHVEECNELTYFNLPDLTNHGRNLRRLSIKS 718  
 QY 711 NKD-DY-----KSPRDSGLPNNLYVLOLEILSLISVDYSLPYIISAKAPATLKKLKL 765  
 DB 719 CHDELYLVTPADFENDMLPS-----LEVLTLSL--HNLRCINISHC-----NKLK- 762  
 QY 766 ERTYLSMSYLDITAELENLVYKLMQD-----DACCGEEMHYVWG--FNRLK----- 810  
 DB 763 ---NWSW-----YOKLPLKEVIELEFDCREIEELISEHESPSVEDPTLFPLKTLRTDRLP 814  
 QY 811 ----LLIKYSFLKFWKATNDNFVLERLMIRSCKNLKEIPFADITHTQLIELRECP 866  
 DB 815 ELNSILPSRSEFQK-----VETLVITNCPRYKKLP--PQERRTQMNLPYVCEE 861  
 QY 867 KLGESAARIQKEQE 880  
 DB 862 KMKKALEKQDPNEE 875

Search completed: September 12, 2002, 13:57:28  
 Job time: 8826 sec







GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2002, 11:30:22 ; Search time 60.59 Seconds  
(without alignments)  
1435.234 Million cell updates/sec

Title: US-09-864-680-3

Perfect score: 4712

Sequence: 1 MAHASVASIMRTISLTFTN.....PVDVRIISNPKESDSEEH 905

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	980	20.8	1824	2	T07589
2	852.5	18.1	1255	2	T06267
3	828.5	17.6	1257	2	T06269
4	741.5	15.7	907	2	P96617
5	717	15.2	908	2	T48899
6	717	15.2	1384	2	P96573
7	696.5	14.8	831	2	T51185
8	684	14.5	906	2	T48898
9	667	14.2	1240	2	T06404
10	666	14.1	899	2	H96617
11	653	13.9	839	2	B96538
12	652	13.8	835	2	T45590
13	651	13.8	820	2	T51186
14	637.5	13.5	847	2	T12977
15	636	13.5	906	2	G96621
16	618.5	13.1	900	2	G96617
17	614.5	13.0	1220	2	T06403
18	614	13.0	821	2	A86243
19	608.5	12.9	852	2	T08416
20	566	12.0	613	2	T52465
21	547.5	11.6	847	2	T12979
22	540	11.5	695	2	T52429
23	531	11.3	926	2	A57072
24	517.5	11.0	560	2	T52438
25	503.5	10.7	1802	2	T00020
26	484.5	10.3	571	2	T02213
27	473.5	10.0	985	2	T06637
28	458	9.7	967	2	G96637
29	457.5	9.7	919	2	T05746

30	456	9.7	889	2	C86257	resistance to Psen
31	442	9.4	889	2	F96637	hypothetical prote
32	432	9.2	921	2	D86293	F7H2.22 protein -
33	429.5	9.1	909	1	A54809	disease resistance
34	420.5	8.9	885	2	B86257	NBS/LRR disease re
35	407.5	8.6	898	2	E96659	hypothetical prote
36	407	8.6	925	2	H96638	protein T1F9.20 (i
37	406.5	8.6	941	2	B96553	hypothetical prote
38	405	8.6	389	2	T04390	NBS-LRR type resis
39	402.5	8.5	470	2	T52440	PRM1 homolog (limp
40	402.5	8.5	884	2	F96659	protein F2K11.26 (
41	392.5	8.3	483	2	T02226	NBS-LRR type resis
42	376	8.0	855	2	T05981	hypothetical prote
43	375.5	8.0	269	2	T04394	NBS-LRR type resis
44	375	8.0	892	2	T01899	disease resistance
45	374.5	7.9	313	2	T03031	NBS-LRR type resis

## ALIGNMENTS

## RESULT 1

T07589

disease resistance protein Prf - tomato

C/Species: Lycopersicon esculentum (tomato)

C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 11-May-2000

C/Accession: T07589

R/Salmeron, J.M.; Oldroyd, G.E.D.; Rommens, C.M.T.; Scofield, S.R.; Kim, H.; Lavelle,

Cell 86, 123-133, 1996

A/Title: Tomato Prf is a member of the leucine rich repeat class of plant disease res

A/Reference number: Z16032; M0UD:96291405

A/Accession: T07589

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 11824 <SAL>

A/Cross-references: EMBL:065391; NID:g1513143; PIDN:AAC49408.1; PID:g1513144

A/Experimental source: strain Rio Grande

C/Genetics:

A/Gene: Prf

A/Map position: 5

A/Introns: 1437/2

C/Keywords: leucine zipper; nucleotide binding

Query Match	20.8%	Score 980;	DB 2;	Length 1824;
Best Local Similarity	30.9%	Pred. No. 2.4e-51;		
Matches 288;	Conservative 167;	Mismatches 342;	Indels 136;	Gaps 33;
QY	26	LSCDHRELCLARKVKSLEVFVKNF-EKNNVFGEKMTDFEYREVAASAEYTI-----	78	
DB	972	LIIDLKQHSVSKGLCLNSFDHFESEYDEHDEAGGLARVASVMAKVEYIDSLAY	1031	
QY	79	-----QRLTGYLGKNSOKKARRRFRSLOQVADMDHIKKESTKI	122	
DB	1032	SHPLMYKVLMISEVLENIKIKVKNVGETCE---RNRIETVREAVKATYYV-----	1079	
QY	123	ODKGVSKESLIVDFSSSTNDILKVKNNVGRDQKOLLEDTFRSYGEPK--VPIY	180	
DB	1080	-----APSFATYQ---RANEMEGPDDTIDELKDKL--LGGSPELDVI	1121	
QY	181	GMGIGKTTAKVEYNDSESLICRPDVHAMATISQHNKKETLLGLHSTFKMDRVKMG	240	
DB	1122	GMGLGKTTAKKIYNDPEVTSRFDVAQCQVWQLYSMRELLIILNDVLEPSDRNEK-E	1180	
QY	241	EAEIADMLQSLKRRKRLVILDIWSEVMDGVARCPTEDMNGSRILLTRNDEVACYA	300	
DB	1181	DGEIADLRFLTKRPLILIDVWDYKVMNDICMCFSDVSNR-SRIILTRLDVAEYV	1239	
QY	301	GVENFSLRMSFMDQESWLSFKSAFSESLAPFEFTVGRQIADCHGLPLTIYVAVGL	360	
DB	1240	KCSDEPHHLPLFDDDESWITLQKEVFGESCPRELEVGFEISCSGGLPLSVLVAGVL	1299	
QY	361	K-SKRTIEDMKTVAKDVKSFTVNDPDERCSRVLGLSYDHLTSLDKTCLLHFGLFPEDSDI	419	



R:Rossi, M.; Gogglin, F.L.; Milligan, S.B.; Kaloshian, I.; Ullman, D.E.; Williamson, V.M.  
Proc. Natl. Acad. Sci. U.S.A. 95, 9750-9754, 1998  
A:Title: The nematode resistance gene Mi of tomato confers resistance against the potato  
A:Reference number: 215577; MUID:98374252  
A:Accession: T07872  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 52-687, 'E', 689-789, 'L', 791-1103, 'A', 1105-1243, 'E', 1245-1257 <ROS>  
A:Cross-references: EMBL:081378; NID:g3426259; PID:AMC32252.1; PID:g3426260  
A:Experimental source: cultivar Motelle  
C:Genetics:  
A:Gene: Mi-1.2  
A:Map position: 6

Query Match 17.6%; Score 828.5; DB 2; Length 1257;  
Best Local Similarity 29.3%; Pred. No. 2.4e-42;  
Matches 288; Conservative 147; Mismatches 317; Indels 223; Gaps 41;  
QY 13 IESLLTPSPWQSLCDHREELCALREKVSLEFVKFEEKNVGEWT-----DFEVE 66  
Db LINDLSDNNAVSISL-----KEEL-----ELVSGELEFIRSF-----FGDAEGGLYKIDMAR 445  
QY 67 VREYASAEYTIQ---LRLTGV-----LGENKSOKKARRRROSLOQVAEDMDHWE 118  
Db VLDVAAYAKVDYIDSLIYRDNGILHLIFSLPTTIKIKLIKELISALDENIPKIDGLIYVN 505  
QY 119 STKIDGKGVKSESLVHSDSSNDILKYNVNGRDQKOLLEDTREYSEPKYIP 178  
Db 506 SPK-----KPEKRSLLTD-----KL---IVGFEENLNLRLKLT--SGPADLDVIS 547  
QY 179 IVGNGIGKTTTAKVYNDSEILCRFDVHAWATISQOHNKKEILLGLSHSTIKMDRYKM 238  
Db 548 ITGPGSGKTTTAYKYNKDSVSRHFDLRAMCTVQDQDKK--LDDTFSGVSSDS--NL 605  
QY 239 IGEELADMLQSLKRRRYLIVDDINSCVWDGVRCPEDNAGSRILITTRNDEYAC 298  
Db 606 SENIDVADKRLKQLEGRKRYLIVDDVMDTTLDELTRPFP--EAKKGSRIITTYREKEVAL 664  
QY 299 YAGVENSILRSPMDODESMISFSAFSSALPYEFETVYKQIADRGHGLPLTIYVAG 358  
Db 665 HGKLTMPDLRLRPDSWELDKRTFGENSCPELDLDGKELAECKGKPLVADLIAG 724  
QY 359 LL---KSKRTIEDMKYAKDVKSFVNDPDERCSRVLGSLYDHLTSDLTLLHFFGIPE 415  
Db 725 VIGREKKRSV--WLEVOSSLSFLLNSEVE--VMKYTELSDHLRPHLAKPCLLHFAEMPK 781  
QY 416 DSDIPVKNLMSMAEGFLKLENDLEG--EYKGC--LOELVDRCLVLYVSKSRDGTKIRSC 472  
Db 782 DTPLTLILFTVYIGAEFVE--KTEMKGIEEVVKIYMDLISLSLVICFNEIGD---ILNF 837  
QY 473 KVNHLIYDLGVREYORINFI-----MNDIYLVDSYPE 505  
Db 838 QIHDLVDFCLIKARKENLEDRISSAPSDLLPQIITIDDEEHGGLNFVMDSKKR 897  
QY 506 CSYLCMTKMPKFKVTGDEINCPYGLYRALLFPVNRQLRDHNNMLKRTSHVSFHE 565  
Db 898 HSGKHTLSL-----RINGD-----QLDSSVD-----AFHLR 924  
QY 566 PLYVVLKSEVYHFKLVLELRHQI---DGFREIISLWLRKLSL-----FSYGN 614  
Db 925 -----HARLIVLDLEPSLIMVNDSLNEICMLNHLRLYLRITQVKKYLPFSFSN 973  
QY 615 FDVPEICRLMNLQTFVQFRSDIILFAEYIEMQLRHLKLPRLFLLPOPSGSGVKGR 674  
Db 974 -----LWNELESFVSN--KGSITVLLPRLIIDLVLKRLV-----SVACS 1010  
QY 675 HLDPSNLQITISYSPROCTEVINGIONVKKLG---ISGNKDYKSFPSDGLPNNLYLQ 731  
Db 1011 FFDMDADSELIANKD---TK-----LENRLIGELLSYSKDTMNIK--RFRP-----LQ 1056  
QY 732 QLELLSLISVDYS-----LLPYIISAKA-----EPAT 759  
Db 1056

Db 1057 VLOELKESMDYSTEOHWPFKLIDCLETELTCVGFKSSNTNHGSSVYTNRPWFHPPSN 1116  
QY 760 LKKIKLEETYSWSWYLDLIAELPNLEVKIMDDACCGEHPIVWG-----FNRKILLIK 815  
Db 1117 LKELLIDPPLTSDSLSTARLPNLENLSTVDTIIOGEEWN--NGEEDTFENLKLFLNIR 1173  
QY 816 YSFLKFWKATNDNFPVLERLMIRSCNKEIPIEFADYHTTLOLIELRCPPKLGESAARI 875  
Db 1174 LTLTKMEVGESESPFNLEKLOECGKLEIPIPSGDIYSLKFIYIV--SPOLEDSALKI 1232  
QY 876 QKEQEDL--GNNPVDY 889  
Db 1233 KKYAEDMRGNDLQI 1247

RESULT 4  
F96617  
probable disease resistance protein P9K23.8 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: F96617  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alon  
Chun, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Huizart, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shim, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wal, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: F96617  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-907 <STO>  
A:Cross-references: GB:AE005173; NID:g11034963; PID:AMG27118.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F9K23.8  
A:Map position: 1

Query Match 15.7%; Score 741.5; DB 2; Length 907;  
Best Local Similarity 26.8%; Pred. No. 2.9e-37;  
Matches 247; Conservative 171; Mismatches 354; Indels 151; Gaps 30;  
QY 25 SLSCDH---REELALREKVSLEFVKNE--KNNVGEKTDPEVEYREYASAEYTIQ 79  
Db 18 SQCEQFQGVBDQYTLKRLDNLSSFLKADAKHTTAAVVRNVVEIKETIYUADIE 77  
QY 80 LRLTGVYGENKSSOKKARR-----RFSLOQVAEDMDHIMESKTIODKQVSK 132  
Db 78 TYLLAKELIMKISGIMKRRRHACIISDRNAL-----DVGI---KRISD----- 121  
QY 133 SLVHDFSS--STNDILKYNVNGRDQKOLLEDTREYSGE----- 173  
Db 122 -VIRDMQSFVQQAIVDQGYQPOGDROREMRQFFSKYEDDFGLVYNAKGLYLVDE 180  
QY 174 --PKYIPVNGGIGKTTIAKEVYNDSEILCRFDVHAWATISQOHNK---EILLGLHS 228  
Db 181 ENVOVVSITGGIGKTTIARQVNHEDVKHQFRLAVVCSQETRRKNVMQILQNTLS 240  
QY 229 TIKMDRVKMGAEIADMLQSLKRRRYLIVDDINSCVWDGVRCPEDNAGSRIL 288  
Db 241 REKDEIILQW--EAEHLHDKLQLETLSSKLIYFPDIDKDEMDLKIPLFP--PNKGMKVL 297  
QY 289 LTRNDEVACYAGYENFSLRMSFMDODESMISFSAF-----SEALPYEFETVQKQIA 343  
Db 298 LFSQNESVAVAGDIKYLINFKRECLAIEDSWLFRIRAPKPKDASGSKYDEMDMGKML 357  
QY 344 DECHGLPLTIYVAGGLKSKRTIEDMKYAKDVKSFV---TNDPDERCSRVLGSLYDHLT 400  
Db 358 KHCGPLAIVLGLLAAKTYTMDWERTLVNISDSIDIVGRTSNNSIYHVLMSFELP 417

QY 401 SDKTCLLHFGIPEDSDIPYKNTMRSMAGFLKLENDLEGEV-----EKCLOELVDRC 455  
 Db 418 SYLHCEFLYLAHPEPDHINVEKLSYCAAEGLSTADYDNGETIYDVGSGSYLEELVRN 477  
 QY 456 LVLSKRSRSDGTIRSCVHDLYDLCVREVORENIFIMNDIVDVSYPECSYLCMYKM 515  
 Db 478 MI-IWERATASRFGCTGLHDMREVCLEFKAKEN--FLQAVASGVGTSSS-----526  
 QY 516 PFKRVYDGE-----INCPYGLYRALLTPVNRQLRDHNNLLKTHVSFSLHP 566  
 Db 527 -----TGNQSPCRSRRLVYQCPTLH-----VERDINNPKLSLVLVMDHMLAVEN---572  
 QY 567 LYYVLAKSEVAFKLLKVLLELRHROIDG--FPRRLSLIMLRYLSLFSGNNDVPELCRL 624  
 Db 573 -WKLGTSTFTRKLLRYLDLFYVDEGKLPFGIGNLHLKLYLSLQDAKVSHPSS---L 628  
 QY 625 WNLQTFIVQFRRSDI-IIFAEIWEIM-QLRHKLKLP-----REFYLP 663  
 Db 629 GNLMLILYLNLDVDEFLTFVDPVFMHMLRYLKLPLMHKKTRLSRLNLYKLETLVYFS 688  
 QY 664 DCPGSGVDKGRHLDPSNLQTSYSPRCCKEV---IMGIONYKKLGISGNKDDYKSF 719  
 Db 669 TWHSSSKDL---CGWTRMLTALRLTRVTSLETLSASISGLRNLLEYLYVGTSH--KKMR 743  
 QY 720 DSGLPNNLVYLOQLEIILSVDSILPVIITSSAKAPATIKKLERTYLSWYLDIIA 779  
 Db 744 EEGI-----VDFEHLKHLLDLYMPRQOHFSPSLTFYKLESCGLEEDPMPLLE 792  
 QY 760 ELPNLEVLKMDACCCEEMHPIYWGFRKLKL-LIKYSFLPKFKNATNDNPFVLERMIR 838  
 Db 793 KLHLKGYILLKSGCYGRMWCSSGGFPQLKKEIVGLKNKEEVLVBEGSNPLLETISIL 852  
 QY 839 SCKNLKEIPIEPADIHVQLIQL 861  
 Db 853 DCEELKEIPDGLRFTYSLEVLML 875

## RESULT 5

T48899  
 disease resistance protein rpp8 [similarity] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 21-Jul-2000  
 C:Accession: T48899  
 R:Mcowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dangl  
 Plant Cell 10, 1661-1674, 1998  
 A:Title: Intragenic recombination and diversifying selection contribute to the evolution  
 A:Reference number: 224999; MUID:99030193  
 A:Accession: T48899  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-908 <MCD>  
 A:Cross-references: EMBL:AF089711; NID:93901293; PIDDN:AACT8631.1; PIDD:93901294  
 A:Experimental source: Columbia  
 A:Gene: rpp8  
 A:Introns: 293/1; 342/1  
 A:Function:  
 A:Description: susceptible allele of a gene that promotes resistance to Peronospora para

Query Match 15.2%; Score 717; DB 2; Length 908;  
 Best Local Similarity 26.1%; Pred. No. 9.1e-36;  
 Matches 252; Conservative 176; Mismatches 377; Indels 162; Gaps 32;

QY 1 MAHASVASIMRTIESLTFPNSP-MOSLSCHREELCALREVVSLEVFVKNFE-KNNVFG 58  
 Db 1 MAEAFVSGLIEKIMDLRESERLOGID----GQIDGKROLRSLOSLKADADAKKHGSD 56  
 QY 59 EMTDEVEVEREVAASAETIQLRLGTVLGENKSKOKKARRR--FRSLQGVADMDHIV 116  
 Db 57 RVNRFLEVDKDLVDAEDITIESYVNLKSGKGVKKHVRRLACFLDRHRKVASDISEIT 116

QY 117 KEST-----KIDCKGKOV---KESLVHDFSSSTNDILKVNKNVRRDDORKQ 161  
 Db 117 KRISVEIGEMQSGIOQIIDGGRSLSLQERQVRQRIQRTYD--SSSEDLVGEOQYKE 174  
 QY 162 LLEDLRSYSGEPKVPPIVGMGIGKTYLAKERYNDESLCRFDYHAAATISQHNKKEI 221  
 Db 175 LVGHIVE--NDVQVVSIGMGIGIKTTLARQVFNHDLVRRHFDGFVAVCVSQOFTQKHV 232  
 QY 222 LGLHSTIKMDRVKMGIEAEADMLQKSLKRRKRLYLDIDISCEVMDVGRCEPRED 281  
 Db 233 WORLELOPHDGLIDQMEYALQKRLFOLLAEGRVLVLDVWMKEDMDYKAVFPK- 291  
 QY 282 NAGSRILITTRNDVACVAGVENFSLRMSFMDQESWLSFKSAF-----SSEALPYFE 336  
 Db 292 -RGKMKLLTSRNGCVGIHADPTCLFPRASILNPEESMKLCERTVPRPRETEVRLDEME 350  
 QY 337 TVGQIADDECHGLPTIIVVAGLLSKRTIEDMKYAKVKSFTYN-----DPDECS--R 390  
 Db 351 AMGKEWVTCGGDLPLAVKALGGLANKHVPKRVFDNIGSOIVGGSWLDNLSNSVYR 410  
 QY 391 VLGSYDHLTSDKTCCLHFGIPEDSDIPYKNTMRSMAGFLKLENDLEGEVEKLOE 450  
 Db 411 ILSLSTEDLPTHLKHFELMAHPEDESEISTYSLEYMAEGIYD-GSTIEDSGEYLEE 469  
 QY 451 LVDRCLVLSKRSRSDGTIRSCVHDLYDLCVREVORENIFIMNDIVDVSYPECSYLC 510  
 Db 470 LVARNLYIADNVL-SWQSKYCCMHDMREVCLSKAKENFL---QIID--PCT---519  
 QY 511 MYKQPFKRVYDGEINCPYGLYRALLTPVNRQLRDHNNLLKTHVSFSLH-----564  
 Db 520 -----STINQSPSRRLSI---HSGKAHHILGHKNK 549  
 QY 565 -----EPLYYVLKSEVH-FKLKYLELRHROIDG--FPRRLSLIMLRYLSL 610  
 Db 550 TKYRSILVPRFEDYWRISASVFNHNTLRLVLDLSWKEGGLKPSIGGLHLKRLSY 609  
 QY 611 SYGNFVPRPEICRLMNLQTFIVQFRSDI--IIFAEIWEIMQLRHKLKLPFVLPDCPS 667  
 Db 610 EAKVSHLP--STMRMLKLLLYLNLRVDTDEEPIHVPNLKEMIQRLYSPLP-----658  
 QY 668 GSVDRKGRHLDPSNLQTSY-----ISPRC--CTKRYIM 698  
 Db 659 -KMDDTKTELGLVLELYFGFSTGHSSVTDLLRMTKRLYAVLSSECKNEFTYSSIR 717  
 QY 699 GIOVKKLGISGNKDDYK-SFRDGLPNNLVYLOQLEIILSVDSYSLPVIITSSAKAP 757  
 Db 718 ELNLELNLNLEFLERYMVDYMGFEVLDFHILKQGG--LAVRSKLP---DQHGEP 769  
 QY 758 ATLKKLLERTYLSWSYLDIIAELPNLEVLKMDACCCEEMHPIYWGFRKLKL-LY 816  
 Db 770 PHLVHFLIYCGMEEDPMPLLEKLHLKSVRLKAFILSRVCSKSGFPOLCVIEISKE 829  
 QY 817 SPLKFNKATNDNPFVLERMIRSCNKLKEIPFADIHVQLIQL-----RECPPL- 869  
 Db 830 SELEEWIVEEGSWPCRLTTLIDDCKLKELPDGLKLTISLEKLEIKGMKREKKEVLVPG 889  
 QY 870 ESARIQ 876  
 Db 890 EDYKYVQ 896

## RESULT 6

E96573  
 protein f12m16.25 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: F96573  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
 Chin, C.W.; Chung, M.K.; Comai, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marzla

OY    740 SVDYSLPIISSAKAFPATLKKLKLERTYLSNSYLDIIAELPNDEVKLMDDACGEEM 799  
     : | : | : | : : : : : : : : : |

Db 530 ---VKRYSSSEKRN---KRMRSILNFGDNL---VGPDEFYTKLLRVLVDYRL---GPPL 577





```

Db 1--KVEGQHONFSE-----TSNOQVSDPEFLINIKKLEDTLETKDLOEQIGLGLKE 148
QY 137 DSSSTNDLTKKNNMVGDD--QRKQLED-----LTSYSGEP-KYPIYMGIGT 188
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 YFDSKLETRPSTSLDEPDIFGROSETEDLIDRLLSGASGKNLTVPIVGMGSLGT 208
QY 189 TLAKEVYNDSEILCRDYNAMATISQOHKKEILLGLSTTKMDRVMKGEAEALAD-- 246
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 209 TLAKAVYNDESCKNHFDLAKMFCVSEAYNAFRTKGLQE-----IGSIDLVYDN 258
QY 247 -----MLOSKLRKRYLLVDDIW--SCVWDGVRRCPTEDMAGSRILLTTRNDVAC 298
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 LNOQVYKLEKEREKKEKFLIVLDVYNDNENWDELNRNF--YOGDLSKLIITTRKDSVAL 317
QY 299 YAGVEFSLRMSFMDDESNLSFKSAFSS-EALPY-EFEYVQKQADCHGIPLTIYV 356
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 318 MKNQDQIS--KGNLSTEASMSLFQRIAFENMDPMGHELEEGROIAACCKGIPALAKTL 375
QY 357 AGILSKRTIEDMKTVAKVYKSFVNDPDRCSRYLGSDYHLSDTKCLLHFGIFEPD 416
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 376 AGMLSKSFEVERKCI--LRSEIMELRNDLIPALMLSYNDLPALKKCFSCAIFPKD 432
QY 417 SDIPVKNMRSMABEGFLKLENDLEGEVEKLOEVLDRCLVYKRSRDTGTRKSCVAD 476
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 433 YPFRKQVILHMLANGLVVEDEI-----IQDLGNQFLELSSRS----- 472
QY 477 LIYDLCVR--EYQRENIFIMNDIVLVSYPECSYLCMTMOPPKRTGTGEINCPYGL-Y 533
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 473 -LFEVRPNPSEGNIKELFLMHDLVNDLQALASSKLCIRLEESOGSHMLQCRHLSYSGY 531
QY 534 RA--LLFPVNR--OLRDNDNNLLKRTSHVPSFHLDEPLYVYKSEVVA-----FKLLV 583
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 532 DGFPEKLPYLYKLEQUR-----TLPTGSSVNF-----YNPLTKVYLNILPTLRSLEA 581
QY 584 LELRRHQIDGFPREI-LSLIMLRYSLSFGNFDVPEICRYLMNLOTPIVORRSDIIF 642
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 582 LSLSHKMEELPNDFIKLRLFLDISRTNIKRLPDSICVLYNLLETLLSSCKLEELP 641
QY 643 AEIEMELMOLRLKLPFLPLPCPSGVKGRHLDPSNLQTSIYSLSPPRCTEYVINGION 702
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 642 QME--KLIMRLHLDISNTHLAMP-----LHLSRLKSLQVL---VGAKFLVGVR 686
QY 703 YKLLISGN-----KDYKSPRDSGLPNLLYLOQLLETLSLSDVS----- 744
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 687 MEDLGEAONLYGSLVYKLENNVDRREAVKPKMKREKNHVEQJLSLENSSEISADNSQTEPD 746
QY 745 LILPVI-----ISSAK-----AFPATLKKLLETTYLSWSY-LDIIAELPNLE 785
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 747 ILDELRLPHKNIGEVKIGRTNFPWVADPLFLKLVKLSLNCKKCYSLPALGOLPCK 806
QY 786 VLKL-----MDACCGEWHPIYMGFNRLKILLIK 815
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 807 FLTVSGMGIRVYTEEYGRSLSSKRPNCLEKLEFEEDMTKQWMAHLAGI----- 856
QY 816 YSLKFWKATNPNFVLERLIRSCKNLK-ELPIEADHITOLIELRSCP 865
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 857 -----EPPLLEKLSIINCPELSLELPDPS--SLKRFVREGCP 892

```

RESULT 10  
H96617  
probable disease resistance protein FRK23.6 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: H96617  
R:Theologian, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: H96617  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-899 <STO>  
A:Cross-references: GB:AE005173; NID:g11034973; PIDN:AG27128.1; GSPDB:GN00141  
A:Gene: FRK23.6  
A:Map position: 1

Query Match 14.1%; Score 666; DB 2; Length 899;  
Best Local Similarity 25.5%; Pred. No. 1,1e-32;  
Matches 234; Conservative 184; Mismatches 376; Indels 124; Gaps 29;

```

QY 32 EELCALREKVSLEEVKKEKNNVFGEMTDFEV-EYREVASAEYTIQLRLGTVLGEN 90
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 27 DQVTELKSNLNLKSLFKDADAKKHISEMVRHCEVEIKDVIYDIEDIET----FLIKK 82
QY 91 KSKK--KARRRROSL--QQVAEDMDHIMKSTKIDCKOVSKESLVHDFSSTND 144
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 VEMKRGIMKRIKRFASITIMDRRELASDIGISKRISKVIQDMOSFVQOITIDGSSSH 142
QY 145 ILK-----VKNNVGRDDQKQLEDLTSYSEPRVPIYVGMGIGTTLAK 192
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 LDRORERMTTESRDSSENFVGEANVKKLVGLVE--KDDYQIVSLTGSGIGKTTLLAR 200
QY 193 EYVNDSEILCRFDYHAMATISQOHKKEILLGLSTIKMD--DRVMKGEAEALADMLOR 250
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 201 QVFNHDVAVDRFGFAMVSVSQEFTRIYVQOTILOMLTSERKDELONMKEADLHDLFR 260
QY 251 SLKRRRYLLVDDIWSCEVWDGVRCPPTEDNAGSRILLTTRNDVACVAGVENSILRMS 310
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 261 LLESSKTLIVLDIWKEDMDLIKPIFPKP--KGVVYLLTSRSTESIAMRDTYIYFSPK 318
QY 311 FMDQDSWGLFSAF-----SEALPYEFYVQKQADCHGIPLTIYVAGLTKSKRT 365
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 319 CSTIPSWTLFOSIAMPKRDTSFKEDEEMNKKMKIKGGLSLAVKYLGLLAKATY 378
QY 366 IEDMKTVADVASFV--TNDPDRCSRYLGSDYHLSDTKCLLHFGIFPDSIDPIVK 422
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 379 LHMKMLSENIGSHYERISGNNSIDHVLVSFEELPNTLKICFLXAHFPEDHEIDVE 438
QY 423 NLMRSMAEGFLKLENDLEGEV-----EKLOELVDRCLVLSKRSRDTGTRKSCVAD 477
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 439 KLHYWAAEG-ISERRRYDGETITROTGDSYIELVRRNMY-ISERVMTSRFEYTCRLHDM 496
QY 478 IYDLCYREVQRENIFIMNDIVLVSYPECSYLCMTMOPPKRTGTGEINCPYGLYR--A 535
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 497 MREICLFKAKEENFLOIVSNHSPISMPQ-----TLGASRRVY 533
QY 536 LITPVNROLRDHNDNNLLKRTSHVPSFHLDEPLYVYKSEVVAHKLKLVLELRHQIDG-- 593
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 534 LHNPTLHVERKKNKPKLSLVYVYDDIGNRRMLSGSIFTRKLLRVLDIYVAKKGGK 593
QY 594 FPREILSIWRLYLSFGNFDVPEICRYLMNLOTPIVORRSDII-IFAEEIW-ELMQ 651
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 594 LPSDICKLHLRLYLSLDAKAVSHLPSS--LRNLVLLIYDITDPTDIFVAVFMGMBE 650
QY 652 LKHLKPRYRLDPCPSGVKGRHLDPSNLQTSIYLS--SPRCTEYVINGIONVYKL-- 706
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 651 LRYLELPR-----MHEKTKELSLNIEKLEALENFSYSSSLEDLGMVRLFTLYI 701
QY 707 -----GISG--NKDYKSFSDSGLPN-----NLVYLOOLELISLSDY 743
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 702 ILSEGSLOTLSASVGLRHLNFKIMENAGVNRMBEEMVADFTYLLKL-----TLISIM 757
QY 744 SLPLVIISAKAPATLKKLLETTYLSWSYLDIIAELPNLEVLKIMDACCGEENHPIY 803
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 758 PLRPKT-----QHLPSHLVLDISYCLEEDPMPILEKLELKLSDIYLSFSGRKMVCSA 813

```

QY 804 MGFRRL-KLLIKYSPFKMFKATNDNFVLERLMIRSCNKLKEIPFIEADHTIQL-LEL 861  
 DB 814 GGFQQLKRLALDEBEMBEWIVBEGSMRSLHTLSIWS-STLKELPDGLRFLYSLSKNIIMG 872  
 QY 862 RECPKLGEASARIQKQ 879  
 DB 873 KSMWERLSERGEFFYKVO 890

## RESULT 11

B96538  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: B96538  
 R:Phenology: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Hultzer, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,  
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719  
 A:Accession: B96538  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-839 <STO>  
 A:Cross-references: GB:AE005173; NID:95734781; PIDN:AAD50046.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F1413.19  
 A:Map position: 1

Query Match 13.9%; Score 653; DB 2; Length 839;  
 Best Local Similarity 24.9%; Pred. No. 6,4e-32;  
 Matches 234; Conservative 175; Mismatches 317; Indels 214; Gaps 34;

QY 1 MAHSAVSLMRTISLTFNSPMOSLSCHREELCALREKSSLEVEFKNF-EKNVNGE 59  
 DB 1 MAEIVSVTVKIQOLL-LEPFLFPGIG--DQYKQLODELKRLNCFLKADDEKQHEER 57  
 QY 60 MTDEVEVEVSAEYTIQRLTGLTVLGNKSK--KKARRF-----RSLDQVAD 111  
 DB 58 VRNNAVIGIREASDAEDLEAF--LKAESRKQKGMKRVRLRACILNEAVSHSVGE 114  
 QY 112 MDHIVKSTKIQ---DKGKOVSKESLVHDFSSTNDILK-----VKNMVGRDQ 158  
 DB 115 IREITSRLSKIAASMLDFG--IKESMGR-GLSLSDLSLRQKQSPFYVVEHNLVGLSOS 170  
 QY 159 RKOLEDLFRSYSGEP-KVPIYVGSGIGTKTLAKEVYNDESILCRFVHMATISQ--- 214  
 DB 171 LEKLVNDLVS--GGEKLRVTSICGSGIGTKTLAKQIFHHKVRHFRFAMVYSQDR 228  
 QY 215 -QHNKEILGLSLSTKMDRVKMGAEADLMLOKSLKRRVLYLVLDIWSCEVMDGV 273  
 DB 229 RRVHMODIFMLYSK--DENQRIILRDEQGEELHFRFLKRNKCLIVDDIMGKAMCCL 286  
 QY 274 RRCPTEDNAGSRILLTRNDEVACYAGVENFSLRSMODESUSLFKSAFSE----- 329  
 DB 287 KHVPRHE--TSEIILTRNKEVALYADPRGVLEHPOLLTCESSELLEKISLSGRENI 344  
 QY 330 -ALYEPFETVGKQIADDECHGLPLTIYVAVGLKSKRTIEDMKTYAKDVKSFTVNDPDR 388  
 DB 345 PMLVKKMEIKQIVRGGGLATIVGLATKSTWNEORVCEKSTVNSGSSNG 404  
 QY 389 SR-----VLGLSYDHLSDTKTCLHFGIPEDSDIPVKMLRSMWAEGFL-----KL 436  
 DB 405 SKNNLVADVLTSLYEYLRPHKQCFYFAHPRDEYEVHGLVSCIALGVMVPMKHTEA 464  
 QY 437 ENDLGEVEKCLQELVDRCLVLSKRSRDGTRKINSCKVHLLIYDLCLVREVORENIFIMND 496

DB 465 GTVEVDVQDYLEELVLRKSMVAVGRDITSEVNTCRHNDLMREVCLOKAKOESFVYID 524  
 QY 497 -----IVLDVSY-----PECSYLQMYMOPFKRYTGOEINVCYGLYRA 535  
 DB 525 SRDDEAEAFISLSTNSRRISVOLHGAEEHHSLSQEPERIDKREGTYIIYW----- 580  
 QY 536 LITFVNRLRDHNNMLKRTHSVFSPFLPELYLVKSEVNFILKLYELRH-RQIDGF 594  
 DB 581 -----KLKYDVDSLVRERATVYSKHLDP-----KTK-----LDLSTLRNLQQLMDF 622  
 QY 595 -----PREILSLWRLYLSFGTGNEDVPEICRLMNLQFFIYOREFSDIITAEETWE 648  
 DB 623 PVGKNCPMDILAMTSLRSLTI-----NLSS-----QNTDFVAVVSSLSKV 661  
 QY 649 IMOLRHLKLPFYLIPDCGSSVNDGRHLD-PSNLOTISYLSPPCCTREVIQGVKLG 707  
 DB 662 LKRLGLTINVPCEPMLP-FYDVTQVLSAFTNL-----CELEFLKLEK----- 704  
 QY 708 ISGNKDYKSPRDSGLPNNLYLQOLEILSLISVDYSLPVIYISSAKAPATLKLKER 767  
 DB 705 -----LPGE-----QSFSSDLGALRLMQ 722  
 QY 768 TYLSMSTYDITAEIPNLEVLKLMDA-----CGEEMHPIYMGFNRLKLLIKYSFLKF 821  
 DB 723 GGLVDDPFWLEKLPNKLILQLEFSGSEVSKLCSK-----NLNLEE 765  
 QY 822 WKATNDNFVLERLMIRSCNKLKEIPFIEADHTIQLLEL 861  
 DB 766 WTVEGAMMRLVYELKCNKLSVPESTRFLKNQVEI 805

## RESULT 12

T45590  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 31-Mar-2000  
 R:Chromosome, N.; Robert, C.; Brothier, P.; Winkler, P.; Cattolico, L.; Attiguenave, F.;  
 submitted to the Protein Sequence Database, December 1999  
 A:Reference number: 223008  
 A:Accession: T45590  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-835 <CHD>  
 A:Cross-references: EMBL:AL133314  
 A:Experimental source: cultivar Columbia; BAC clone F12A12  
 C:Genetics:  
 A:Map position: 3  
 A:Note: F12A12.50  
 C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein rep

Query Match 13.8%; Score 652; DB 2; Length 835;  
 Best Local Similarity 25.2%; Pred. No. 7.4e-33;  
 Matches 235; Conservative 164; Mismatches 314; Indels 220; Gaps 36;

QY 31 REELCALREKYSLEVEFKNEKNVFGEMT-----DEVEVEVSAEYTIQRL 82  
 DB 28 KEDLEELTELTCITGVLYKDYAREDEVEKSKVLVDPAVYDEVLD---TYHLKL 83  
 QY 83 TGYVLGENKSKKARRF-----RSLDQVADMDHIVKSTKIQDKGKOVSKESLVHD 137  
 DB 84 -----EERSORGLRLTRNIGRMDAVSIYDDIRILKRLDITRRRETYGIGLEP 137  
 QY 138 FSSSTNDILTKYK-----NNMVGRDQKQLLEDLRLRSYSGEKKVPIYMGSGIG 186  
 DB 138 QGGNGTSLKVRQLRRASVDQEEVYVGLDEDKLLKLEKLNKFTISITFGMGLG 197  
 QY 187 KTLIAKEVYNDESILCRPDVAMATISQHNKKEILGLSLSTKMD-----DRVAMIGA 242  
 DB 198 KTLARAKIYNSRDVKEKREYRAMVYVSEYKGTGDIIMIIISLGMTSGEELKIRKFADE 257



A:Molecule type: DNA  
 A:Residues: 1-847 <CHO>  
 A:Cross-references: EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.240  
 A:Experimental source: cultivar Columbia; BAC clone T6H20  
 C:Genetics:  
 A:Gene: ATSP:T6H20.240  
 A:Map position: 3  
 C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 13.5% Score 637.5; DB 2; Length 847;  
 Best Local Similarity 26.5%; Pred. No. 5.7e-31;  
 Matches 237; Conservative 162; Mismatches 311; Indels 185; Gaps 37;

QY 31 REELCALREKVSLEFVKNF---KNVFGEMT---DFEVEVREVAASAEYTIQ--- 79  
 DB 28 KDLLELTTELTCIHGYLKDVEAREDESKETKLVLDIADYEDVDYFVLEERS 87  
 QY 80 -----LRLGTVLGEMKSOQKARRFRQSLQOVAEDMDHIKESTKIDCKQVSKESL 134  
 DB 88 LRRGLRLT-----NKIGKR-----DAYNIVEDIRTLKRRLIDYTRKRETFGIGSF 134  
 QY 135 VHDSSSTNDI-----LKVNNMGRRDQKOLLEDL-----TRSYSGEPKVI 178  
 DB 135 NEPRRENTNVRVROLRAPPVDOELVVGLEDVYKILVLLSDNEKDKST-----IIS 189  
 QY 179 IVMGIGIKTTLAKENVDESLCRFDYHAMATISQHNKKEILGLHS-----TIKMD 234  
 DB 190 IFMGIGIKTTLAKRLYNSGDVYKRRFCRAMTVYSEYKTRDILIRISLGISAEEME 249  
 QY 235 RYKMGIE-AELADLMQSLKRRRIYIVDDIVSCVWDGVRCEFTEDNAGSRILLTRN 293  
 DB 250 KIKMEDEEELVYLYGLLEGKNYVVDVWDPMESLKALPC-DHRSKVIITTRI 308  
 QY 294 DEVACYAVEN--FSLRSPFMDQDESLSKSAFSS--EALPYEFTYVKQIADCHGP 350  
 DB 309 RAIA--EVEGVYVYHAKRLFLFEESWTLFEKAFSNEKEDEDLQRTGKEKWKCGGIP 366  
 QY 351 LTIIVVAGILSKRTIEDMTKTVADVKSFTVNDPERCSRVLGSLYDHLTDLTKCLHF 410  
 DB 367 LAIVVLSGLISRKRT-NEMHEVCASIMRRL-KDINSIHISTVEDLSFKEMRHELCIFLYE 424  
 QY 411 GIEPDSIDIPYKNIMRSMAGFLKLENDLGE-VEKC-LOELVDRCLVYKSRDGT 468  
 DB 425 SVFPEYDIYKVKLHLHVAAGFIOEDEMMEDVARYCIDELVRSIVKMERIERG--K 482  
 QY 469 IRSKVHDLIYDLCVREYORENI-----FIMNDIVDVSPECY 508  
 DB 483 VMSCRIDLDLAIKKAKELNFVNVYNEKQSSDICREYVHHLMNDY-----Y 532  
 QY 509 LCATKMOFPKRVGTDEINCYCYGLRALLTPVNRQLRDHNNNLKRTHSVFSFHEPLY 568  
 DB 533 LCDRRVNV--KRM-----RSFLFIGERGEGYVNTNLK----- 563  
 QY 569 YLKESEVYHFLKLVLELR-----HROLDG--FPREILSLIWLRYLSTFSGNFDVPRIC 622  
 DB 564 -----LKLRYLMEGLLEFVSKNLSNTLPVYIGELHLYRIYGLADTVYSILPASIS 614  
 QY 623 RLWNLQFTIVORFSDIIFAEIEMELQMLHLKLPREFYLPDPCSGSVADKGRHLDPSMD 682  
 DB 615 NLRFLOT--LDASNDPQYVTTDLTKLSLNRH--IGKR-VEGCLIG-----EGVNLQ 662  
 QY 683 TISTLSPPCCCK---EVIAMGIONVKKIGISGNKDYK---SFRDSGLPNNLVLYQ-OLEI 735  
 DB 663 TLRISISSYSKMLHMLRNLDLEIYDHSKMWQDRVPLVFEFSKPKNRVILKEMRN 722  
 QY 736 LSLISVYSLPVIITISSAKAPATLKLKLERTLSWSYLDITAEPLRLEVLKMDACC 795  
 DB 723 FKLSSESRTITGLADVNV--FP-SLESITLVGTLLENSMPLQKLPRLLELVKDCYS 778  
 QY 796 GEEWHPI-VMGFNRLKLLIKYSFLKFWKAVNDNFPVLERIMRISCKKILKPIE 849  
 DB 779 GVKIMTISAGFGRLK-----NLEKSMERGRIGLDLELRIE 813

# RESULT 15

696621  
 Probable disease resistance protein F23H11.10 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: G96621

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
 Ansen, N.F.; Hughes, B.; Hulzar, L.  
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.V.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marzia  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tello  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: Ab6141; MUID:21016719  
 A:Accession: G96621

A:Molecule type: DNA  
 A:Status: preliminary  
 A:Cross-references: GB:AE005173; NID:g5080812; PIDN:AD039321.1; GSPDB:GN00141

A:Gene: F23H11.10  
 A:Map position: 1

Query Match 13.5% Score 636; DB 2; Length 906;  
 Best Local Similarity 24.9%; Pred. No. 7.8e-31;  
 Matches 223; Conservative 178; Mismatches 361; Indels 132; Gaps 32;

QY 32 BELCALREKVSLEFVKNF---KNVFGEMTDFEVEVREVAASAEYTIQ-LRTGTVGE 89  
 DB 34 EOTITLRODLKMLAFSLSDADAKKOTRLARNCELEIKETIYDADITIEFLKGSV--- 90  
 QY 90 NKSQKARRRRRQSLQOVAEDMDHIKESTKI-----ODKQVVS-KE 132  
 DB 91 ---NMRSIACPGGRREIALQITSKRISKVIGQVQNLGKSIDMGVDSHAQLEKR 146  
 QY 133 SLVHDFSSSTINDILVKNMNGRRDQKOLLEDLTRSYSGEPKVIPIYMGIGIKTTLAK 192  
 DB 147 ELRHTFSSES-----ESNLVGLKRVKVELELVGNDSSHG--VSITGLGIGKTTIAR 198  
 QY 193 EYVNDESILCRFDYHAMATISQHNKKEI--LGLSLSTIKMDRVAMIGAEALADMLQ 249  
 DB 199 QIFDHDKKSHFDGLAWCVSOEFTKRDYMTIIGNLSPKTKDSD---LPEDIQKKLF 254  
 QY 250 KSLKRRYLIYLDIVSCVWDGVRCEFTEDNAGSRILLTRNDEVACYAVENFSLRM 309  
 DB 255 QLETKKALIVFDDIMKREDWYRIAMFP--ERKAGWKVLLTSRNDIAIRPHC---VTEKP 309  
 QY 310 SFMDQDESLSKSAFSS-----ALPYEFTYVKQIADCHGLPLTIYVVGALLSK 363  
 DB 310 ELTHDEBCWKLQRIAFSKQTKITGYITDKKEMVAKKMTYHCKRPLAVKLLGLDLAK 369  
 QY 364 RTIEDMTKTVADVKSFTVNDPERCSRVLGSLYDHLTDLTKCLHFGIEPED 416  
 DB 370 HTRQWKILSINIISHIYVGGTSSNENDSSVNVHLSLSPFGLPGYKHLKCLILASYED 429  
 QY 417 SDIPYKNIMRSMAGFLKLENDLGE-----VEKCLQELVDRCLVYKSRDGTKIRS 471  
 DB 430 HEIETERLSYVMAEG--ITYPGNAGATIRVDADLYIELVKRVNV--ISERDALTSRPEK 487  
 QY 472 CKVHDLIYDLCVREYORENIIMNDIVDVSYPCCSYLCKMKMPKRVGTDEINCYG 531  
 DB 488 COLHDLMEKICLLAKKEENFL--QIVTDP-----SSSVHSLASS 526  
 QY 532 LYRALLTPVNRQLRDHNNNLKRTHSVFSFHEPLYVYKSEVYHFLKLVLELRHQI 591  
 DB 527 RSRRLVY--YNISITSGENDMKNKSLRSLIFPVGYSRFSMSNFIELPLRLAVLDLDAKF 585





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2002, 13:58:42 ; Search time 31.22 Seconds  
(without alignments)  
1122.396 Million cell updates/sec

Title: US-09-864-680-3  
Perfect score: 4712  
Sequence: 1 MAHASIASIMRTESILTFPN.....PYDVIRISNPLKESDSEEH 905

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	238.5	5.1	1248	1 APAF_HUMAN
2	236	5.0	1249	1 APAF_RAT
3	232.5	4.9	1249	1 APAF_MOUSE
4	186.5	4.0	1261	1 APAF_BRARE
5	152.5	3.2	1036	1 YOB6_CABEL
6	152	3.2	1679	1 YIO9_YEAST
7	149	3.2	1692	1 CYAA_SCHPO
8	147	3.1	1928	1 MYSL_YEAST
9	145.5	3.1	950	1 Y511_RICPR
10	143.5	3.0	3911	1 AKAG_METJA
11	139	2.9	1064	1 Y108_HUMAN
12	139	2.9	1828	1 CWTJ_SCHPO
13	138.5	2.9	4092	1 DYHC_YEAST
14	138	2.9	2663	1 CENE_HUMAN
15	135	2.9	904	1 TLR3_HUMAN
16	134.5	2.9	1269	1 FLIH_HUMAN
17	134	2.8	2077	1 TEGU_HSV7J
18	133.5	2.8	2059	1 TEGU_HSV7J
19	133.5	2.8	2145	1 CYAA_PODAN
20	132.5	2.8	1257	1 FLIH_CABEL
21	131.5	2.8	1427	1 REST_HUMAN
22	130.5	2.8	1428	1 YAB4_SCHPO
23	130	2.8	1046	1 SBCC_LACIA
24	130	2.8	1839	1 CYAA_SACKL
25	127.5	2.7	1256	1 FLIT_DROME
26	127	2.7	810	1 CLPC_BACSU
27	126.5	2.7	1258	1 YS00_ANASP
28	126.5	2.7	1315	1 CHAO_DROME
29	126.5	2.7	2300	1 CYAA_NEUCR
30	126	2.7	1041	1 TLR4_HUMAN
31	126	2.7	1312	1 RASO_YEAST
32	126	2.7	1727	1 ALML_SCHPO
33	125.5	2.7	2238	1 RRPL_BUNYW

34	125.5	2.7	5430	1 ACE7_HUMAN	O9upn3 homo sapien
35	125	2.7	864	1 CHEA_BORBU	O44737 borrelia bu
36	125	2.7	1169	1 SMC_METJA	O56037 methanococ
37	124.5	2.6	856	1 CLPB_HELPY	P71404 hellicobacte
38	124.5	2.6	944	1 NOF1_YEAST	P32380 saccharomyc
39	124.5	2.6	959	1 LONM_HUMAN	P36776 homo sapien
40	124.5	2.6	2418	1 SPCA_HUMAN	P02549 homo sapien
41	124	2.6	905	1 TLR3_MOUSE	O99mb1 mus musculi
42	124	2.6	908	1 H104_YEAST	P31539 saccharomyc
43	124	2.6	2198	1 YLJ2_CABEL	P34367 caenorhabdi
44	123.5	2.6	784	1 TLR2_MOUSE	O9gun7 mus musculi
45	123.5	2.6	1939	1 MYH6_HUMAN	P13533 homo sapien

## ALIGNMENTS

RESULT	1	STANDARD:	PRT: 1248 AA.
ID	APAF_HUMAN		
AC	O14727; O9UB5; O9U58; O9U59; O9U60; O9U61; O9U62; O9U63; O9U64; O9U65; O9U66; O9U67; O43297; O9BX26; O9UGN8; O9UGN9; O9UGP0; O9UNC9;		
AC	O9UGP0; O9UNC9;		
DT	15-JUL-1998 (Rel. 36, Created)		
DT	01-MAR-2002 (Rel. 41, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Apoptotic protease activating factor 1 (Apaf-1).		
GN	APAF1 OR KIA0413.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
LN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.		
RC	TISSUE=Cervical carcinoma;		
RX	MEDLINE=97410306; PubMed=9267021;		
RA	Zou H., Henzel W.J., Liu X., Lutsch A., Wang X.;		
RT	"Apaf-1, a human protein homologous to C. elegans CED-4, participates in cytochrome c-dependent activation of caspase-3.";		
RL	Cell 90:405-413(1997).		
LN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 4 AND 5).		
RC	TISSUE=Peripheral blood, Heart, and Cervical carcinoma;		
RX	MEDLINE=99373149; PubMed=10441496;		
RA	Hahn C., Hirsch B., Jahnke D., Duerkop H., Stein H.;		
RT	"Three new types of Apaf-1 in mammalian cells.";		
RL	Biochem. Biophys. Res. Commun. 261:746-749(1999).		
LN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM 2).		
RC	TISSUE=T-cell;		
RX	MEDLINE=9929765; PubMed=10364241;		
RA	Saleh A., Striniwasula S.M., Acharya S., Fisher R., Alnemri E.S.;		
RT	"Cytochrome c and dATP-mediated oligomerization of Apaf-1 is a prerequisite for procaspase-9 activation.";		
RL	J. Biol. Chem. 274:17941-17945(1999).		
LN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE-Kidney;		
RA	Benedict M.A., Nunez G.;		
RT	Submitted (May-1999) to the EMBL/GenBank/DBJ databases.		
LN	[5]		
RP	SEQUENCE OF 385-1248 FROM N.A. (ISOFORM 1).		
RC	TISSUE-Brain;		
RX	MEDLINE=98116655; PubMed=9455477;		
RA	Ishikawa K., I., Nagase T., Nakajima D., Seki N., Ohira M.;		
RT	Myajima M., Tanaka A., Kotani H., Nomura N., Ohara O.;		
RT	"Prediction of the coding sequences of unidentified human genes. VIII. 78 new cDNA clones from brain which code for large proteins in vitro.";		
RL	DNA Res. 4:307-313(1997).		
LN	[6]		
RP	SEQUENCE OF 810-864 AND 866-883 FROM N.A.		
RA	Roberts D.L., Dalgleish R., Cohen G.M., MacFarlane M.;		

RT "The mammalian CED4 homologue, APAF1, exists as two distinct forms in  
 RT human cells."  
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 1-138 FROM N.A. (ISOFORM 1/4/5).  
 RA Won M., Lee J.-W., Ohn H.-H., Kim D.-U., Chung K.-S., Lee M.,  
 RA Yoo H.-S.;  
 RT "Cloning of variant Apaf1."  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP APAF-1-MEDIATED OLIGOMERIZATION.  
 RX MEDLINE-96815378; PubMed-9651578;  
 RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Alnemri E.S.;  
 RT "Autoactivation of procaspase-9 by Apaf-1-mediated oligomerization."  
 RT Mol. Cell 1:949-957(1998).  
 RN [9]  
 RP INDUCTION BY E2F AND P53.  
 RX MEDLINE-21283226; PubMed-11389439;  
 RA Moroni M.C., Hickman E.S., Denchi E.L., Caporaso G., Coll E.,  
 RA Cecconi F., Mueller H., Helin K.;  
 RT "Apaf-1 is a transcriptional target for E2F and p53."  
 RT Nat. Cell Biol. 3:552-558(2001).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS) OF 1-97.  
 RX MEDLINE-20013059; PubMed-10543941;  
 RA Vaughn D.E., Rodriguez J., Lazebnik Y., Joshua-Tor L.;  
 RT "Crystal structure of Apaf-1 caspase recruitment domain: an alpha-  
 RT helical greek key fold for apoptotic signaling."  
 RT J. Mol. Biol. 293:439-447(1999).  
 RN [11]  
 RP STRUCTURE BY NMR OF 1-97.  
 RX MEDLINE-20047184; PubMed-10578182;  
 RA Day C.L., Dupont C., Lackman M., Vaux D.L., Hinds M.G.;  
 RT "Solution structure and mutagenesis of the caspase recruitment domain  
 (CARD) from Apaf-1."  
 RT Cell Death Differ. 6:1125-1132(1999).  
 RT -1- FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent  
 RT autocatalytic activation of pro-caspase 9 (Apaf-3), leading to the  
 RT activation of caspase-3 and apoptosis. This activation requires  
 RT ATP.  
 CC -1- SUPPLEMENT: Monomer. Oligomerizes upon binding of cytochrome c and  
 CC dATP. Oligomeric Apaf-1 and pro-caspase-9 bind to each other via  
 CC their respective NH2-terminal CARD domains and consecutively  
 CC mature caspase-9 is released from the complex.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: 5 isoforms; 1/Apaf-1XL (shown here), 2/Apaf-  
 CC 1L, 3/Apaf-1S, 4/Apaf-1M and 5/Apaf-1XS; are produced by  
 CC alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest levels of expression in  
 CC adult spleen and peripheral blood leukocytes, and in fetal brain,  
 CC kidney and lung. Isoform 1 is expressed in heart, kidney and  
 CC liver.  
 CC -1- INDUCTION: BY E2F and p53 in apoptotic neurons.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).  
 CC -1- SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.  
 CC -1- CAUTION: Ref.7 sequence differs from that shown due to a  
 CC frameshift in position 109.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL; AF013263; AAC51678.1; -;  
 DR EMBL; AJ243003; CAB55579.1; -;  
 DR EMBL; AJ243004; CAB55580.1; -;  
 DR EMBL; AJ243005; CAB55581.1; -;  
 DR EMBL; AJ243006; CAB55582.1; -;  
 DR EMBL; AJ243007; CAB55583.1; -;

DR EMBL; AJ243008; CAB55584.1; -;  
 DR EMBL; AJ243009; CAB55585.1; -;  
 DR EMBL; AJ243010; CAB55586.1; -;  
 DR EMBL; AJ243011; CAB55587.1; -;  
 DR EMBL; AJ243048; CAB55588.1; -;  
 DR EMBL; AJ243107; CAB56462.1; -;  
 DR EMBL; AF134397; AAD38344.1; -;  
 DR EMBL; AF149794; AAD34016.1; -;  
 DR EMBL; AB007873; BAA24843.1; -;  
 DR EMBL; AJ133643; CAB65085.1; -;  
 DR EMBL; AJ133644; CAB65086.1; -;  
 DR EMBL; AJ133645; CAB65087.1; -;  
 DR EMBL; AF248734; AAK28401.1; ALT\_FRAME.  
 DR PDB; 1CV5; 01-DEC-99.  
 DR PDB; 1CWV; 21-JAN-00.  
 DR MTM; 602233; -;  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR002182; NB-ARC.  
 DR InterPro: IPR001680; WD40.  
 DR Pfam; PF00619; CARD; 1.  
 DR Pfam; PF00931; NB-ARC; 1.  
 DR Pfam; PF00400; WD40; 11.  
 DR PRINTS; PR00320; GPROTEINRPT.  
 DR SMART; SM00320; WD40; 10.  
 DR PROSITE; PSS0209; CARD; 1.  
 DR PROSITE; PSS0678; WD\_REPEATS\_1; 4.  
 DR PROSITE; PSS0082; WD\_REPEATS\_2; 9.  
 DR PROSITE; PSS0294; WD\_REPEATS\_REGION; 1.  
 DR Apoptosis; ATP-binding; Repeat; WD repeat; Alternative splicing;  
 KW 3D-structure.  
 KW DOMAIN 1  
 FT NP\_BIND 104 415  
 FT REPEAT 154 161  
 FT REPEAT 613 652  
 FT REPEAT 655 694  
 FT REPEAT 697 738  
 FT REPEAT 741 780  
 FT REPEAT 796 836  
 FT REPEAT 838 877  
 FT REPEAT 880 919  
 FT REPEAT 959 998  
 FT REPEAT 1001 1040  
 FT REPEAT 1042 1080  
 FT REPEAT 1083 1122  
 FT REPEAT 1125 1164  
 FT REPEAT 1175 1212  
 FT DOMAIN 95 98  
 FT VARSPPLIC 99 109  
 FT VARSPPLIC 575 575  
 FT VARSPPLIC 824 866  
 FT VARSPPLIC 1113 1154  
 FT CONFLICT 108 108  
 FT CONFLICT 134 134  
 FT CONFLICT 145 145  
 FT CONFLICT 161 161  
 FT CONFLICT 370 370  
 FT CONFLICT 383 383  
 FT CONFLICT 544 544  
 FT CONFLICT 580 580  
 FT CONFLICT 608 608  
 FT CONFLICT 620 620  
 FT CONFLICT 639 639  
 FT CONFLICT 708 708  
 FT CONFLICT 742 742  
 FT CONFLICT 746 746  
 FT CONFLICT 757 757  
 FT CONFLICT 795 795  
 FT CONFLICT 798 798  
 FT CONFLICT 825 825  
 FT CONFLICT 871 871  
 FT CONFLICT 876 876  
 FT CONFLICT 949 949  
 FT CARD.  
 FT NB-ARC.  
 FT ATP (POTENTIAL).  
 FT WD 1.  
 FT WD 2.  
 FT WD 3.  
 FT WD 4.  
 FT WD 5.  
 FT WD 6.  
 FT WD 7.  
 FT WD 8.  
 FT WD 9.  
 FT WD 10.  
 FT WD 11.  
 FT WD 12.  
 FT WD 13.  
 FT POLY-SER.  
 FT MISSING (IN ISOFORM 2 AND ISOFORM 3).  
 FT E -> ETIGESKK (IN ISOFORM 5).  
 FT MISSING (IN ISOFORM 3, ISOFORM 4 AND  
 FT ISOFORM 5).  
 FT MISSING (IN ISOFORM 5).  
 FT S -> P (IN REF. 7).  
 FT N -> S (IN REF. 7).  
 FT G -> C (IN REF. 2; CAB55587).  
 FT S -> F (IN REF. 2; CAB55586).  
 FT Y -> T (IN REF. 2; CAB55581).  
 FT I -> H (IN REF. 2; CAB55584).  
 FT F -> L (IN REF. 2; CAB55584).  
 FT A -> T (IN REF. 2; CAB55585).  
 FT R -> C (IN REF. 2; CAB55585).  
 FT H -> R (IN REF. 2; CAB55587).  
 FT L -> F (IN REF. 2; CAB55583).  
 FT T -> A (IN REF. 2; CAB55579).  
 FT H -> R (IN REF. 2; CAB55584).  
 FT V -> A (IN REF. 2; CAB55582).  
 FT L -> P (IN REF. 2; CAB56462).  
 FT E -> G (IN REF. 2; CAB55581).  
 FT D -> G (IN REF. 2; CAB55587).  
 FT E -> A (IN REF. 2; CAB55585).  
 FT S -> T (IN REF. 2; CAB55587).  
 FT A -> L (IN REF. 2; CAB55581).  
 FT I -> V (IN REF. 2; CAB55585).



Query Match 5.1%; Score 238.5; DB 1; Length 1248;  
 Best Local Similarity 20.2%; Pred. No. 8.2e-07;  
 Matches 176; Conservative 116; Mismatches 268; Indels 313; Gaps 41;

QY 96 KARREROSLOQVAD-----MDH-----WKESTKIQDKGKQVSK-----131  
 DB 4 KARNCLQHRALKEIKTYIMDMHISDGLTISEEKVANEPTQOORAMLIKMLK 63  
 QY 132 -----ESLVH-----DSSSTNDILKAKNNVGRD-----157  
 DB 64 DNDYSVFYNALHKGKYLALHLDGIPVYSSSGKDVSGINSYVTVLCGGVDPOR 123  
 QY 158 -----OROLLEDLFRS-----GEPKVIPIYMGIGTKTAKVEYNESIL--C-RPDVH 207  
 DB 124 VVETPRKVLVAIQKLSKLGEGPWTTHMACGKSVLAELVRDHSLEGGCPGGVH 183  
 QY 208 AMATISOOHNKKEILLGLHSTIKMDRVKM-----IGELADLMOKSLKR--RYLIIV 260  
 DB 184 -WVSVGRO-DKSGILMKLQNCRLDDESPQRPLNTEAKRRLRIMLRKHPRLILI 241  
 QY 261 LDIWSEVMDGVRCPPTEDNAGSRILLTTRNDEVACYA-----GVE 303  
 DB 242 LDDVW--DSW--VLKAPDSQ---CQILLTRDKSVSDVWGPXYVPVSSLEKEGLE 293  
 QY 304 NLSLRMSFMODESWSLFKSAFSSALPYEFETVGKQIDEGCHGLPTIIVVAGLLKSK 363  
 DB 294 ILSLFVMMKRAKAD-----LPEGAHSILK-----ECKGSPILVSLIGALLRD- 333  
 QY 364 RTEDMTKVAKV--KSF-----VTNDPDERCSRVLGSDYHLSJDKTCLHAGIPEP 416  
 DB 334 -FPRRWETYLKQLOKQFKIRKSSSYDYERLDEAMSISVEMLEDIKDYTTDLISLOKD 392  
 QY 417 SDIPVKMLMSWAEGLKLENDLE-GEVEKCLQELVDRLVLSKSRDGTAKRSCKVH 475  
 DB 393 VKPVTKLVLCTIM-----DMETEVEDIIOLEFVNSKLLFC--DRNGKSPR-YLIH 438  
 QY 476 DLIVDLCVREVORENIFIMNDIVLVSPECSYLCMYKMPKRVGTGEINVCYGLYRA 535  
 DB 439 DLOVDFLEK-----NCS-----451  
 QY 536 LITPVNQLRDHNNMLKRTHSVSFHLBPLYVLKSEVHFILKLELRHQIDGFP 595  
 DB 452 -----QIQD-----LHKIITQFOXYHOPHLSP 475  
 QY 596 REIISLWLRKILSFSGNEDVPEICRLMNLQTFIVORESDIITPAEIIWELMQLRHL 655  
 DB 476 DQEDCMYWNFLA-YHMASAKMHELCALMFSLDML--KATTELIVGPAHLIHEVEYRHI 532  
 QY 656 KLPREYLPDGPSSGVDRHLPFSLQTFISLSPRCTKEVIMGIO--NVKKGISGNK 712  
 DB 533 LDEK-----DCAVS-----ENFQEFSLNCH-----LIGRQPPNVLQGLCE- 570  
 QY 713 DDYKSPFSDGILPNNLVYIQLLEILSLSDVSYSLPVIISAKAPATLKIKLERTLSW 772  
 DB 571 -----PEISEVYQAKIQAKQEVONGM-----YLEW 597  
 QY 773 SYLDITLPLNLEVLKAMD--DACGGEEMHPIV-MGFNRL-----KLILITY-- 816  
 DB 598 INKNININLRLVVRPHTDVYHACFESDGRIASCADKTLIQVKAETGEKLEIRAKE 657  
 QY 817 -SFLKFWKATNDNFPVLERLIRISCKNLKEPI 848  
 DB 658 DEVILCAFSIDRF-----IATCSYDKVKYKI 683

DE Apoptotic protease activating factor 1 (Apaf-1).  
 GN APAF1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC SMPAIN=Sprague-Dawley;  
 RA Itoh T., Itoh A., Pleasure D.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RP [2]  
 RP DEVELOPMENTAL REGULATION, AND INDUCTION BY BRAIN INJURY.  
 RX MEDLINE=21450943; Pubmed=11567033;  
 RA Yakovlev A.G., Ota K., Wang G., Moysesyan V., Bao W.-L., Yoshinara K.,  
 RA Faden A.I.;  
 RT "Differential expression of apoptotic protease-activating factor-1 and  
 RT caspase-3 genes and susceptibility to apoptosis during brain  
 RT development and after traumatic brain injury.";  
 RL J. Neurosci. 21:7439-7446(2001).  
 CC -1- FUNCTION: Regulates programmed cell death; necessary for normal  
 CC brain development. Participates with caspase-9 (Apaf-3) in the  
 CC cytochrome c-dependent activation of caspase-3, leading to  
 CC apoptosis. This activation requires ATP (by similarity).  
 CC -1- SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and  
 CC dATP. Oligomeric Apaf-1 and pro-caspase-9 bind to each other via  
 CC their respective NH2-terminal CARD domains (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -1- DEVELOPMENTAL STAGE: Highly expressed in brain cortex in embryos  
 CC (E17) and new-born rats up to day 7. Very low expression  
 CC thereafter.  
 CC -1- INDUCTION: By brain injury.  
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 13 WD REPEATS (TRP-ASP DOMAINS).  
 CC -1- SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF320222; AAC35067.1; -.  
 DR InterPro: IPR001315; CARD.  
 DR InterPro: IPR002182; NB-ARC.  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00619; CARD. 1.  
 DR Pfam: PF00931; NB-ARC. 1.  
 DR Pfam: PF00400; WD40. 13.  
 DR PRINTS: PR00320; GPROTEINRPT.  
 DR SMART: SM00114; CARD. 1.  
 DR SMART: SM00320; WD40. 13.  
 DR PROSITE: PS50209; CARD. 1.  
 DR PROSITE: PS50294; WD\_REPEATS\_1; 4.  
 DR PROSITE: PS50082; WD\_REPEATS\_2; 9.  
 DR PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
 KW Apoptosis; ATP-binding; Repeat; WD repeat.  
 FT DOMAIN 1  
 FT 106 415 NB-ARC.  
 FT NP\_BIND 154 161 ATP (POTENTIAL).  
 FT REPEAT 613 652 WD 1.  
 FT REPEAT 655 694 WD 2.  
 FT REPEAT 697 738 WD 3.  
 FT REPEAT 741 780 WD 4.  
 FT REPEAT 796 837 WD 5.  
 FT REPEAT 838 877 WD 6.  
 FT REPEAT 880 919 WD 7.  
 FT REPEAT 959 998 WD 8.  
 FT REPEAT 1001 1040 WD 9.  
 FT REPEAT 1042 1080 WD 10.  
 FT REPEAT 1083 1122 WD 11.



DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00320; WD40; 12.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 4.  
 DR PROSITE; PS50082; WD\_REPEATS\_2; 9.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 KW Apoptosis; ATP-binding; Repeat; WD repeat; Alternative splicing.  
 FT DOMAIN 1 90 CARD.  
 FT NP\_BIND 106 415 NB-ARC.  
 FT REPEAT 154 161 ATP (POTENTIAL).  
 FT REPEAT 613 652 WD 1.  
 FT REPEAT 655 694 WD 2.  
 FT REPEAT 697 738 WD 3.  
 FT REPEAT 741 780 WD 4.  
 FT REPEAT 796 837 WD 5.  
 FT REPEAT 838 877 WD 6.  
 FT REPEAT 880 919 WD 7.  
 FT REPEAT 959 998 WD 8.  
 FT REPEAT 1001 1040 WD 9.  
 FT REPEAT 1042 1080 WD 10.  
 FT REPEAT 1083 1122 WD 11.  
 FT REPEAT 1125 1164 WD 12.  
 FT REPEAT 1176 1213 WD 13.  
 FT VARSPLIC 99 110 GKDTGGGITSFV -> A (IN ISOFORM 2).  
 SQ SEQUENCE 1249 AA; 140888 MW; 53D91539CE6025C CRC64;

Query Match 4.9%; Score 232.5; DB 1; Length 1249;  
 Best Local Similarity 24.0%; Pred. No. 1.9e-06;  
 Matches 114; Conservative 75; Mismatches 161; Indels 125; Gaps 25;

QY 96 KARRRROSLOQVAED-----MDHIK-----ESTKIDCKGVSK----- 131  
 DB 4 KARRRROSLOQVAED-----MDHIK-----ESTKIDCKGVSK----- 63  
 QY 132 -----ESLVH-----DESSSTNDILKVNMMVGRDDQ----- 158  
 DB 64 DNCAVIFSYNNLHEGYDLAALQSGPLIVSSSGKDTGITSFVTVLCEGVPQRP 123  
 QY 159 -----KQLEDLTR-----SYSGEKVPIYVGMGIGKTTAKVEYNDSIL--CFEDVHA 208  
 DB 124 VIFETKRLVHAIOCKLMKLMGEPGWVYIYMACGKSVLAEEVVRHSLLEGCGSGGVH 183  
 QY 209 WATISOQHKKKEILLGLLSTIKMDRVKM-----IGEAELADMLQSLKKR--RYLIVL 261  
 DB 184 WVSIGKQ-DKSGLLMKLQNLCKRDLQDESEQRPLINEEKKRLRVYLMKKHRSLLIL 242  
 QY 262 DDIVSCVWDGVRRCFPTEDNAGSRILLTTRNDEVA--CYAGVENFSLRMSFMDQ--ES 317  
 DB 243 DDVW--DPM--VLKAF--DNO--COILLTRDKSVTDSVMGPKHVVPESGLGREKLEI 294  
 QY 318 WSLFKSAFSEALPYEFETVQKQIADCHGLPLTIYVAVGLLS-----KTIID- 368  
 DB 295 LSLFVN--MKKEDLPAAEHSTIK--ECKGSPVLSLIGALLDFPNRMAYYLKQIUNK 348  
 QY 369 -WKTAVDVKSFVNDDEKSRVLSYDHLTSLKTLHFGIFEDSDIPVKNILRS 427  
 DB 349 QFKRIRKS-----SSYVEALDEAMSTISVEMLRDINDYDLSLCKDVAVPKVLCYL 403  
 QY 428 WMAEGFLKLENDL-GEVEKCLQELVDRCLVLSKRSRDGKIRSC--KVHDLIYD 480  
 DB 404 W-----DLTEVEEDILQEFVNSKSLFCNRNGS-----FCYLLHDLQYD 443

RESULT 4  
 APAF\_BRARE STANDARD; PRT; 1261 AA.  
 ID APAF\_BRARE  
 AC Q919H8;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 GN Apoptotic protease activating factor 1 (Apaf-1).  
 DN APAF1.

OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20373792; PubMed=10917738;  
 RA Inohara N., Nunez G.;  
 RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."  
 RL Cell Death Differ. 7:509-510(2000).  
 CC -! FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent autocatalytic activation of pro-caspase 9 (Apaf-3), leading to the activation of caspase-3 and apoptosis. This activation requires ATP (by similarity).  
 CC -! SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and dATP (by similarity).  
 CC -! SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 CC -! SIMILARITY: CONTAINS 1 CARD DOMAIN.  
 CC -! SIMILARITY: CONTAINS 13 WD\_REPEATS (TRP-ASP DOMAINS).  
 CC -! SIMILARITY: CONTAINS 1 NB-ARC DOMAIN.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: AF251502; AAF67189.1; -  
 CC ZFIN; ZDB-GENE-000616-4; apaf1.  
 CC InterPro; IPR001315; CARD.  
 CC InterPro; IPR002182; NB-ARC.  
 CC InterPro; IPR001680; WD40.  
 CC Pfam; PF00619; CARD; 1.  
 CC Pfam; PF00931; NB-ARC; 1.  
 CC Pfam; PF00400; WD40; 12.  
 CC PRINTS; PR00320; GPROTEINBRPT.  
 DR SMART; SM00114; CARD; 1.  
 DR SMART; SM00320; WD40; 11.  
 DR PROSITE; PS50209; CARD; 1.  
 DR PROSITE; PS00678; WD\_REPEATS\_1; 2.  
 DR PROSITE; PS50082; WD\_REPEATS\_2; 7.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 KW Apoptosis; ATP-binding; Repeat; WD repeat.  
 FT DOMAIN 1 90 CARD.  
 FT NP\_BIND 106 417 NB-ARC.  
 FT REPEAT 154 161 ATP (POTENTIAL).  
 FT REPEAT 613 654 WD 1.  
 FT REPEAT 657 696 WD 2.  
 FT REPEAT 700 743 WD 3.  
 FT REPEAT 746 785 WD 4.  
 FT REPEAT 798 836 WD 5.  
 FT REPEAT 840 879 WD 6.  
 FT REPEAT 882 921 WD 7.  
 FT REPEAT 964 1003 WD 8.  
 FT REPEAT 1006 1045 WD 9.  
 FT REPEAT 1047 1088 WD 10.  
 FT REPEAT 1091 1130 WD 11.  
 FT REPEAT 1133 1172 WD 12.  
 FT REPEAT 1184 1223 WD 13.  
 SQ SEQUENCE 1261 AA; 142933 MW; F80CC9CB41764F1C CRC64;

Query Match 4.0%; Score 186.5; DB 1; Length 1261;  
 Best Local Similarity 20.7%; Pred. No. 0.0011;  
 Matches 116; Conservative 80; Mismatches 187; Indels 177; Gaps 27;

QY 94 KKKARRRROSLOQVAED-----MDHIWKESTKIQDK-----GKQVSK----- 132  
 DB 2 EERARRRLRSKATLEQDIKASVLMHMSDGLVLTNDEARVLSKATRKQDAVALLETLL 61

QY 133 -----SLVHD-----FSSSTNDILKYKNNMV 153  
 DB 62 KADNRAYISFYNNALLRESYGDASLHSDLPILSPBEGEKSPADGVSPTQALIS-----V 116  
 QY 154 GRDDQR-----QLEDLTRSYSGEPVPIVGMGIGKTTLAKVEYNDESIL- 201  
 DB 117 GVPQRPVFEVSPRLNIRRELYQRLDPTGCVTFGMAAGSKSVMAAEVVRDRLIKE 176  
 QY 202 CRDVANAMTISQHNKKRILLGLHSTFKMDRVMKIGALADMLQK----- 250  
 DB 177 CEPDGVHMLSVG-QCERADL-----VRMOSLCFRLEQCCSDPTSQRPSTVEAKER 228  
 QY 251 ----SLKR-KRYLIVLDDIMSCVMDGVRCPTEDNAGSRILTTNR-----DEVACYAG 301  
 DB 229 LRFLMRRPRRSLILDDVMD-----SSSLRSPDIQ-----CRLLTTRNNAALDSV-----SG 277  
 QY 302 VENESLRMSFMDQESWLSFKSAFSSSEALPYEFETVGKQIADCHGLPLTIVVAGLKL 361  
 DB 278 VREYEVENGDLDEKALEIL-----ALYVNGMKMKLPEQARSIVSECKSPFLVSLIGALLR 334  
 QY 362 S-----KRTIEDKRTVAKDVKSFTVNDPERCS-----RVLGISYDHLTSDLKTCL 408  
 DB 335 EEPDRMSYLRLOQKQFRIRKS-SSYDEALDQAMASLQVLEAEHOELTRDL----- 388  
 QY 409 HEGIFPEDSDIPYKNLMRSMMAEGFLKLENDLEGEVEKCLQELVDRCLVLSKRSRDGK 468  
 DB 389 --SVMKDKIKVPAKVLSTVM-----GLELE-----EVEDVLOEFVKSLL----- 426  
 QY 469 INSK-----VHDLIYLCVREVORENIFIMNDIVLDSYSPESYLCMYMPFKRYT 521  
 DB 427 FRDCNORPRYRYLHDLQLEF-LAEONRDOIAELHKMKVR-----QYRFYSKRPPDSAD 479  
 QY 522 GDEI-----NYCPGYLRYALLT 538  
 DB 480 KSLIYVYQFPIHMAKAGLS 499  
 RESULT 5  
 YOB6 CAEEL  
 ID YOB6 CAEEL STANDARD; PRT; 1036 AA.  
 AC Q09259;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Hypothetical 118.2 kDa protein C30G12.6 in chromosome II.  
 GN C30G12.6.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RC STRAIN-BRISTOL N2;  
 RA Lateille P.;  
 RL Submitted (Jul-1995) to the EMBL/Genbank/DBJ databases.  
 RL  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL: U21319; AAC46675.1; -  
 DR Wormpep: C30G12.6; CE01837.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1036 AA; 118234 MW; FE5A40D301780B82 CRC64;

Query Match 3.2%; Score 152.5; DB 1; Length 1036;  
 Best Local Similarity 18.9%; Pred. No. 0.099;

Matches 177; Conservative 137; Mismatches 277; Indels 347; Gaps 46;  
 QY 118 ESTIADKQKGVSKESLVHDESSSTNDILKYKNNMVGRD-----ORQL----- 162  
 DB 37 DSQFASSKANPEPNDSDPERQSS-----VSKQSDANDEDEINEVEIOEKELDNEEDFN 93  
 QY 163 -----LEDLTR-----SYGEPVPIVGMGIGKTTLAKVEYNDESILCRED 205  
 DB 94 LLTIEEVLVDVLFARIRRVFEVYRAEPALALFDVA-----KHIFKSTMLDCKRN 146  
 QY 206 VHMAATISQHNKKRILLGLHSTFKMDR-----VMMIGAEALADMLQSLKR 254  
 DB 147 -----TVID-----SILEGL--SILDERERDQAGEAEHVLMTIATKLA-TKNSMK 193  
 QY 255 K-----RYLIVLDDIMSCVMDGVRCPTEDNAGSRIL-TLTRNDEVACYAGVENESLR 308  
 DB 194 SDLYKLLILVDRILYLA--DSFVRC-----RIVRLIACMEANRYAYV----- 236  
 QY 309 MSFMDQESWLSFKSAFSSSEALPYEFETVGKQIADCHGLPLTIVVAGLKSRTIED 368  
 DB 237 MREHGD-----AFLEDEDEPTESE-----VMIPEGVNR----- 265  
 QY 369 MKTYAKDVKSFTVNDPERCSRVLGIS-YDHLTSDLKT-----LHFGIFPEDSDI 419  
 DB 266 W--MGKLSKSLDKSPVEKCAVATALSMDHDIKCTTCODEVTYNDLKKSVHVDSEV 323  
 QY 420 PVKNLMRSMMAEGFLKLENDLEGEVEKCLQELVDRCLVLSKRSRDGKTRSCRVHDLIY 479  
 DB 324 RVNARVRHIAN-----END-----IDKCIDY-ETSKD-NRVKQAIYRLAS 364  
 QY 480 D--LCVREVORENIF-IMNDI-----VLDSYSPESYLCMYMPFKRYTGEINCPYG 531  
 DB 365 DVSLSEFEKQRFRLVNLNNSDSARVODVIH-----OLLVESMKVAGDEI----- 411  
 QY 532 LYRLALPVYNQRLDHNNNLKRTHSVSPHLEPL-----YYVLSEVHFKLKVLE 585  
 DB 412 -----ISPSIFPPDSDNNNIPKEFPSTILEYDPLVDPTAVYVFKFAVRIQSTVQ 466  
 QY 586 LRHROID--GFPREILSL-----IMLRYLSLF-----SYGNPDVPEICRLMNLQ 629  
 DB 467 QACGSLDVEKFMKDLISMTIPDCERVGLMRTTFRLLPKNONGNEDIRKIFSR 521  
 QY 630 FIVQFRSDIITFAEELIEMQLRHLKLPRIYLPDCSGSVXKGRHLDFSNLOTISLSP 669  
 DB 522 FISRCFVDVIFNFAKGRIDLATHSRAL-TFFLPD----- 555  
 QY 690 RCGTKEYVIMGONKKGISGNKDYKSPRSGLPNNLVYLOQLEILSLASVDSLPLVI 749  
 DB 556 -----VTFVEHLEK-----FCDAIFHRM-----STDTCKDLY 585  
 QY 750 I-----SSAKAPATLKLKLEKRTYLSVSYLDIAELPNLEVLKLMDD 792  
 DB 586 LYNLLHLMNNAATKYGDLDHDKMLYKHALKITIGNSSVF-----SNDVKQLCDW 634  
 QY 793 ACCGEMHPHYMGFRNLKLLIKISFLKFKATDNFPVLERMIRS-----CKR--- 842  
 DB 635 MC-----DTAKQMLSHEEVLNLEAKKNKRVLEQWLRSATMLATCKHEEV 662  
 QY 843 -----LKEIPFADHTIQLIELRECPPIGSAARIK 877  
 DB 683 ESPFASMSLEKTIIPALGNKNELOGLIELIGFAT--SIDPENCEPIKLKLTLLIOR 740  
 QY 878 EQEDLGNPNVDVRI-----SNPLRESDSSEE 904  
 DB 741 GDEVLTSTGVVTLKVIKSGQFPRTANALFQGEQOTED 778  
 RESULT 6  
 YIO9 YEAST  
 ID YIO9 YEAST STANDARD; PRT; 1679 AA.  
 AC P40457;  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

Query Match	3.2%;	Score 152;	DB 1;	Length 1679;	
Best Local Similarity	19.4%;	Pred. No. 0.2;			
Matches	216;	Conservative	157;	Mismatches	341;
				Indels	402;
				Gaps	53;

QY	20	NSPMOSLSCDHREELCALREKVVSLFEVVKFNEKNVFGMTDEVEYREVAASAEYITQ	79
		:	:
Db	10	NVPFESLQGVWYPPYLRKRYKRIA	58
		:	:
QY	80	LRLTGTVLGEMKSOKKA	125
		:	:
Db	59	ISKKLQLDSEEQAKNTAKEELNGIKDOLNEBRKRYRREIDALKQOL-HVSHEARVEND	117
		:	:
QY	126	GKOVKESLIVHDF	156
		:	:
Db	118	EKRVAEE--YDIWGSRQGNDSLUNDINKKKLLRLRLMEMENTLQCKSNALSLOLKY	174
		:	:
QY	157	-----DORKQLEDLTRSYSGEKVYPIYMGIGICTTLAKV-----	194
		:	:
Db	175	DTSVQEKELMLOSKKLIIEKLSFS-	219
		:	:
QY	195	-----YN-----	223
		:	:
Db	220	LYQMSNTESVFTYKFKLLNOKQLOLSQVVEEVLEMKMLKDTASVEKAEFSKEMTLQKNM	279
		:	:
QY	224	-GLHSTI-----KMDRVKMGH-----AELAD--MLQSKLRKRYL-I	259
		:	:
Db	280	NDLRSQGLSLEKQCSLRAIEKNDNSCRNPHTVIDELDTKRLERKSKNKGCRLONI	339
		:	:
QY	260	VLDIDWISCEVMDGVRCPTEPDNAGS-----RILLTRNDEVACYAGVENSLEPM----	309
		:	:
Db	340	VMDCTKEEBEATTTSAVSPYQKLFESDJKVLKROLIKERNOKFQLOLQDELFIIELEHKT	399
		:	:
QY	310	-----SEFMODEKWSLFFKSAFSSSLAPFEFFVGQ-----IADECHGLPFIIVAVGL	359
		:	:
Db	400	PELLISFKEETK--SLEHELKSTELLETVSLTKRKQEBELTISLRKINGCEANT--HSL	454
		:	:
QY	360	LKSKRTIEBWKTVADVQSVFYND--DERGSRVGLGSLYDHLTSDIKTLCTLFGFIPEDS	417
		:	:
Db	455	VKQRDL-----ANQVALLLLNTAISAIQETAS--PLSDDELIS-LRKIL-----ESS	497
		:	:

ID	CVAA_SCHPO	STANDARD;	PRT;	1692 AA.
AC	PI4605;			
DT	01-APR-1990	(Rel. 14, Created)		
DT	01-APR-1990	(Rel. 14, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenyl1l cyclase).			
GN	CYR1 OR SPBC19C7.03.			
OS	Schizosaccharomyces pombe (Fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC	Schizosaccharomyces.			
OX	NCBI_TaxID=4896;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=90046723;	PubMed=2682634;		
RA	Young D., Riggs M., Field J., Vojtek A., Broek D., Wigler M.;			
RT	"The adenyl1l cyclase gene from Schizosaccharomyces pombe."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:7989-7993(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=89345533;	PubMed=2668944;		
RA	Yamawaki-Katooka Y., Yamachi T., Choe H.-R., Tanaka H., Katooka T.;			
RT	"Adenylate cyclases in yeast: a comparison of the genes from Schizosaccharomyces pombe and Saccharomyces cerevisiae."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:5693-5697(1989).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RA	Lyne M., Rajandream M.A., Barrell B.G., Lucas M., Galliard C.;			



[illegible]



```

Db 1320 LMLFVYDLKRLQDIEFRAHYDAENAIISALHSKFRKIQGE-----SSLSDDSIYKLKFEA 1373
QY 338 VG---KQIADDECHGLPL---TIVYVAGLLSKRTIEDMTAKVDK-----SFVTNDPD 385
Db 1374 SEERYKSLDEKLTMLRDRTNLPVGDIIKRNDSISKYEERLYKLENYKLOLEINEN 1433
QY 386 EERCSTRLGSDYHLSLSDTKLHFIQIPEDSDIP---VKNILMRMAEGFLKEN--- 438
Db 1434 GLTSLQ---LTLDLROSKSEALLSEDLRLQDLDESTEROKELISSTIQCKQOQFENCMD 1490
QY 439 DLGG-----EVEKQLQELVDRCLVLSKRSRSGTKIRSCVKYDLIYDLCVREORE 489
Db 1491 DLQGNELRLREHIALKQAEEDVKNMAISIEK-----LTKQMKQEKLIWE---REMERN 1542
QY 490 NIFIMNDIYDVSYPCSTLCMKYKQPKRYVGEDEINCPYGLY---RALLTPVAKOR 545
Db 1543 D---SDMQLQETLE---LKRQVDYKLLSDLAHLKERLSAVEDSSQYTDIEINRLK 1593
QY 546 DHNNNL-----LKRTHSVFPHLE-----PLYVYLKSEVHFKLLKVELRHRQID 592
Db 1594 EELNCSLKAEFTNLKKEFATLKKLETSTNDESAKISDLK-QLDHY--TKVYEMLNNE-- 1648
QY 593 GEPREILSL---IMLRYSLSFYGNFVDPPEICRLMNLQTFIVQFRSDIIFAEIWE 648
Db 1649 ---KDAISLAERELYOKYKAL---NTECESLKGKIVSL-TRIKQELIESDL---NQKTD 1696
QY 649 LMQLRLHLKPRFVLPDPCSGSVDKGRHLDPSNLQTSYLSPPCKREVIAMGION----- 702
Db 1697 ALQISNAL-----SSSTQKNKEI---TEKIKYLE---TLQLOME-QNSNGEEL 1739
QY 703 VKRLGISGNKDDYKFSRSGLPNNLVYLOLELISLVYSLLPVIISAKAFPAATLK 762
Db 1740 VKTLQASCN--GYKQKFEDEKQKIDLYEENQTLQKLNITDQL-----QLKN 1784
QY 763 L--KIERTYLSMSYDITIAELPNEVLK 788
Db 1785 LHERLSDTTEKNAMLSKIHLENVSL 1812

RESULT 9
VS11_RICPR STANDARD: PRT: 950 AA.
AC Q92D36;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Hypothetical protein RP511.
GN RP511.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_Taxid=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Almark U.C.M., Podowski R.M., Neeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AJ235272; CAA14963.1.
DR InterPro; IPR001646; Pentapeptide.

```

```

DR Pfam: PF00805; Pentapeptide: 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 950 AA, 108612 MW, C047F8BC063F715 CRC64.

Query Match          3.1%; Score 145.5; DB 1; Length 950;
Best Local Similarity 18.2%; Pred. No. 0.23;
Matches 179; Conservative 172; Mismatches 309; Indels 321; Gaps 46;

QY 1 MAHASVASIMRTIESLITNSPMQSLSCDHREL-----CALREKVS 42
Db 64 LAKSSNIYLDPEFOKSLNESPWFELKRNHSDLPKIGILAKAGREFODKSALDE-- 121
QY 43 SLEVFYKFNENKNNVFGEMTDFEVEYREVASAEYTIQLRGTGLGENSEKOKKARRRR 102
Db 122 GLKILKECFKNEKYLKIDDIAEVQ-----ERTMKNTVSIIDMLVTDK-----NQ 171
QY 103 QSLQVAAEDMDHIWKSESTKIDQKGVSKESLVHDFSSTNDILKYNKNVGRDQKOL 162
Db 172 KFEFKSKDITHYIRSG-----ATEILPSDYMKSFDDIL-----QKPEKKTL 213
QY 163 LEDLTYSYSGEYVIPYVGMGIGKTTLAKEVYNDSEILCRPDVHAMATISQOHKKEL 222
Db 214 L---KIFNTHDY-----KQELVNNI--NNENILKRF-----NKLFTKQETM 250
QY 223 LGILHSTIKMDRVRKMGAEELADMLQSKLR-KRYLIYLDIWSG-----EYWDGV 273
Db 251 LHSFLKEK-----AQSKPFLQEHFESKIDKILDIIPTLNKPDKELFDL 300
QY 274 RCFPTEDNAGSRILLTTNDEVACYAVENF-----SLRSMFMDDES-WSLEKS 323
Db 301 ----NAPKGVAMISLEKALEMAGDOLKSEFANNKTIIPNALGLINTFSVOSITNE 355
QY 324 AAFSSALPYEEFYGVK-QIADDECHGLPLTIYVAGLLSKRTIEDMTAKVDKSFVN 382
Db 356 YNQDQMLVIVGEVMSKPELAHE-----IADLNGK-----DYSLGTGNIISIT-N 400
QY 383 DDERCSRVL-----GLSYDHLTSDKTYCLHFGIFPDSIDIPVKNLMRMAEGFLK 436
Db 401 DPSFKLDILVQSKKGL-FDNLIN-----GVLEQD--IKN----- 433
QY 437 ENDLSEVEKCIQELVDRCLVLSKRSRSGTKIRSCVKYDLIYDLCVREORENITMD 496
Db 434 -----SOLIKQDILNMGAGVTKL--TKIPILLD----- 463
QY 497 IYLDVSYPCSTLCMKYKQPKRYVGEDEI--NYCPGLYRALLTPVNRDLRHDNN-- 551
Db 464 -----KPSLKKVFRDFIKGNTTKTKRELISLITKNPKIKETLNNRAI 507
QY 552 ---LKRRT---HSVFSFHLPEPLYVLKSEVNH---FKLKVLELRH----- 588
Db 508 FASILDKTLMDIPGINNLDKQELYNILPSMLNHPDELKIVIEVEKSHGAVSAIYNLA 567
QY 589 RQIDGPRRILSLIMLRYSLSFYGNFVDPPEICRLMNLQTFIVQFRSDIIFAEIWE 648
Db 568 KSTNFFEGQLPNIKAGFNSGFNATEKVK-----DVSSSSDFEKDYI--DEIT 616
QY 649 LMQLRLHLKPRFVLPDPCSGSVDKGR--HDFSNLQTSYLSPPRCTKREVIAMGIONVKRL 706
Db 617 RKLHDKIQNGKRLN---EGAILLGLNSNIDFSG-----VSLKNADLT 655
QY 707 GISGNKD-DYKSEFR--DSGLPNNLVYLOLELISLVDSYSLPVIISAKAFPAATLKL 763
Db 656 KYSLSKDCNFKNNLVADAKLPNLIWF--TDYVNLDKAIPTLAPRLIKAQA----- 705
QY 764 KIERTYLSMSYDITIAELPNEVLKLMADACCGEEHNPVYMGFNRLKLLIKYSLFKWK 823
Db 706 KLVADKIDVVFQVQKAE-----EKKILFSKKEFLQYQV 738
QY 824 ANDNPPVLERMINSCKLKEIPEFADITHTLOLELRECPPKLGEASARIQKEQEDG 883
Db 739 -----ITLEENQIVKDYIIDKLSFPMNVTNLE-TPKIQO-----YKHTTNHV 781

```





```

FT DOMAIN 3587 3689 COILED COIL (POTENTIAL).
FT DOMAIN 3726 3730 POLY-LEU.
FT DOMAIN 203 292 GLN-RICH.
FT DOMAIN 321 1010 GLU-RICH.
FT DOMAIN 1846 2772 GLU-RICH.
FT VASPLIC 17 28 MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT VASPLIC 1637 1642 OLOEI -> LATRED (IN ISOFORM 4).
FT VASPLIC 1643 3911 MISSING (IN ISOFORM 4).
FT VASPLIC 2175 2182 MISSING (IN ISOFORM 3).
FT VASPLIC 2175 2183 SADTFQVE -> Q (IN ISOFORM 6).
FT VASPLIC 2895 2907 VEGFYNNCFSLC -> GSSIPELASHDAVQTRICSS
FT VASPLIC 2895 2948 (IN ISOFORM 2, ISOFORM 3 AND ISOFORM 6).
FT VASPLIC 3901 3911 MISSING (IN ISOFORM 5).
FT VASPLIC 3901 3911 STOFHAGMR -> ALSITSMQHSARPTAPLEFELSH
FT VASPLIC 3901 3911 SLG (IN ISOFORM 6).
FT VASPLIC 3901 3911 K -> Q.
FT VASPLIC 3901 3911 /FTID-VAR_010926.
FT VASPLIC 3901 3911 E -> Q (IN REF. 3).
FT VASPLIC 3901 3911 M -> I (IN REF. 3).
FT VASPLIC 3901 3911 E -> G (IN REF. 3).
FT VASPLIC 3901 3911 R -> S (IN REF. 3).
FT VASPLIC 3901 3911 N -> S (IN REF. 3).
FT VASPLIC 3901 3911 H -> N (IN REF. 3).
FT VASPLIC 3901 3911 K -> N (IN REF. 3).
FT VASPLIC 3901 3911 QKH -> PKP (IN REF. 1 AND 2).
FT VASPLIC 3901 3911 Q -> P (IN REF. 1 AND 2).
FT VASPLIC 3901 3911 Q -> P (IN REF. 1 AND 2).
FT VASPLIC 3901 3911 N -> D (IN REF. 3).
FT VASPLIC 3901 3911 V -> E (IN REF. 3).
FT VASPLIC 3901 3911 R -> P (IN REF. 1 AND 2).
FT VASPLIC 3901 3911 N -> T (IN REF. 3).
FT VASPLIC 3901 3911 V -> G (IN REF. 3).
FT VASPLIC 3901 3911 MISSING (IN REF. 5).
FT VASPLIC 3901 3911 A -> P (IN REF. 3).
FT VASPLIC 3901 3911 I -> V (IN REF. 3).
FT VASPLIC 3901 3911 V -> D (IN REF. 5).
FT VASPLIC 3901 3911 EI -> HE (IN REF. 7).
FT VASPLIC 3901 3911 E -> V (IN REF. 3).
FT VASPLIC 3901 3911 L -> R (IN REF. 3).
FT VASPLIC 3901 3911 T -> N (IN REF. 8).
FT VASPLIC 3901 3911 E -> D (IN REF. 3).
FT VASPLIC 3901 3911 P -> S (IN REF. 3, 7 AND 8).
FT VASPLIC 3901 3911 Q -> H (IN REF. 3).
FT VASPLIC 3901 3911 Q -> H (IN REF. 3).
FT VASPLIC 3901 3911 ESE -> OSO (IN REF. 3).
FT VASPLIC 3901 3911 P -> A (IN REF. 3).
FT VASPLIC 3901 3911 T -> S (IN REF. 3).
FT VASPLIC 3901 3911 SEQUENCE 3911 AA; 453664 MW; 3FBICBIC819B47AA CRC64;

```

```

QY 285 SRILITRNDVACAGYENFSLRMSFMDQDESNLSFKSAARSSALPYEFTVGKOLAD 344
DB 844 LKQOQIOLNEE-----TEKORNTFSFAKN-----FEVNYOEOE 878
QY 345 ECHGLPLTIVVAGLAKSKRTIEDKRTAKADKVSFTVNDPDERCSRVLGSLVD-HLTS-D 402
DB 879 E-----YACLKVKDDLEDSK-----NKQELFYKSLALANELHLORIN 918
QY 403 LKTCILHGIIPEDSDIPYKNLMRSMAGFLKLENDL-GE-VKQLOELVDRCLYL-- 458
DB 919 PTVYMKSSVPEDED-----KTFVAB-----TLEMGEVYKVDTELMKLEVKR 962
QY 459 -----VSKSRD-----GTRKRSKVHDLIDYDQVREVO-----RENI- 491
DB 963 EKLELSQRLSDSEQLKQKHGHSIFLNEVYKSLKQKEQVSLRCBDELIINHNAENVO 1022
QY 492 -----FIMNDIV-----LDVSYPECSYLCYKMPKRYT-GDE----- 524
DB 1023 SCDDTVSSILDDGVMTSGAGSVSKYKSPGESEKINVEDKVSFENMTVGEESKOEOL 1082
QY 525 -INCPYGLYRALPLPVNRQLRDHNNULKRTSHVSPFHEPLLYVLKSEVYHFKLKV 583
DB 1083 ILDLPLSVTKESL-----RATQPSENDKIQKELN-----VLKSEQNDLRL- 1123
QY 584 LELRRQIDGFPREILSLIWLRYL-SLFSYGNFVDVPEICRLMNLQTFYVQFRSDIIF 642
DB 1124 -----QMEA-QRTLSLVYTHVQVREYEMENEDKALCSL-----KEELIF 1164
QY 643 AEE-TWELMOLRLHLKLPFYLPDCPSGVYDKGRHLDFSNO-----TISYSPRCCKE 695
DB 1165 AOEERIKELQKHOLELQTMKTOE--TGDECKPLHLIGLKQKAVSECSYELQRLCS-- 1220
QY 696 VIMQIONKKGIGISGNKDKYKFRSDGLPNNLVYLOOLE-----TLISLVNDY 743
DB 1221 -VLGEYTPALKEVNAEDKENSVDYISENEDPELODYREYODPOENMHTLNVTEY 1279
QY 744 SLPLVIIS-AKAPFATLKLKL-----ERTYLSWSYDITAEPLNLEVLKMDPA 793
DB 1280 NKULVLOTRLSKIMQOQDGMKLEGEENLPKEET-----EFLISHQMTNLEIDVYNKS 1335
QY 794 CGGEEMHPVWGNFRLKLLIKYSLFKWKAT--NDNPFYELRLMIRSKNLIKELPIEF- 850
DB 1336 -----KLSSLODELKRYKLEVOLESLISSLOOQOQTEYONVE 1374
QY 851 ADIH-----TLQILRECPKLGESARIRQKEQDGLNPNVVRISNPKESDS 900
DB 1375 AEHCLQKRLQAVSESTVPPSL-----PVD--SVVITSDA 1408

```

```

RESULT 11
Y08.METJA
ID Y08.METJA STANDARD: PRT: 1064 AA.
AC Q60307;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJC808.
GN MJC808.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

```





```

FT DOMAIN 1042 1063 COILED COIL (POTENTIAL).
FT DOMAIN 1681 1705 COILED COIL (POTENTIAL).
FT DOMAIN 1894 1922 MICROTUBULE-BINDING (POTENTIAL).
FT DOMAIN 2993 3092 COILED COIL (POTENTIAL).
FT DOMAIN 3242 3300 COILED COIL (POTENTIAL).
FT DOMAIN 3532 3608 COILED COIL (POTENTIAL).
FT NP_BIND 1796 1803 ATP (POTENTIAL).
FT NP_BIND 2074 2081 ATP (POTENTIAL).
FT NP_BIND 2418 2425 ATP (POTENTIAL).
FT NP_BIND 2760 2767 ATP (POTENTIAL).
FT CONFLICT 589 601 Y -> C (IN REF. 3).
FT CONFLICT 1364 1364 V -> A (IN REF. 3).
FT CONFLICT 2118 2119 E -> A (IN REF. 1).
SQ SEQUENCE 4092 AA: 471337 MW: 309DF447E8E2D6B CRC64;

Query Match 2.9%; Score 138.5; DB 1; Length 4092;
Best Local Similarity 18.2%; Pred No. 4.3;
Matches 168; Conservative 148; Mismatches 289; Indels 319; Gaps 44;

QY 32 EELCALREKVSLEVEKFEKNVGEVMDPEVEVREVAASAEYITQLRTGTVLGEMK 91
DB 1051 EDNRDRREAVEDMDINFTSLKNTIYIEAVN-VNKRHL--TERDIQIKLGSVMRAL 1105
QY 92 SOKKARRR-----ROSLQOYAEEMDMHWKSTIKODKQVSKESL----- 134
DB 1106 KAKRREPHEVYIDOLDNDFSSLSRSLSYEOL-----OKHRVYIAKSEEGV 1154
QY 135 --VHDSSSTNDILKYKNMNVGRDORCOLLEUTRSYSGEPKVPYIVGSGIGKTTLAK 192
DB 1155 ENINNLISQSLNESWSV-----RKPISPILT-----PPRAKIL----- 1187
QY 193 EYVNDSEILCRFDVHAMATISQOHKKKEILLGLHSTIKDDRVKIMGEALDMLQKSL 252
DB 1188 EEFNESITTKLKKHSHVAAAKK-----LLIPVLMQDLTHVEEVKYVDLWRSI 1238
QY 253 KRRRYLIVDDIMSCVWGVRCFPEPDNAGSRILITFNDEVACVAGVENSLSRSEM 312
DB 1239 K-----NLMEOVQRTFEP-----WCWVDVLLQLQSDIANFLRRADEL 1275
QY 313 DOD-ESMSLEKSAFSESEALPYEFETVGRQIADCHGLPLTIYVAVGLSKSRITEDMKT 371
DB 1276 PRAVKQFEMWKS-LFSQVNNLTISVNNKIIVELKD-----GALKPRH-----WNM 1317
QY 372 VAKDV--KSFVNDPDE-----RCSRVLGSLSYD--LTSDLTKCLLHFGIFPDSIDPVK 422
DB 1318 IFRDIGKRQIQKMLDKLEFSLKDVAVMLNTLNEILTKIIRAKOKEFYI-----EKSLN 1372
QY 423 NLMRSMABEF-----LKLEND--LEGVEKCLQELVDR-----CLAVY 459
DB 1373 RIKKFKKAOYEIVIEHSSGLKLVREMDVLEQACKEDLEELVSKMASNYKIFEDCLDLE 1432
QY 460 SKRSRDTKIRSKVDL--IYDLCEVRORENIFIMNDIVDVSYSPESYICMYMQP 516
DB 1433 SKL-----TKISEIQVMWVEQFYWLDLXGILGENLDIQLNPLRLETS-----K 1475
QY 517 FKRVGDEINVCYGLYRALLPVNRQLRDHNNNLKRTHSVFSHLEPLYLVLSSEV 576
DB 1476 FKSLTSE-----YKMTT-----RAFQDLPTTEIVIHIPFDTTLKLTID 1514
QY 577 HFRLLK-----VLELHRQIDGFRRELISIMWRLYSLSFYGVNDVPELCRLMNQTFI 631
DB 1515 SLKMIKSSLSFLEKRRQ--FPR-----FYFLGNDL----- 1545
QY 632 VQFRSDIILIFAEIWEIMQLRHLKLPFYLPDPCSGSVYKGRHLD-----FSNLQ 682
DB 1546 -----LKI-----IGSGNHQVSKFMKMGSTIE 1570
QY 683 TISYLSPRCCTKEVINGIONVKKLGISGNKDYKSFSDGLPNNLVYLOQLLEILSLSD 742
DB 1571 STFL-----EDFITGVHSVE--GEVLNLEKIELEKDS-----IQAGEWLNIIDTE 1614

```

```

QY 743 YSLPVIITSSAKAPATPKKIKLERLYLSMYSYIDILAEPLNLEVLKIMDDACGSEWHPI 802
DB 1615 IKL-----SVFTQPRDCLGOLK-----DGTDLVAVSKTIFQAILLSAQ----- 1653
QY 803 VMGFNRLLKLLIYSEFKFKAQNDNPPVLERLIMRSCKMLKE-----IPLEFADHRLQL 858
DB 1654 VMTELVKELQINQFQSKYKEVDMKIKGLIDKLNKSSDVNKKIEALVEY--LHNNV 1711
QY 859 I-ELRECPPLGESA---ARIOR 877
DB 1712 IGLKNCSTK--SEARLMAKVK 1733

RESULT 14
CENE_HUMAN STANDARD; PRT; 2663 AA.
ID CENE_HUMAN
AC 002224;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Centromeric protein E (CENP-E protein).
GN CENPE.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93024922; PubMed=1406971;
RA Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
RT "CENP-E is a putative kinetochore motor that accumulates just before
RT mitosis.";
RL Nature 359:536-539(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95196755; PubMed=7889940;
RA Thresher D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
RT "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
RT microtubule motor.";
RL EMBO J. 14:918-926(1995).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98437347; PubMed=9763420;
RA Chan G.K.T., Schaar B.T., Yen T.J.;
RT "Characterization of the kinetochore binding domain of CENP-E reveals
RT interactions with the kinetochore proteins CENP-F and hBUBR1.";
RL J. Cell Biol. 143:49-63(1998).
CC -1- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE
CC KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE
CC OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
CC AND/OR SPINDLE ELONGATION.
CC -1- SUBUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.
CC -1- SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CC CONGRESSION. RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: 215005; CAA78727.1; -.
CC PIR: S28261; S28261.
CC HSSP: P17119; 3KAR.
CC KIM: 117143; -.
CC InterPro: IPR001752; kinesin.
CC Pfam: PF00225; kinesin; 1.
CC PRINTS: PR00380; KINESINHEAVY.
CC SMART: SM00129; KISC; 1.

```



DR SMART; SM00369; LRR\_Type: 2.

DR SMART; SM00255; TIR: 1.

DR Receptor; PS50104; TIR: 1.

KW Receptor; Immune response; Inflammatory response; Signal;

KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.

FT SIGNAL 1 21

FT CHAIN 22 904

FT DOMAIN 22 704

FT TRANSMEM 705 725

FT DOMAIN 726 904

FT REPEAT 50 73

FT REPEAT 75 97

FT REPEAT 98 121

FT REPEAT 123 145

FT REPEAT 147 169

FT REPEAT 170 193

FT REPEAT 196 219

FT REPEAT 247 270

FT REPEAT 273 296

FT REPEAT 298 320

FT REPEAT 354 377

FT REPEAT 379 403

FT REPEAT 406 429

FT REPEAT 431 454

FT REPEAT 455 478

FT REPEAT 480 504

FT REPEAT 505 528

FT REPEAT 530 552

FT REPEAT 561 584

FT REPEAT 586 608

FT REPEAT 610 632

FT REPEAT 634 659

FT DOMAIN 754 896

FT CARBOHYD 52 52

FT CARBOHYD 57 57

FT CARBOHYD 70 70

FT CARBOHYD 124 124

FT CARBOHYD 126 196

FT CARBOHYD 247 247

FT CARBOHYD 252 252

FT CARBOHYD 265 265

FT CARBOHYD 275 275

FT CARBOHYD 291 291

FT CARBOHYD 398 398

FT CARBOHYD 413 413

FT CARBOHYD 507 507

FT CARBOHYD 636 636

FT CARBOHYD 662 662

SQ SEQUENCE 904 AA: 103828 MM: 034E05ECA7AAD2F7 CRC64;

Query Match 2.9%; Score 135; DB 1; Length 904;

Best Local Similarity 23.8%; Pred. No. 0.93;

Matches 67; Conservative 48; Mismatches 111; Indels 56; Gaps 13;

QY 599 LSLIMRLVSL-PSYGNFVPPFICRLM--NLQTFIVQRKSDIIFAEIWMQLRL 655

DB 269 LGLKWTNLTMLDLSTNNLVNNDSPAWLPQLVFFLE-YNNIQHLFSLHGLFNVRYL 327

QY 656 KLPFRFLPDCPS-GSVDKGHLDFSNLQTSYLSPR-----CCTKEYIMGIQVKKLGIS 709

DB 328 NLKRSTKQGISLASLPKIDDFSFQWLKCLEHNMEDNDIPGKSNMFTGLINLKYISLS 387

QY 710 GNRDYSKSPFSDGLPNNLVYLOQLLSLSVSYSLPVIISAKAFPATLKL-KLERT 768

DB 388 -----NSFTSLRTLTNETFVSLASPLHL-----NLTKNKISKIESD 425

QY 769 YLSWSYLDITIAELPNEVYKL---MDDACGGEWHPIYMGFNRLKILLIKYSFLKFWKA 824

DB 426 AFSW-----LGHLEVDLGLNEIGQELTGOEWKLENIFE-----IYLSYNYQL 471

QY 825 TNDNF---PYLERLMIR--SCKMLKEPIEFADIHLLQLIEL 861

DB 472 TRNSFALVPSLQRLMLRVALKNVDSPPSPQPLRNLTJIDL 513

Search completed: September 12, 2002, 14:08:19  
Job time: 577 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 12, 2002, 13:57:37 ; Search time 80.61 Seconds  
(without alignments)  
1942.196 Million cell updates/sec

Title: US-09-864-680-3  
4712

Perfect score: 1 MAHASVASLMRTIESLTLTFN.....PVDYRISNPKESDSEEH 905

Sequence: BLOSUM62

Scoring table: GaPop 10.0 , GaPop 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_ARCHA:.\*  
2: SP\_BACTERIA:.\*  
3: SP\_FUNGI:.\*  
4: SP\_HUMAN:.\*  
5: SP\_INVERTEBRATE:.\*  
6: SP\_MAMMAL:.\*  
7: SP\_MHC:.\*  
8: SP\_ORGANELLE:.\*  
9: SP\_PHAGE:.\*  
10: SP\_PLANT:.\*  
11: SP RODENT:.\*  
12: SP\_VIRUS:.\*  
13: SP\_VERTEBRATE:.\*  
14: SP\_UNCLASSIFIED:.\*  
15: SP\_RVIRUS:.\*  
16: SP\_BACTERIAP:.\*  
17: SP\_ARCHAEP:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4712	100.0	905	09SNW0	09SNW0 capsicum ch
2	1257.5	26.7	933	09LKO0	09LKO0 solanum tub
3	1245	26.4	938	09SM52	09SM52 solanum aca
4	1242.5	26.4	912	09S704	09S704 solanum tub
5	1234.5	26.2	937	09XGF5	09XGF5 solanum tub
6	980	20.8	1824	09LJL4	09LJL4 lycopersico
7	980	20.8	1824	09A485	09A485 lycopersico
8	970	20.6	1825	09LJL0	09LJL0 lycopersico
9	901	19.1	1245	09A109	09A109 lycopersico
10	875.5	18.6	1245	09A109	09A109 lycopersico
11	864	18.3	1241	09A105	09A105 lycopersico
12	852.5	18.1	1255	09A105	09A105 lycopersico
13	849.5	18.0	1271	09A107	09A107 lycopersico
14	848.5	18.0	1263	09A106	09A106 lycopersico
15	834.5	17.7	1206	09SNO9	09SNO9 lycopersico
16	834.5	17.7	1257	09SBC3	09SBC3 lycopersico

17	828.5	17.6	1257	10	081137	081137 lycopersico
18	741.5	15.7	907	10	09C644	09C644 arabidopsis
19	723.5	15.4	909	10	09M5A1	09M5A1 arabidopsis
20	717	15.2	908	10	09ZSY3	09ZSY3 arabidopsis
21	717	15.2	1584	10	09MAG6	09MAG6 arabidopsis
22	716.5	15.2	908	10	09FJK8	09FJK8 arabidopsis
23	707	15.0	1049	10	09A4H3	09A4H3 arabidopsis
24	698	14.8	901	10	09FJH5	09FJH5 arabidopsis
25	696.5	14.8	831	10	09M6E8	09M6E8 arabidopsis
26	684	14.5	906	10	09ZSY4	09ZSY4 arabidopsis
27	669	14.2	1266	10	09XET3	09XET3 lycopersico
28	667	14.2	1240	10	024016	024016 lycopersico
29	666	14.1	899	10	09C646	09C646 arabidopsis
30	656.5	13.9	894	10	09AGC0	09AGC0 oryza sativ
31	653	13.9	839	10	09SX38	09SX38 arabidopsis
32	652	13.8	835	10	09SNC5	09SNC5 arabidopsis
33	651	13.8	820	10	09M6E7	09M6E7 arabidopsis
34	637.5	13.5	847	10	09STE7	09STE7 arabidopsis
35	636	13.5	906	10	09XJF0	09XJF0 arabidopsis
36	632.5	13.4	1155	10	09AHW5	09AHW5 arabidopsis
37	629.5	13.4	1297	10	0945S6	0945S6 lycopersico
38	618.5	13.1	900	10	09C645	09C645 arabidopsis
39	614.5	13.0	1220	10	024015	024015 lycopersico
40	614	13.0	821	10	004093	004093 arabidopsis
41	612.5	13.0	904	10	038834	038834 arabidopsis
42	608.5	12.9	852	10	09SVK4	09SVK4 arabidopsis
43	608.5	12.9	926	10	09ATQ3	09ATQ3 triticum ae
44	600	12.7	920	10	09ATQ8	09ATQ8 triticum ae
45	596.5	12.7	959	10	094G20	094G20 oryza sativ

## ALIGNMENTS

RESULT 1  
ID 09SNW0 PRELIMINARY; PRT; 905 AA.  
AC 09SNW0;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE DISEASE RESISTANCE PROTEIN BS2.  
GN BS2.  
OS Capsicum chacoense.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; easterids I; Solanales; Solanaceae; Capsicum.  
OX NCBI\_TaxID=107817;  
RN [1]  
RS SEQUENCE FROM N.A.  
RX MEDLINE=20040692; PubMed=10570214;  
RA Tai T.H., Dahlbeck D., Clark E.T., Gajiwala P., Paslon R.,  
RA Whalen M.C., Stahl R.E., Staskiewicz B.J.;  
RT "Expression of the BS2 pepper gene confers resistance to bacterial  
RT spot disease in tomato."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:14153-14158(1999).  
DR EMBL: AF202179; AAF09256.1; -  
DR InterPro: IPR000767; Disease\_resist.  
DR InterPro: IPR002182; NB-ARC.  
DR Pfam: PF00931; NB-ARC.1  
DR PRINTS: PR00364; DISEASEREST.  
SQ SOURCE 905 AA; 104459 MW; 8ED897D30E67A75B CRC64;

Query Match 100.0%; Score 4712; DB 10; Length 905;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 905; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAHASVASLMRTIESLTLTFNSPMOSLSCDREELCALREKYSLEVFYKNEKNVFGEM 60  
Db 1 MAHASVASLMRTIESLTLTFNSPMOSLSCDREELCALREKYSLEVFYKNEKNVFGEM 60  
OY 61 TDFEVEVEVSAEYTIQLTLGTIVLGENSKKKARRRRRQSLQYAEWDHIMKEST 120

```

Db      61 TFEVEVREVASAEYTIOLRLGTVLGENKSOQKARRRFRQSLQOVAEDMDHKES1 120
Qy      121 KIODKGVKSVESLVDSSSTNDILKVNKNWGRDQKOLLEDTKRSYSGEPKIPY 180
Db      121 KIODKGVKSVESLVDSSSTNDILKVNKNWGRDQKOLLEDTKRSYSGEPKIPY 180
Qy      181 GNGIGKTTLAKEVYNDESILCRFDVHANATISQHNKKEILLGLHSTIKMDRVKMIG 240
Db      181 GNGIGKTTLAKEVYNDESILCRFDVHANATISQHNKKEILLGLHSTIKMDRVKMIG 240
Qy      241 EAEIADMLQSKLRKRYLLVDDINCEVWDGVRCPPEEDNAGSRILLTTRNDEVACYA 300
Db      241 EAEIADMLQSKLRKRYLLVDDINCEVWDGVRCPPEEDNAGSRILLTTRNDEVACYA 300
Qy      301 GVENFSLRMSFMDQESWLSFKSAFSSALPPEFETVGOJADECHGLPLTIVVAGLL 360
Db      301 GVENFSLRMSFMDQESWLSFKSAFSSALPPEFETVGOJADECHGLPLTIVVAGLL 360
Qy      361 KSKRTIEDKTYAKDVKSVTNDPDERCSRVILGLSYDHLTSDLCTCLHFGIFPEDSDIP 420
Db      361 KSKRTIEDKTYAKDVKSVTNDPDERCSRVILGLSYDHLTSDLCTCLHFGIFPEDSDIP 420
Qy      421 VKNLRSMWAEGLKLENDLBEVEKLOELVDRCLVYVSKRSRGTKIRSKVHDLIYD 480
Db      421 VKNLRSMWAEGLKLENDLBEVEKLOELVDRCLVYVSKRSRGTKIRSKVHDLIYD 480
Qy      481 LCVREVORENIFIMNDIVLVSYPECSYLCMKQPFKRTVDEINCYCYGLRALLTPY 540
Db      481 LCVREVORENIFIMNDIVLVSYPECSYLCMKQPFKRTVDEINCYCYGLRALLTPY 540
Qy      541 NQOLDHNNNLKRTKTHSVFPHLEPLYYVAKSEVYHFKLLVLELRHQIDGPREILS 600
Db      541 NQOLDHNNNLKRTKTHSVFPHLEPLYYVAKSEVYHFKLLVLELRHQIDGPREILS 600
Qy      601 LITMLRYSLSFGYNDVPEICRLNLOTFTYQRRSDIIFAEELIMOLRHLKLPRE 660
Db      601 LITMLRYSLSFGYNDVPEICRLNLOTFTYQRRSDIIFAEELIMOLRHLKLPRE 660
Qy      661 YLPDPSGVKGRHLDFSNLTQITISYLSPRCTKEVINGIONVKRLGISGNDYKSPFD 720
Db      661 YLPDPSGVKGRHLDFSNLTQITISYLSPRCTKEVINGIONVKRLGISGNDYKSPFD 720
Qy      721 SGLPNNLVYLOOELTSLISVDYSLPLVITISAKAPFATLKKLERTYLSWSYDIIAE 780
Db      721 SGLPNNLVYLOOELTSLISVDYSLPLVITISAKAPFATLKKLERTYLSWSYDIIAE 780
Qy      781 LPNLEVLKMDACCGEEMHPYVMGFNRLKLLIKYSFLKFPKATNDNPPYLERLMIRSC 840
Db      781 LPNLEVLKMDACCGEEMHPYVMGFNRLKLLIKYSFLKFPKATNDNPPYLERLMIRSC 840
Qy      841 KNLKEIPIEFADITLQILRECPKLGESAAARIQOEEDLGNNPVDRISNPLKESDS 900
Db      841 KNLKEIPIEFADITLQILRECPKLGESAAARIQOEEDLGNNPVDRISNPLKESDS 900
Qy      901 DSEEH 905
Db      901 DSEEH 905

```

```

Ox      NOBL_TaxID=4113;
Rn      [1]
Rp      SEQUENCE FROM N.A.
Ra      van der Vossen E.A.G., Rouppe van der Voort J.N.A.M., Kanyuka K.,
Rb      Bendahmane A., Sandbrink H., Baulcombe D., Bakker J., Stiekema W.J.,
Rc      Klein-Lankhorst R.M.;
Rd      *Homologs of a single resistance gene cluster of potato confer
Re      resistance to distinct pathogens: a virus and a nematode.*;
Rf      Plant J. 0:0-(2000)
Rg      EMBL: AF26747; AF76163.1; -
Rh      InterPro: IPR000767; Disease_resist.
Ri      InterPro: IPR002182; NB-ARC.
Rj      Pfam: PF00931; NB-ARC; 1.
Rk      PRINTS: PR00364; DISEASERESIST.
Rl      NON_TER 933
Rm      SEQUENCE 933 AA; 107303 MW; A8197F92A1B9755E CRC64;

Query Match      26.7%; Score 1257.5; DB 10; Length 933;
Best Local Similarity 35.1%; Pred. No. 4.4e-76;
Matches 345; Conservative 148; Mismatches 348; Indels 141; Gaps 30;

Qy      1 MAHASVSLMRITLESILTNSPMOISCDHREBLALREKVSLEVFKNFEKN-NVEGE 59
Db      1 MAHAATSLMRTI-----HOSMELTGC-----IQPFYKLSRLAIL---EKSCNIMGD 47
Qy      60 ---MTDFEVEVREVASAEYTIOLRLGTVLGENKSOQKARRRFRQSLQOVAEDMDHIW 116
Db      48 HEGITLIKAEIYEVATTTEDWDVDSERNVFLAONLEKSRAMEIFVLEQALECIDSTV 107
Qy      117 KESTKIODKGVSKRE--SLVHDFSSTNDILKVNKNWGRDQKOLLEDTKRSYSGEP 174
Db      108 KOMMAASDMKDLKPQTSLV---SLPEHDVQOPDINIVGRENEFPMUQLARG-GRLL 163
Qy      175 KYIPIVGMGIGKTTLAKEVYNDESILCRFDVHANATISQHNKKEILLGLHSTIKMD 234
Db      164 EYVSTVGMGIGKTTLAALVSDPYIMSRFDIARAIVSQEVYCVRVVFGILSTLSDPD 223
Qy      235 RYKMGAEIADMLQSKLRKRYLLVDDINCEVWDGVRCPPEEDNAGSRILLTTRND 294
Db      224 -----DQLADRLQKHLKGRYLVYIDDIWTEAMDKDLKCPFCYN-GSILLTTRNV 275
Qy      295 EVACYAGVENFSLRMSFMDQESWLSFKSAFSS-ALPYEFETVGOJADECHGLPLTI 353
Db      276 EVAENASSGKPPHNRIMNFDESNNLHKIKIETEGSVSPERENIGKQALCKGGLPLAI 335
Qy      354 VYVAGLL-KSKRTIEDKTYAKDVKSVTNDPDERCSRVILGLSYDHLTSDLCTCLHGI 412
Db      336 TVIAGLSKMGORDKWKQIENVSSVSTDEAQCNRVLAHSLPDLPCFLYFAI 395
Qy      413 FPEDSDIPVKNLMRSMWAEGLKLE--NDLBEVEKLOELVDRCLVYVSKRSRGTKIR 470
Db      396 FAEDEIYVKNLVDMANAEGLNEEGKSIEVEPTCINELVDRSLISIHNSIPFG-KIE 454
Qy      471 SKVYHDLIYDLCEVQVENFIMNDIVLVSYPEC--SYLCMKQPPKRYTGD-EINY 527
Db      455 RCENHDVTRRELREAR--NNMFVAVIRGNSDQNSCAQSMOCSEKRSRISIHNEELW 512
Qy      528 CPYGLRALLTPVNNQOLDHNNNLKRTKTHSVFPHLEPLYYVAKSEVYHFKLLVLELR 587
Db      513 C-----RNS-----EASIIIF-----CGKFTVLELSRFLVAVLDLG 545
Qy      588 HROIDGPREILSLIWLRLSL-----FSYGNFDPPEICRLMNLQTF-- 630
Db      546 STCPIPEPVSGLSLIHLRLSLCENPCIKQYRGSLANPSSIIIDPLSISLCTVQTQKL 605
Qy      631 -TVQRFNSD--IIFAEIYELMOLRHLKLPREYLPDPSGVKGRHLDFSNLTQITISYL 687
Db      606 CFPPEYRDVYVPEILPSEILTMPLRKLCMGMYL---RSHPEIENR-LVLSQCLHQQL 661
Qy      688 SPCRTKEVINGIONVKRLGISGNDYKSPRDGRLNNLVYLOOELTSL----- 738
Db      662 NPMYCTGSFFRLIPNLKLVFGIQODFRNRKD---PYDFRYLQLEKLEFSIRWPAQOV 718

```

OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

```

QY 739 -----ISVDYSL-----PVIISSAKAPATLKKLE-RT 768
DB 719 AACILKNTAPSGSTPEQPLRFOTELFHRTYFEMWETAPLTLPPDAPFONLKLSTFRCGEF 778
QY 769 YLSMSTYLIITAEPLMVEYLKMDACCGEEMHPYMGFRNKLKLLIKSFLKFKWATNDN 828
DB 779 FLAWMDLSIVGKLPKLEVLKLSYNPFKEWVEVAEGEPHKLFLDLKVIYIKWRASSDH 838
QY 829 PPVLERLIMRSGCNLKEIPFEPADITHLQLELRCPCPLGESAARIOKEOEDLNNPVD 888
DB 839 PPYLERLIRACYFDLSDIPRDPADITTLALDITRCQOSVGNASAOIODIDONTGSSIE 898
QY 889 VRISNPL-----KESDSE 903
DB 899 VTRNLIVFSDVSTYDDEDDDD 920

RESULT 3
ID 09SM52 PRELIMINARY; PRT; 938 AA.
AC 09SM52;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
DE NBS-LRR PROTEIN.
GN RX2.AC15.
OS Solanum acule (Wild potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBL_TaxId=103871;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RX MEDLINE=20117531; PubMed=10652152;
RA Bendaehmane A., Quercl M., Kanyuka K., Baulcombe D.C.;
RT "Agrobacterium transient expression system as a tool for the isolation
RT of disease resistance genes: application to the Rx2 locus in potato.";
RL Plant J. 21:73-81(2000).
DR EMBL: AJ249448; CAB56299.1; ".
DR InterPro: IPR000767; Disease_resist.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00560; LRR; 1.
DR Pfam: PF00931; NB-ARC; 1.
DR PRINTS: PR00364; DISEASESIST.
SQ SEQUENCE 938 AA; 107529 MM; 43853213B07327AB CRC64;

```

Query Match 26.4%; Score 1245; DB 10; Length 938;  
 Best Local Similarity 35.2%; Pred. No. 3.1e-75;  
 Matches 351; Conservative 139; Mismatches 330; Indels 176; Gaps 32;

```

QY 1 MAHAYASIMLRTESSLTFTNSPMQSLCDHREELCALREKVSLEVEVKNEFN-NVFG- 58
DB 1 MAYAAVTSIMLRTESSLTFTNSPMQSLCDHREELCALREKVSLEVEVKNEFN-NVFG- 58
QY 59 -EMTDEVEVEVSAEAETIQLRLGTVLGNKSSOKKARRRPROSLQOAVADMHIW 116
DB 48 HEELTILEVEILVAYTTEDMVDSEKSVFLAONLEERNRAMEIFVLEVALECIDSTV 107
QY 117 KESTKIDOKKOYSKE--SLV-----HDESSSTDILKVKNNMGGRDOOROLLEDLRSY 170
DB 108 KOMMATSDSKDKLPOTSSIVSLPDAFE-----OPENIMVGREVEFEMLDQVLRG- 159
QY 171 SGEPTKPIYVGMGIGTTLAKREYNDSEILCREVDHAMATISQAHNKEILLGLHSTI 230
DB 160 GRELEVSVIYMGIGTTLATKLISYDPIYMSRDIKAKATVSGEVCVRNVLLGLSLTS 219
QY 231 KMDRYAMICEAELADMLOKSLKRRKRLYLVDIWSCEVNDGVAKRCPTEEDMAGSRILLT 290
DB 220 DEPD-----DQIADRLQKHLKGRRLVYIDITWKAMDGIKLP-DCYKGSRIILT 271

```

```

QY 291 TRNDEVACYAGVENFSLRSMDEDSMELFKSAAPFSE-ALPYEPFVQIOIADCHGL 349
DB 272 TRNVEVAEFASSGKPPHNRKLMMFDESNMLKKITFEKGSYSPEPENIGKOLAKCGGL 331
QY 350 PLTIYVAGIL-KSKRTIEDMKTVAKDVKSFTYNDPDERCSRVLGISYDLHLSDTKTL 408
DB 332 PLATIVYAGILKISKTIDEMQNVAMENSVYSTDEACRMVALSYHHLSPKPCFL 391
QY 409 HGEIPEPDSIDIPYKNIMRSMABGLKLE--NDLGEVEKCLQELVDRLVYLSKRSRG 466
DB 392 YFAIFEDERISVTKLVEILMAVEGFINEEGRKSIEEVAETCINELVDRSLISYHLSFG 451
QY 467 TKIRSKVNDLIDLCVREVORENIFIMNDIYLVAVPCCSYLCMKMPKFKVTGDEIN 526
DB 452 -KIESCGMDVIRELCLEARR--NMNFVNI-----RGKSDQ-N 486
QY 527 YCPYGLRALTPVNRQLDHDNNNLKRTHSVSEHLEPLYYVLKSEV----- 575
DB 487 SCAQSMQSRFSK--RSRIH-----KLEELAMCRNSEAHISIMLGFGEC 529
QY 576 ---VHFKLLVLELNRHROIDGFPREILSLMIRYSL-----FSYGNPD 616
DB 530 VLELSEFKLVRLVDLGTNTWPIFPGSVLSLILRLYLSLRNPCLQOYQGSKEAVPSSID 589
QY 617 VPPEICRLMNLQTFIYO-RPRSDI-IIFAEIEMQLRLKLPREFLPDPCPGSYDKGR 674
DB 590 IPIISISLCYLOTFKINLPFPSPYFPIIPSEILTMQRLKMDWYL--RSHEPTENR 646
QY 675 HDFSNIQATISYSPRCCTKEVIMGIQNVAKIGISGNKDDYKFSRSGLPNNIYVLOLE 734
DB 647 -LVKMLQCLNQNLNPRCTGSFRLPNLKLQVFGVEPDERNSODL--YDRRYTQLE 702
QY 735 ILSL-----ISVDYS-----LTPVITSSAK 754
DB 703 ELTFRLYPPYACFLKNTAPSGSTPODPLRFOTELHKEIDFGTAPPTLLP-----PPD 758
QY 755 APPATLKKLLEKTY-LSMSYLDIIAELPMLEVLKMDACCGEEMHPYMGFRNKLKLL 813
DB 759 AFQONLKLSTLRFREFSVAMKDLIVGKLPKLEVLISLWNAFICGMEVVEGPHLNFLE 818
QY 814 IKYSFLKFKWATNDNPPVLERLMIRSGCNLKEIPFEPADITHLQLELRCPCPLGESSA 873
DB 819 LDVYIRYWRASSDHPFYLERLILRDCRNDSIPRDPADITTLALDIDYCOQSVNVSAS 878
QY 874 RIKOEQEDLNNPVDVRI-----SNPLKESDSDS 902
DB 879 QIOODIODNYGSSIEVTRHLFTPKSVTYVEDDDDS 914

```

RESULT 4  
 ID 09S704 PRELIMINARY; PRT; 912 AA.  
 AC 09S704;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)  
 DE NBS-LRR PROTEIN.  
 GN GPA2.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OX NCBL\_TaxId=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ROOT;  
 RA Bendaehmane A., Kanyuka K., Baulcombe D.C.;  
 RT "Agrobacterium transient expression system as a tool for disease  
 RT resistance genes isolation: application to Rx2 locus in potato.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 SQ SEQUENCE FROM N.A.

RA Van der Vossen E.A.G.;  
 RL Submitted (OCr-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AJ249449; CAB55838.1; -  
 DR EMBL: AF195939; AAF04603.1; -  
 DR InterPro: IPR000767; Disease\_resist.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR002182; NB-ARC.  
 DR Pfam: PF00560; LRR; 2.  
 DR Pfam: PF00931; NB-ARC; 1.  
 DR PRINTS: PR00364; DISEASERST.  
 SQ SEQUENCE 912 AA; 104551 MW; 65EFD9C86688F768 CRC64;

Query Match 26.4%; Score 1242.5; DB 10; Length 912;  
 Best Local Similarity 35.1%; Pred. No. 4.4e-75;  
 Matches 340; Conservative 146; Mismatches 333; Indels 149; Gaps 29;

QY 1 MAHASIASIMRTIESLITFNSPMQSLSCDHRELCALREKVSLEVFYKNEKN-NVGE 59  
 DB 1 MAYAAVTSIMRTI-----HQSMELTQCD---LQPFYEKLKSLRAIL---EKSCHIMGD 47  
 QY 60 ---MTDFEVEVEVASAAEYTIQLRTGLTVIGENKSQKKARRRROSLOQVAEDMDHT 116  
 DB 48 HEGITILEVEITLVAATYTDMDVDESRRVFLARNGKRSRAMWGIFVLEQLAECIDSTV 107  
 QY 117 KESTRIQDKGKOVSK--SLVHDFSSSTNDILKVNKNMGRDQKOLLEDTLSYSGEP 174  
 DB 108 KQMATSDSMKDLKQTSLSV---SLPHDVQBPENIMVGNRENEFMMDQLARG-GRGL 163  
 QY 175 KVIPIVGMGIGKTTLAKVYNDESILCFDYHAMATISQOHKKKEILLGLHSTIKMD 234  
 DB 164 EVASIVGMGIGKTTLAKVYNDESILCFDYHAMATISQOHKKKEILLGLHSTIKMD 223  
 QY 235 RVKMGAEALADMLCKSLKRRYLIYDDIWSCEYWDVGRCEFPEDNAGSRILLTTND 294  
 DB 224 ---YQADQLOKHLKGRYLVYDDIWTTEAMDIDKLCFPCODN-GSRILLTTNRV 275  
 QY 295 EVACYAGVENFSLRMSFMDODESMFLKSAFASSE-ALPYEFYVQKQIADCHGLPLTI 353  
 DB 276 EVAEYASGKRPNNHRLMNFDESNNLHKKIFKEGSSYSPENINGKQALACGGGLPLAI 335  
 QY 354 VYVAGLL-KSKRTIEDKTVAKDVSPYTNPDDEKSRVLGISTYHLSIDKTLIHGCI 412  
 DB 336 TLIACTLISKISTDEWONVAVNSVSTDEAKCMRLAISTYHLSIDKTLIHGCI 395  
 QY 413 FPEDSIDPVKNLMRSMAGELKLE--NDLEGEVEKCLQELVDRCLTVYKSRSDGTKR 470  
 DB 396 FAEDRIYVNNLVELMAVEGLNEEGKSIEVAETCINELVDRCLTVYKSRSDGTKR 454  
 QY 471 SKCHADLIYDLCEVQRENTIFIMNDIVLDSYSPC--SYLCMYKQPEFKRVTGDEINVC 528  
 DB 455 RCGMDVTRICLREAR--NNMFVAVIRGKSDQNSCAQSMCCSFKR----- 499  
 QY 529 PYGLYRALLTFVNRLRHDNNNL---KRTHVSFHLERPLIVYLKSEVYHFKLVL 584  
 DB 500 ---SKSTIHNEBELWCRNSEAHSTITLCI---FKCVTLLESLFIVRL 542  
 QY 585 ELRRHROIDGPREILSLTLRYLSL-----PSYGNFVDPPEICRLMNTQT 629  
 DB 543 DLGLTCTGFPSGVLSTLHLRYLSLRFNPRLOQYRGSKENAPSSIDIDPLISISLCYTQT 602  
 QY 630 F-IYQRRSDI-TTFAETIWMQLRHLKRLPYLPDCSSVDKGRHLDSNLOTISYL 687  
 DB 603 FKLHPNCPYPLIPSELITMPQRLKLCGMWNL---RSHEPTENR-LVLSLQCLNEL 658  
 QY 688 SPKCTKEVINGIYNNKLGISGNKDYKSKPRDGLPNNLVLVYLOOLETSLISVDYS--- 744  
 DB 659 NPKICTGSLFLFNLKLEEVGYKEDRNKDL---YDFRYLVQLEKLA-FSTYISSA 714  
 QY 745 ---LLPVIISAKAPATLKK 762  
 DB 715 CELKNTAPLGSTPDPLRFQWETLHLETHSRATAPPTDVTFFLLP---PPDCFPQNLKS 770

QY 763 LKLERT-YLWSYTLIIAEPLNLEVLKMDACCGEEMHPIVGNFNKLILIKISFLK 821  
 DB 771 LTRSGDFLAKMDLSVIGKLPKLEVLQLSHNAKGEWEVEGFPKLFLLDSITIRY 830  
 QY 822 WKATNDFPVLERIMTRSCNKLKEIPFADHTLQILBELRECPKIGESARITOEQD 881  
 DB 831 WRASSDHPFLYERLFLSDCYLSDIRDFADITTLALIDIFRCQOSGNSAKQIQQDID 890  
 QY 882 LGNNPDV 889  
 DB 891 NVGSIEV 898

RESULT 5  
 ID Q9XGF5 PRELIMINARY; PRT: 937 AA.  
 AC Q9XGF5;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE RX PROTEIN.  
 GN RX.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; eunsterids I; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID:4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. CARA;  
 RA MEDLINE:99264301; PubMed:10330465;  
 RA Bendahmane A., Kanyuka K., Baulcombe D.C.;  
 RT "The Rx gene from potato controls separate virus resistance and cell  
 RT death responses.";  
 RL Plant Cell 11:781-791(1999).  
 DR EMBL: AJ011801; CAB50786.1; -  
 DR InterPro: IPR000767; Disease\_resist.  
 DR InterPro: IPR002182; NB-ARC.  
 DR Pfam: PF00931; NB-ARC; 1.  
 DR PRINTS: PR00364; DISEASERST.  
 SQ SEQUENCE 937 AA; 107489 MW; 98F96B2EE31D3490 CRC64;

Query Match 26.2%; Score 1234.5; DB 10; Length 937;  
 Best Local Similarity 35.1%; Pred. No. 1.6e-74;  
 Matches 345; Conservative 144; Mismatches 343; Indels 131; Gaps 32;

QY 1 MAHASIASIMRTIESLITFNSPMQSLSCDHRELCALREKVSLEVFYKNEKN-NVGE 59  
 DB 1 MAYAAVTSIMRTI-----HQSMELTQCD---LQPFYEKLKSLRAIL---EKSCHIMGD 47  
 QY 60 ---MTDFEVEVEVASAAEYTIQLRTGLTVIGENKSQKKARRRROSLOQVAEDMDHT 116  
 DB 48 HEGITILEVEITLVAATYTDMDVDESRRVFLARNGKRSRAMWGIFVLEQLAECIDSTV 107  
 QY 117 KESTRIQDKGKOVSK--SLVHDFSSSTNDILKVNKNMGRDQKOLLEDTLSYSGEP 174  
 DB 108 KQMATSDSMKDLKQTSLSV---SLPHDVQBPENIMVGNRENEFMMDQLARG-GRGL 163  
 QY 175 KVIPIVGMGIGKTTLAKVYNDESILCFDYHAMATISQOHKKKEILLGLHSTIKMD 234  
 DB 164 EVASIVGMGIGKTTLAKVYNDESILCFDYHAMATISQOHKKKEILLGLHSTIKMD 223  
 QY 235 RVKMGAEALADMLCKSLKRRYLIYDDIWSCEYWDVGRCEFPEDNAGSRILLTTND 294  
 DB 224 ---DQADQLOKHLKGRYLVYDDIWTTEAMDIDKLCFPCODN-GSRILLTTNRV 275  
 QY 295 EVACYAGVENFSLRMSFMDODESMFLKSAFASSE-ALPYEFYVQKQIADCHGLPLTI 353  
 DB 276 EVAEYASGKRPNNHRLMNFDESNNLHKKIFKEGSSYSPENINGKQALACGGGLPLAI 335  
 QY 354 VYVAGLL-KSKRTIEDKTVAKDVSPYTNPDDEKSRVLGISTYHLSIDKTLIHGCI 412

Db 336 TVIAGLSKMGRLDEMORIGENSVSTDEPAOCMRVLAISTHHLKPCFLYPAI 395  
 Qy 413 PEPEDSDIPKNIIMRSMMAEGFLKLE--NDLEGEVEKCIQELVDRCLVYSKRSRGTIR 470  
 Db 336 FIEDQISVNEVELMPPVGFLENEEGKSIEVATTCINELDRSLIFHNPSRGT-IE 454  
 Qy 471 SCKVHDLIYDLCEVREVORENIFIMNDIYLVSYPECSYICMVKMOPKAVTGDEINCY 530  
 Db 455 SCGMHVDYRELCRLBR--NMNFVNYI-----RGKSDQ--NSCAQ 490  
 Qy 531 GLYRALTPVNNQOLDHONNLL-----KTHSVF--SPHLPLVYLVKSEVYHFKLV 583  
 Db 491 SMOSEKRS--RSRIKHVEELAMCNSPASHIIMGFECVTL-----ELSEKLVAV 541  
 Qy 584 LELRHROIDGFPREILSLIMRYLSL-----FSGNFDVPPETICRLMNO 628  
 Db 542 LDGLNTWPIFFSGVSLHLRLYLSRFNPCLQOYOGSKAVPSSIIDIPLSISLCYIO 601  
 Qy 629 TTVVO-REFSDI-IIFAEIWMLOLRHLKLPFYLPDPPSGSVKGRHLDPSTQITISY 686  
 Db 602 TKRLNLPFSYYPFLIPSEILTMPRLTLCMGWNYL--RSHEPTENR-LVKNLQCLQ 657  
 Qy 687 LSPRCCTKRVINGIOVKKIGISGNKDYKSPFDSGLPNNLVYLOLEILSL----- 738  
 Db 658 LNPRTYGTSGFPLFPYKLTQVGFVEDPFRNSQDL--YDFRYLYOLELTFRLYYPVA 714  
 Qy 739 -----ISVDYS-----LLPVITSSAKAPATIKLKLK 767  
 Db 715 CELKNTAPSGSTODPLRFQTEILHKEIDFGTAPPLLP--PPDAPQNKSLTFPG 770  
 Qy 768 TX-LSMSYDITAEPLNLEKIMDDACGGEWHPIVMGFNRLIKLKYSPFKWATN 826  
 Db 771 ERSVAKDLSYVKRLKLEVLISNNAPFKSEVYVEEGPHKLPFLDVIYIRYMRAS 830  
 Qy 827 DNFVLERLMTIRSKNLKEIPFADITHLQLELRECPKIGESAPRIQKECEDJGNNP 886  
 Db 831 DHPYLERVILRDCRNLDSPROFADITLALIDYCCQSVNSAKOIODIDYNGSS 890  
 Qy 887 VDVRI-----SNPLKESDSDS 902  
 Db 891 EVHTRHLFLPKSVTTVEDDDDS 913  
 RESULT 6  
 Q9LID4 PRELIMINARY; PRT; 1824 AA.  
 AC Q9LID4;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE PRF.  
 OS Lycopersicon pimpinellifolium (Culant tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; eusterids I; Solanales; Solanaceae; Solanum.  
 OC NCBI\_TaxID=4084;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. RIO GRANDE 76R; TRANSPOSON-RETROTANSPOSON TOTOTI;  
 RA Lavelle D.T., Oldroyd G.E.D., Dalbeck D., Staskiewicz B.J.,  
 RA Michalmore R.W.;  
 RT "the structure and evolution of the Pto locus in tomato."  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP20602; AAF76308.1;  
 DR InterPro: IPR000767; Disease\_resist.  
 DR InterPro: IPR001916; Lactalbumin\_lysozyme.  
 DR InterPro: IPR002182; NB-ARC.  
 DR Pfam: PF00931; NB-ARC; 1.  
 DR PRINTS: PR00364; DISEASERISN.  
 DR PROSITE: PS00128; LACTALBUMIN\_LYSOZYME; UNKNOWN\_1.  
 SQ SEQUENCE 1824 AA; 209574 MW; 1F14E7D662DEBAC6 CRC64;

Query Match 20.8%; Score 980; DB 10; Length 1824;  
 Best Local Similarity 30.9%; Pred. No. 56-57;  
 Matches 288; Conservative 167; Mismatches 342; Indels 136; Gaps 33;  
 Qy 26 LSCDHREELCALREKVSLEVEYKNE--EKNVFGEMTDEVEVEYASAAEYI----- 78  
 Db 972 LIIDLKHOLESYKEGELLCRSFIDHSESSEYDEHDEACGLIARVSVAAYAEYIDSCLAY 1031  
 Qy 79 -----QRLTGVLDGENKSQKKARRRFRQSLQOYAEEDHDMKRSKTL 122  
 Db 1032 SHPLWYKVLWISSEVLBNIKVYKRVGECE-----RRNIEVYHEVAKTTTY----- 1079  
 Qy 123 QDKGRKVSKEVLHDESSGNLILKYNMVGGRDQKOLJEDITRSYSGEPK--VPIYV 180  
 Db 1080 -----APFSATQ-----RANEHEGQODIIDEKDL-----LGSPELDIY 1121  
 Qy 181 GMSGIGKTTLAKENVYDESLICFEDVHAMATISQHNKKEITLGLHSTIKMDPRKMIG 240  
 Db 1122 GMPGLGKTTLAKKIYNDPEYTSRFDVAOCVYQYLSWRBELLTLLINDVLEPSDRNEK-E 1180  
 Qy 241 EELADMLQKSLKRRKRYLYVLDIWMSCVWDGVRCFPEPDNAGSRITLTTRDEVACYA 300  
 Db 1181 DGEIADBLRFFLTFRFLIIDDYWDKYVNDNLCMCESDVSNR--SRITLTTRLDVAEYV 1239  
 Qy 301 GVENFSLRMSFMDQDSWSLFSKSAFSSALPYEFETVGQIADDECHGLPLTYVYVAGL 360  
 Db 1240 KCESDPHHLRLFRDDESWTLQKEVFGESCPPELEDVGEISKSGPLSVYLVAVGL 1299  
 Qy 361 K-SKRTIEPMKYAKKDVKSQSVTNDPDERGSRVGLSYDHTLSDTKTLHFJGFPEDSDI 419  
 Db 1300 KKKKTLTDSKVVYQSLSSORISLESIS-IIGFSKNIPLHYKPCFLIFGGILOGKDI 1358  
 Qy 420 PKNLMRSMMAEGFLKLEND--LEGEVEKCIQELVDRCLVYSKRSRGTIRSKCYVHL 477  
 Db 1359 HYSKMTKLMWAEQVQANNKKGEDTAQGLDLDIGNVYAMAK-RPNKTKVKTCRIHDL 1417  
 Qy 478 IYDLCVREVORENIFIMNDIYLVDS-----YPCSYICMVKMOPKAVTGDEINCYCYGL 532  
 Db 1418 LHKFCWEKAKQE-----DELLQINSGEVGPE--RLEERYL--FVHYSODEID-----L 1462  
 Qy 533 YRALTPVNNQOLRDH--DNNNILKTHSVFSPHLEPLVYLVKSEVYHFKLVLELRHROI 591  
 Db 1463 WRPSRSVVRSLLENADIDPNLMPRDISFTPE-----SKIKVYVLDLESFNI 1509  
 Qy 592 DG-FPREILSLIMRYLSLSYGNFDVPPETICRLMNOITFIQVRFSDIIFAEIWMEL 650  
 Db 1510 GGFPTFLOVLIQMKYFAAQIDAN-SIPSSIAKLENIETFEVVRGIGEMILPC-SLIKMV 1567  
 Qy 651 QLRHLKLPFRYLPDPPSGSVKGRHLDP-----NIQITVSLPRCC-----TKEVI 697  
 Db 1568 KLRIIHV-----NDRVSGFJHEHNDVLTGNSQLPNLETFS--PRLEFYGKDAEKVL 1616  
 Qy 698 MGIONVKKL-----GISGNKDYKSPFDSGLPNNLVYLOLEILSLISVDYSLPVISS 752  
 Db 1617 KMKPKLKLKSLISFGTIGYSKSLKG-KCYVRP-RLDPLSHLESIAKIVSNS--PAKLP 1671  
 Qy 753 AKAPATLKKLLETRYLSWSYDIIAELPNLEVLKIMDDACGGEWHPIVMGFNRLIKL 812  
 Db 1672 KFNPPSOARELTLSKFRLPWQISIIAELPNLVILIKLILRAFGDHWEVVKSEFLEKYL 1731  
 Qy 813 LKTSFLKFKATNDPNPVLERLMTIRSKNLKEIPFADITHLQLELRECPKIGESA 872  
 Db 1732 KIDMLKVYQWISIDAPAEKLLHVLTKCKLEKIPREDAVCLARVEVNMNANVANS 1791  
 Qy 873 ARIQKEO-EDLGNPVDYRISNP--LKESDSDS 902  
 Db 1792 ODITQMOHEVIANDSFYVTIOPDMSKQPIIDS 1824  
 RESULT 7  
 Q96485  
 ID Q96485 PRELIMINARY; PRT; 1824 AA.  
 AC Q96485;

```

DT      01-FEB-1997 (TREMBLrel. 02, Created)
DR      01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      PRF.
GN      Lycopersicon esculentum (Tomato).
OS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
RN      [1]
RX      NCBI_TaxID=4081;
RP      SEQUENCE FROM N.A.
RC      STRAIN=RIO GRANDE;
RX      MEDLINE=96291405; PubMed=8689679;
RA      Salmeron J.M., Oldroyd G.E., Rommens C.M., Scottfield S.R., Kim H.S.,
RT      Laveille D.T., Dahlbeck D., Staskavics B.J.;
RT      "Tomato PtoI is a member of the leucine-rich repeat class of plant
RT      disease resistance genes and lies embedded within the Pto kinase gene
RT      cluster."
RL      Cell 86:123-133(1996).
DR      EMBL, U65393; AAC49408.1; -.
DR      InterPro: IPR001916; Lactalbuma_lysozyme.
DR      InterPro: IPR002182; NB-ARC.
DR      Pfam: PF00931; NB-ARC: 1.
DR      PROSITE: PS00128; LACTALBUMIN_LYSOZYME; UNKNOWN_1.
SO      SEQUENCE      1824 AA; 209388 MW; B6a63CEbCAc98BE82 CRC64;

```

QY	241	EAADADLOSIAKRRVLYLVDIMSCVMDVGRCCFPEDNAGSNILITFTNDYACA	300
Db	1182	DGELATERRRLTKRLLILDVMDYKWDNLCMCFSPVSNK-SKILITLTDVAEYV	1240
QY	301	GVENFSLRMSFMODESWSLFSKAASFSLAPYEFETVGOIADBECHGLPTIVVAGL	360
Db	1241	KCESDPIHHLRFNRDESWITLLQKEVFOGSCCPRELDVDFELISKSGRLPSVLVAGL	1300
QY	361	K-SKRTIEDKTYAKDVKSVTYNDPDERGSRVIGLSYDHLTSDLTCLLHSGIPEDSDI	419
Db	1301	KOKKRTITDSKRVVQEOSLSISORIGLSLEESIS-IIGFSYKMLPYHLKCFELYFGFGLOGKDI	1359
QY	420	PVKMLMSMAAEGKIKLENO--LEGEVEKLOELVRCVILVSKRSROSTKIRSCVNDL	477
Db	1360	HYSKMTLMTVAEEGVVANNKSGEDPDAQGFIDLIRNLVMAEMK-RPNAKAKTCHIDL	1418
QY	478	IYDLCVREVORENIFIMDVIDVS-----YPCSYLCMKMQPFKRYGTDEINYCPYL	532
Db	1419	LHKCKMEKAAQ-----DPLQINSGEVGFPE--RLEBYRL--FVHSYODEID-----L	1463
QY	533	YRALTFVNNQLRDH--DNNLLKRTHSVSEFHLERPLYYLKSGVYHFKLYKLELRHQI	591
Db	1464	WRSPRSNVRSLIFENADPDMLMPRODISLFE-----SFKLVKVLDESNI	1510
QY	592	DG-FPRPILSLIMLRYLSLFSYGNPVPVPEICLMMIQTPIYQRFSDRIIIPAEIEIWM	650
Db	1511	GGTFPEIQLVLOMKRYAAQTGAN-SIPSSIAKLEMLFVVRGLGEMILPC-SLKNV	1566
QY	651	QLRHKLKPRYLLPDCSGSGVDKGRHL-----DESNLQTSIYSIPRCC---TKVYIMGIQ	701
Db	1569	KLRIH-----HVNDRVSFGLREMMADVLTGNSOLPNEFTS--TPRLFYGKAELKIRKP	1621
QY	702	NVKLT-----GISGNKDDYSFSPDSGLPNNLYVLODELISLSDVSYLLPVIISAKAF	756
Db	1622	KLRLKSLCIFSGTFGYSKRLG-RCVRRP-RLDLSHLESLKLVSNY--PAKLHKENE	1676
QY	757	PATLKTKLERTYLSWSYDIIIAELPNLEVLKIMDACCGEENHPYVMGFNLKILLIKY	816
Db	1677	PSQIRELTLSKFRLPWQIITIAELRNVLTKILLRFAFGDMWEKDSFELKTKLKDND	1736
QY	817	SFLKFWKATNDNFPVLERLWIRNSCKNIKETPIEFADITHTLQLELRECPKLGESAARQ	876
Db	1737	LKVQWMSISDAPKLEHILVLTCKKLEKIPSRFEEDAVCLNVEVWCMNVANSAODIQ	1796
QY	877	KEQ-EDLGNPNPVYRISNP--LKESDS	902
Db	1797	TMOHEVIANDSTVTIOPPWMSKEQPLDS	1825
RESULT	9		
ID	094108	PRELIMINARY;	PRT: 1246 AA.
AC	094108;		
DT	01-DEC-2001 (Tremblrel. 19, Created)		
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)		
DE	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DN	TOSPOVIRUS RESISTANCE PROTEIN B.		
GN	SW5-B.		
OS	Lycopersicon esculentum (Tomato).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots.		
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
ON	NCBI_TaxId=4081;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. STEVENS;		
RA	Folkertsma R.T., Spassova M.I., Prins M., Stevens M.R., Hille J.,		
RA	Goldbach R.W.;		
RT	"Construction of a bacterial artificial chromosome (BAC) library of		
RT	Lycopersicon esculentum cv. Stevens and its application to physically		
RT	map the Sw-5 locus."		
TL	Mol. Breed. 5:197-207(1999).		

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, STEVENO;  
RA Prins T.W., Spassova M.I., Prins M., Klein Lankhorst R.,  
RT Goldkette R.T., Hille J., Goldbach R.W.;  
RU "The sv-5 locus confers resistance to 'respiruses'";  
DR Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
EMBL; AY007366; AAG31014.1; -  
DQ SEQUENCE 1246 AA; 143889 MM; EC334B327ECC413C CRC64;



Db 1133 EYLOL-HDVCFPOSEKCLDITPHKLLKLYKLNISR-WDYSESPLETLTVIKCI 1190

QY 842 NLKEPIEFADITLQLEL-RECPKLGSAARIKEQED 881

Db 1191 DLKEPIELFADITLQLEL-KLIGSKWVLEDSAVAKKEIKD 1231

RESULT 10

Q94109 PRELIMINARY; PRT; 1245 AA.

AC 094109

DT 01-DEC-2001 (TREMELREL. 19, Created)

DT 01-DEC-2001 (TREMELREL. 19, Last sequence update)

DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)

DE TOSPOVIRUS RESISTANCE PROTEIN A.

GN SW5-A.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4081;

OX 11

RP SEQUENCE FROM N.A.

RC STRAIN-CV. STEVENS;

RA Folkertsma R.T., Spassova M.I., Prins M., Stevens M.R., Hille J.,

RA Goldbach R.W.;

RT "Construction of a bacterial artificial chromosome (BAC) library of

RT Lycopersicon esculentum cv. Stevens and its application to physically

RT map the Sw-5 locus."

RT Mol. Breed. 5:197-207 (1999).

RN 121

RP SEQUENCE FROM N.A.

RC STRAIN-CV. STEVENS;

RA Prins T.W., Spassova M.I., Prins M., Klein Lankhorst R.,

RA Folkertsma R.T., Hille J., Goldbach R.W.;

RT "The Sw-5 locus confers resistance to Tospoviruses."

RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY007367; AAC31013.1; "

DR SEQUENCE 1245 AA; 143538 MW; 251BEFA58FB00B46 CMC64;

Query Match 18.6%; Score 875.5; DB 10; Length 1245;

Best Local Similarity 29.2%; Pred. No. 3.1e-50;

Matches 272; Conservative 167; Mismatches 341; Indels 153; Gaps 33;

QY 8 SLMTIESILTFNPMOSLSDHREICALEKYSLEVVKNKKNVNGEMTD----- 62

Db 394 SLKRLKEMSTSKSGLGFLM--KPLGLNLEKELSLTSLIEK-ELSSIFSVDVHHEHNT 449

QY 63 -----FEVEYEVASAEYTIQLRL--TGTVLGENKSKQKKARRRROSLQ 107

Db 450 PKDQRTINLAEEVAIDSLAQYNAFLHIFCSLPTIYK-----IKQ 494

QY 108 VAEDMDIWEKSTKIQDKGVKSVLHDESSSTNDILKYKNNMGRDQRKQLEDLT 167

Db 495 INVEVTEKMSDIDPLNHYAAPLKHLPDRHSNLYTD-----EEVVGFEKQAEELIDYL 549

QY 168 RSYGGEPRVPIVGMGGIGKTTAKKEYNDESLCRFDVHAMATISQOHKKEILGLH 227

Db 550 RG-TNEDDVPIVGMGGIGKTTAKKLYNDLIYSRFDVAMCTISQYHIELLQDIFS 608

QY 228 STIKMDRVKMGIEALADMLQSLKRRRYLIADDIMSGVDGVRCPTEEDNAGSRI 287

Db 609 QVTFENNGATVD--VLADMLRRLKRRKRYLIYDDMDMCMWMDLRLSP-DVGIRSI 665

QY 288 LITTRNDENVACYAGVENFLSMFSMDQESWSLFKSAFSEALPYFFETVGAQIADCH 347

Db 666 VVTRLEEVGKQVYKHYDPSLPLTTEESQQLQKVFQEKDCLPLQDVSAVAKECK 725

QY 348 GLPLTIYVAGLLSKRTIEDMKTVARD-VKSFYTNPDRCRSVGLSDHLTSDLKTC 406

Db 726 GLPLTIYVAGLLSKRTIEDMKTVARD-VKSFYTNPDRCRSVGLSDHLTSDLKTC 785

QY 407 ILAHGIFPESDIPYKNNLMRSMAGFLKLEND-----LEGEVEKQLOELVRCILVSK 461

Db 786 LLYMGAFESDARIPTASTILSLMTADGF--VENTESGRMLKEEBAEGLMDLLSNLVMISK 843

QY 462 RSRDGKIRISCVHDLIYDLCAREVORENIFIMDVIDVSYPECSYLKMKQPFKRYT 521

Db 844 RSYKG-KVYKQGVHVVHNFCL-EKSRKAFYL-----AVK 877

QY 522 GDEINCPYGLYRALLTPYNNRQLRDHNN--NLKRTYSVSFHLPELY-----YV 570

Db 878 GQCIQFOPSD-WKG--TRVSFSESLSEKFAVSKTKPFGHQLLITNNRAKSIDVI 934

QY 571 LKSEVHVFELVLELRHQIDGFPREILSLIWLTYLSFSY-----GNFVPEICFLW 625

Db 935 LECQISELRLLVLDL-----SYVEFLSLAKFPYLMQKYLAVKADKFFEDG-SILP 988

QY 626 NLQETIVORFRSDIIFAEELWELMQLRHLKPRYLPDCPSGSYDK-GRHLDFSNIQT 683

Db 989 HIEFTIVKFCYGMGL-PVSEFMKKLRHAF-----GNAEFDKQGLEGSSTLENL 1039

QY 684 -----ISYISPCCTKEVIMGIONVKKIGISGNKDDYSEFRSGLPNNLVYLOQ 732

Db 1040 RLKNIIGFDGVLSRR-----PNIQLOLITFGNDEEFTPK--LENLTQLOQ 1088

QY 733 LEILSLISVDSLPLVLISSAKAPATLKLTERTYLSWSYLDIAPLNVLEKLMDD 792

Db 1089 LQD-----SFARPHLSGLQPSNKLKVLLEGHIE-SVISIAPLSLEYQL-QD 1138

QY 793 ACC--GEEMHPYVGMFNRLKLLIKYSPLKPKATNDNPFVLERMITSCKNAKEIPEF 850

Db 1139 VCFPOSEEWCLDITFPKRLKLVNLPISRWDSSESPLETLTVIKCODLEPIPSF 1198

QY 851 ADIHTLOLEL-RECPKLGSAARIKEQEDL 882

Db 1199 VDIPLTEQIKLGSKWVLEDSAVAKKEIKDI 1231

RESULT 11

Q94105 PRELIMINARY; PRT; 1241 AA.

AC 094105

DT 01-DEC-2001 (TREMELREL. 19, Created)

DT 01-DEC-2001 (TREMELREL. 19, Last sequence update)

DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)

DE TOSPOVIRUS RESISTANCE PROTEIN E.

GN SW5-E.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4081;

OX 11

RP SEQUENCE FROM N.A.

RC STRAIN-CV. STEVENS;

RA Folkertsma R.T., Spassova M.I., Prins M., Stevens M.R., Hille J.,

RA Goldbach R.W.;

RT "Construction of a bacterial artificial chromosome (BAC) library of

RT Lycopersicon esculentum cv. Stevens and its application to physically

RT map the Sw-5 locus."

RT Mol. Breed. 5:197-207 (1999).

RN 121

RP SEQUENCE FROM N.A.

RC STRAIN-CV. STEVENS;

RA Prins T.W., Spassova M.I., Prins M., Klein Lankhorst R.,

RA Folkertsma R.T., Hille J., Goldbach R.W.;

RT "The Sw-5 locus confers resistance to Tospoviruses."

RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY007367; AAC31017.1; "

DR SEQUENCE 1241 AA; 143224 MW; EF64DCDEC0378082 CRC64;

Query Match 18.3%; Score 864; DB 10; Length 1241;

Best Local Similarity 30.5%; Pred. No. 1.8e-49;



Matches 277; Conservative 163; Mismatches 327; Indels 142; Gaps 35;

```

QY 35 CALREVSSLEFVKNFEK-----NNVFGEHTDEFEVEYREVASAETITQLRLTGTVL 89
DB 393 CMEKQSTL---ISMLEKSLSSIFRDVKNHEHNDL--QRTTNLAYEAGVSD 446
QY 90 NKSOKKARRRPROSLOQVAEDMDHIMWKESTKIQDGKOVSKESLWDF-----SSST 142
DB 447 SICAKYNVWHCCSLPTLLEIKQINAEYTEMMSADILNPIYVAPKHLPTRRSNPI 506
QY 143 NDLKYNKNNVGRDQKQLEDLRSYSGEKPVIVYMGIGTGTAKAYVNDSEIIC 202
DB 507 TDEEIDESEIVGRIKKEKIIQCLLNG-TNDLDVPIVEMGGCKTIAKYNVNSNIYS 565
QY 203 RRDVHAMATISQOHNKEKILLGLHSTIKMDRVKMIIGAELADMLQKSLKRRYILVD 262
DB 566 HEDVRAWCTIVSOTYNNRKLQELTLOVTSKQD--KGEYEDLDLDELKSLKRRYILVD 623
QY 263 DIMSCVMDGVRCFPTEDNAGSRILLTTR---NDEVACVAGENFSLRMSFMDQESM 318
DB 624 DMMDCAMMDLRLSPDFEGR--SRIVYTRLEKVEGQVCH--TDPYSL--PRLTTEESC 678
QY 319 SLFKSAFSSSEALPYEFETVQKQIADCHGLPLTIVVAGLLKSKRTIEDMKTAVDVS 378
DB 679 KLLQKVFQKEDCPRELQOVVAKCKGLPLVIVVAGIIRKRMESMWNELKDSILF 738
QY 379 FYTNPDDECSR-VLGLSDHLSLSDKLTCLLHGIIFPESDIPYKMLMSMAEGKLKE 437
DB 739 DYLDCHSEQYSTRATMQLSDNLADLCKPLLYMGMPEDACIKVSLSLTMAEDVQ-- 796
QY 438 NDLEGEVEKCLQELVRCVAVLSKRSRDTKIRSCVHDLIDYLCREYORENFIIFM-- 494
DB 797 -NIE-SAEYILANLISNNVMSKEYNG-KIYCEVHVVYHLFCLEKSEENFMVLAAG 853
QY 495 -----NDIADVSYPECYLCMKQPFKRVYTGDELNYCPYGLYRALLTPVNRQLDHND 549
DB 854 NNSQSFVWKS--RVSPSLSEENSKFASKT---RKCSHQLRSLIT----- 896
QY 550 NMLKRTHSVFSEHLEPLYYVLSKEVYHFKLLKYLELRHQRQIDGPRELLS-LIMRYIS 608
DB 897 -----NGASFEDI---ISLSWIMHRLKLVLSNHEVDVTSATLKLPLNHLKYL 944
QY 609 LFS--YGFNDVPEICRLMNLQTFIVORFSDIIFFAEIEYLMQRLHLKLPREFYLPDC 665
DB 945 VRAITFY--FD---RESHLPHLETILYKNDRS--VMLRCFPMEDLRAVEI----- 989
QY 666 PEGSYDK-GRHLDFSNLQTI-----SYLSPRCTKEVIMGIQVYKLLGISG 710
DB 990 SDAEFQKGLFEGSSKLEMLRLIKNIYGFPIRADVLSRRC-----PNLQGHIEF 1040
QY 711 NKDDYKSPFSDSLPNNLVYLOQELISLISVDSLPIVSISSAKAPATILKIKLEERTYL 770
DB 1041 SIDAADSFCLTEN---LTQLOKRLRISTECHSVL---SRLQLPMSIKKIKVLSNTCI 1091
QY 771 SMSYDILIELFNLEVLKILMD-----DACCGEEMHPIYMGFNKLTLLIKYSPFKM 822
DB 1092 E-NLTSFLEGLTSLLEIQLRDYIFPQSKCKLGD-----ITFHLKILIKLVQDISM 1144
QY 823 KATNDNFVLEIRMLIRSCNLEKPIEFADITLQILIELRECPK-LGESAARIQEOED 881
DB 1145 DVSSESEFPLETITIRRCQNLTEIPISFADVPLTKQIKLILHCKKSLDSSAVRIKQVED 1204
QY 882 -LGNRPVYV 889
DB 1205 NEGNDRIDL 1213

```

RESULT 12  
081136  
ID 081136 PRELIMINARY; PRT: 1255 AA.  
AC 081136;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

```

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PLANT RESISTANCE PROTEIN (DISEASE RESISTANCE GENE HOMOLOG MI-COPY1).
GN MI-1.1
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. VENT CHERRY; TISSUE=UNINDUCED ROOT;
RX MEDLINE=98374252; PubMed=9707547;
RA Ross J. M., Goggin F. L., Milligan S. B., Kaloshian I., Ullman D. E.,
RA Williamson V. M.;
RT "The nematode resistance gene Mi of tomato confers resistance against
RT the potato aphid."
RL Proc. Natl. Acad. Sci. U.S.A. 95:9750-9754(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. VENT CHERRY; TISSUE=UNINDUCED ROOT;
RA Milligan S. B., Bodeau J., Yaghoobi J., Kaloshian I., Zabel P.,
RA Williamson V. M.;
RT "The root knot nematode resistance gene Mi from tomato is a member of
RT the leucine zipper, nucleotide binding, leucine-rich repeat family of
RT plant genes."
RL Plant Cell 10:0-0(1998).
RN [3]
RP SEQUENCE OF 52-1255 FROM N.A.
RC STRAIN=CV. MOTELLE;
RA Bodeau J. P., Kaloshian I., Milligan S., Williamson V. M.;
RT "Isolation and large-scale sequencing of bacterial artificial
RT chromosomes (BACs) spanning the tomato Mi1 nematode-resistance
RT locus."
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039681; AAC67237.1; -.
DR EMBL; U81378; AAC32253.1; -.
DR InterPro: IPR001064; CrystalIn.
DR InterPro: IPR000767; Disease_resist.
DR InterPro: IPR002182; NB-ARC.
DR InterPro: IPR003880; Phosphopant_attach.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERIST.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS00102; PHOSPHOPANTETHEINE; UNKNOWN_1.
SQ SEQUENCE 1255 AA; 144354 MW; DF923D28BC7FEE6F CRC64;

```

Query Match 18.1%; Score 852.5; DB 10; Length 1255;  
Best Local Similarity 30.1%; Pred. No. 1.1e-48;  
Matches 274; Conservative 156; Mismatches 336; Indels 145; Gaps 34;

```

QY 31 REELALREKVSLEFVKNFEK---NNVFGEHTDEFEVEYREVASAETITQLRLTGTV- 86
DB 413 KEIELELVKQDLKIFRSFFDAEQGLKYLDMARVLDVAAYEAKVDID-----SIIVRDNGLIH 468
QY 87 ----LGENKSQKKARRRPROSLOQVAEDMDHIMWKESTKIQDGKOVSKESLWDFSSST 142
DB 469 LIFSPLITTKIKLILKEISALDENIPKDGILVNSPK-----KPERKSLTVD----- 518
QY 143 NDLKYNKNNVGRDQKQLEDLRSYSGEKPVIVYMGIGTGTAKAYVNDSEIIC 202
DB 519 ----KT---TVGEFEETNLILKLT--SGSADLDVIVITGHPGSGKTTIAKYNVNDKSVSS 570
QY 203 RRDVHAMATISQOHNKEKILLGLHSTIKMDRVKMIIGAELADMLQKSLKRRYILVD 262
DB 571 RFDLRAMCTVDOGCDCK--LLNTIFSOVS--DSQSKLSENIDVADKLRLKQLFGKRYILVD 628
QY 263 DIMSCVMDGVRCFPTEDNAGSRILLTTRNDNVACVAGENSLMSFMDQESMFLK 322
DB 629 DVMDDTTWELTRPP--ESKSGSRITLTTRKREKVALHGLKLNDDPLDLRLRPDESWELE 667
QY 323 SAFSSEALPYEFETVQKQIADCHGLPLTIVVAGIL--KSKRTIEDMKTAVAKVKSF 379

```

Db 688 KRAFGNESCPELDLVGKEIAENCKGLPIVADLIAGIAGREKKRSV--WLEVOSSLSSE 745  
 QY 380 VTNDPDRCSRVGLSDHILTSIDKTCCLHFGIPEPESDIPVKNLMASMAEGFL-KLE- 437  
 Db 746 ILNSEVE-VKRYIELSDYDHLPHHKLPCCLYFASFPEKDTSLTIELVNFGEAEFVKTEM 804  
 QY 438 NDEGEKCLQELVDCVLSKRSNDGKIKSCAKVHDLYDLCVREYRENIIFI----- 493  
 Db 805 NSMEEVKITYMDLIYSLVICF--NEIGYAL-NFOIHDVHPCLIKAKKEMLPQINS 861  
 QY 494 -----MNDIVLVSYECSYLCMKQOPKRYTGDINTCPYG 531  
 Db 862 SAPSDLPPIROITIDCEEHGILNFWFDSNKKRHSGLHLSL-----RIIGD----- 909  
 QY 532 LYRALLPVRQLDHDHNNMLKRTHSVSPHLEPLLYVLKSEVFKLLVLELRHQI 591  
 Db 910 -----QIDDSVSD-----AFHLR-----HRLRLVLDLHRTSFI 937  
 QY 592 ---DGFPEILSLTILWYLSLFSYGNEDVPPEICRLMNIOTFIYOHFRSDIIFAEIWE 648  
 Db 938 MKKSLNELICMLNHLAYSLIDQVKY-LPLSFSNLMNLESLEFVSTNRS-ILVLLRLID 995  
 QY 649 LMOIRHLKL-P-RPYLPDCSGSYDKRHLDFSNLOTISYL--SPRCCTEVIIMGIQNK 704  
 Db 996 LVKRLVLSVACSFEDMADE-SILIAEDYKLENLRILTELLIYSKDTKNIFKREPNO 1054  
 QY 705 KLGISGNKDOVKSPRDSGLPNNLYLQOELLISLVYDLYLLPVIISAKA----- 755  
 Db 1055 ILSEF-LKESNDYSTBOHWSSELDLFELETL---SVGFSSNTDNGSSVAIINRPRDI 1110  
 QY 756 FPATIKLKLETRYLSMSYLDIIAELPNLEVLKIMDACCGEEMHPIVMG---FNRKL 811  
 Db 1111 FPMILKILMIREPLTSDSLSTARLPNLELSYHTIIGSEEMN--MGEDPTFEMIKF 1167  
 QY 812 LLITSLKLPKAKANDPVLERIMISCKNLKEIPLEFDHTILOLELRBPCKIGES 871  
 Db 1168 LNFQVSIKWEESFPNLEKIKLGRKLEIPSFSDIYSLAKSIKIV--SPOLEDS 1226  
 QY 872 AARIQKQEDL 882  
 Db 1227 ALKITEVAEDM 1237  
 RESULT 13  
 ID 094107 PRELIMINARY; PRT; 1271 AA.  
 AC 094107;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
 DE TOSPOVIRUS RESISTANCE PROTEIN C.  
 SM5-C.  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Asteridae; eusteleids I; Solanales; Solanaceae; Solanum.  
 OC NCBI\_Taxid=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. STEVENS;  
 RA Folkesta R.T., Spassova M.I., Prins M., Stevens M.R., Hille J.,  
 RA Goldbach R.W.;  
 RT "Construction of a bacterial artificial chromosome (BAC) library of  
 RT Lycopersicon esculentum cv. Stevens and its application to physically  
 RT map the Sw-5 locus";  
 RL Mol. Breed. 5:197-207(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. STEVENS;  
 RA Prins M., Spassova M.I., Prins M., Klein Lankhorst R.,  
 RA Folkesta R.T., Hille J., Goldbach R.W.;  
 RT "The Sw-5 locus confers resistance to Tospoviruses";  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY007367; AAC31015.1; "-"  
 SQ SEQUENCE 1271 AA; 147392 MW; 07D43B369C34E001 CRC64;  
 Query Match 16.0%, Score 849.5; DB 10; Length 1271;  
 Best Local Similarity 27.6%; Pred. No. 1.8e-48;  
 Matches 279; Conservative 184; Mismatches 324; Indels 223; Gaps 41;  
 QY 4 ASVASLMRTIESLILFNPSMOSLSODHRE--ICLR--EVSSLEVYVKNFKNVNF-- 57  
 Db 336 AAGVLYVYIOKL-----LSIKKDNKSKISLSIQIWEKTKDLKAOVEYVTSKFTP 390  
 QY 58 -----GEMTDEVEVREY-----ASAAYTI-----QLRLGTVLGKNSOKK 96  
 Db 391 SQFPYVGSFIDSLIRKLKEMSKSKSCLDFLMKRLGNLEKLSIQISLEKDS----- 446  
 QY 97 ARRRFROSLQOVAEDMDHMKESTKIQDKK-----QVSKESLV-----HDFSS 140  
 Db 447 -----SLSSILRDVAVYHHEHILDLHRTIMAYAEVAIDSLAQYVFWHIFCS 499  
 QY 141 STNDILKVK-----NNMYGRDQQRKL 162  
 Db 500 LPTILKEIQIVQYQOMKADIALKPCYVVAPEFYFTRHINPTDIDYVGFQNDIEKM 559  
 QY 163 LBDLTRSYSGEPRVPIPVGMGIGKTTLAKEYNDESILCRFDYHAMATISQAHNKEIL 222  
 Db 560 FQYLIRG--INDIDIVPYGMGOGKTVARRYNSDNIHSHFDVRAVCIVSQYVRRKLL 618  
 QY 223 LGLLHSTIKMDRVKMGIAELADMLQKSLKRRRLVLDIOWSEVWDVGRRCPTEDN 282  
 Db 619 OELISQVTSKD--RGYEDDILADELRKSLMGKRLTLLDWDMDAMADILRSPDSGN 676  
 QY 283 ACSRIILTR-----NDEVACYAGVENFSLRMSFMDODESWLSFKSAFSSALPYEFETV 338  
 Db 677 R-SRIVYTRLKVEGQVQKCH--TDPSYL--PELTKBESCELLQKKVQKQKDFPELODV 731  
 QY 339 GQOIADECHGLPITYVAVAGLKSRTIEDMKTVAKDYKSFYTDNDRCSR-VLGLSYD 397  
 Db 732 SOAVAKCKGGLPVLIVVAVAGIIRKRMESWMNELKDLFYLCHSQQYRARMOQLSFD 791  
 QY 398 HLTSDIKCCLHFGIPEPESDIPVKNLMASMAEGFLDLEGEVCKQLQELVDRCLV 457  
 Db 792 NLADCKPCLLYGMPEPESDIPVKNLMASMAEGFLDLEGEVCKQLQELVDRCLV 847  
 QY 458 LVSKRSRDTGKIRSCVHDIYDLCVREYORENIFIM-----NDIVLVSYPECSYL 509  
 Db 848 MYSKKEYNG-KIKYCKVHYVHLFCLERSRENEFLVAKGNHSGQSPVYMKOS--RVSFS 904  
 QY 510 CMYKMQPFRVYTGDEINCPYGLYRALLTPVNRQLDRHDNNMLKRTHSVFSHLEPLY 569  
 Db 905 LSEENKFFASKT-----RKCSHQPLRLSLIT-----NGASFIDISL-- 939  
 QY 570 VAKSEVH-FRLIKVLELRHQIDGF-----PREILSLIMRLYLSFSGYNDPPEIC 622  
 Db 940 ----SSILHRLRLKVLVLSHSEVDYNSATLKLPLMLLYLGFRASYF---FD---RES 989  
 QY 623 RLMLNLOTFIYQFRSDIIFAEIWEIMQLRHLKLPREFLPDCPSGSYDK-GRHLDFSNL 681  
 Db 990 HLPHELETLIVKNNRS--VMLRGCFWEMQLRHVEL-----SDAEFDKQGLFGSGSKL 1039  
 QY 682 QTIYSLSPRCCTKEYIMGIQNVKKGIGGNKDKYKSFDSGLPNNLYLQOELT----- 735  
 Db 1040 EMLRLT-----KNI--VGFIIDRADVYSR--CPN-----LQDLHIEFEYFA 1077  
 QY 736 -----LSLISVDSLLPVIISAKAFPTATLKLKLETRYLSMSYLDIIAELPN 783  
 Db 1078 EPPFWLTGLNLTQDLIDLSFRLSHW--SGDLPSNLMLVLRADLE-KLTSYAGLPS 1134  
 QY 784 LEVLKIMDACCGEEMHPIVMGFNRLKILLIKYSLKFMKATNDFPVLERIMRSCNKL 843  
 Db 1135 LEVLOITNNYFQSBMCGLDIFHKLKLLKLVQDLISMDVSESEFPLEIIIRMCNLT 1194  
 QY 844 KEIPLEFADHTILOLELRBPCKIGES-IGESAARIQKE-QEDLGNNPDVRI 891

DB 1195 EIPISFADVPTLQIKILHCKKSLDSDSAVRKIKDVEENEGNDRIDLI 1244

## RESULT 14

ID 094106 PRELIMINARY; PRT: 1263 AA.

AC 094106;  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE TOSPOVIRUS RESISTANCE PROTEIN D.  
GN SWS-D.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; eusterids I; Solanales; Solanaceae; Solanum.  
NCBI\_TaxID=4081;  
OX [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CV. STEVENS;  
RA Folterisma R.T., Spassova M.I., Prins M., Stevens M.R., Hille J.,  
RA Goldbach R.W.;  
RT "Construction of a bacterial artificial chromosome (BAC) library of  
RT Lycopersicon esculentum cv. Stevens and its application to physically  
RT map the Sw-5 locus."  
RL Mol. Breed. 5:197-207(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. STEVENS;  
RA Prins T.W., Spassova M.I., Prins M., Klein Lankhorst R.,  
RA Folterisma R.T., Hille J., Goldbach R.W.;  
RT "The Sw-5 locus confers resistance to Tospoviruses."  
RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY007367; AAC31016.1;  
SQ SEQUENCE 1263 AA; 146026 MW; D3275C734BE358AD CRC64;

Query Match 18.0%; Score 848.5; DB 10; Length 1263;  
Best Local Similarity 29.1%; Pred. No. 2.1e-48;  
Matches 278; Conservative 168; Mismatches 331; Indels 177; Gaps 38;

QY 8 SLIMRT-----ESLTFNSMOSICDHREE---LCLAREKSYLFEVFNKKNVGE 59  
DB 391 SLIRKLNMSRSKRYGDFLMLKPIFCLEKQOSTILNLKELSSLSIRDTYK--VHHE 448  
QY 60 MTD-----FEVEVREVASAEYTIQLRL--TGIVLGENKSOKKARRRFRSL-- 105  
DB 449 OKDQRTINLAVGAVSIDISICAKYVFWHCFCSLPTLEIKQINAEVTEWMSADIP 508  
QY 106 --QVAEDMDHI--WKESTKIQK-----GKQVSKESLHMFSSSTNDILKKNMVG 154  
DB 509 NPHYVAAPKHLPTRHSDNITDEIYDEIVGIDKEKTIQCVIRGTNDL----- 559  
QY 155 RDOQRKQLLEDLTRSYSGEPKVIPIVGMGIGIKTKLAKEYYNDESILCFEDVHAMATISQ 214  
DB 560 -----DVPVIVGMGGOGKTTIARVYVNSDNIYSHEDVAMQVISO 599  
QY 215 QHNKKELILGLHSTIKMDRYKMGCEALADMLOKSLKRRKRLIYLDIMISCEVWDGVR 274  
DB 600 TYRRKRLIQOIIISQVYGRD--KGVEDDILADELRKSLMGKRYLIYLDIMDMAMDDELR 657  
QY 275 RCPPTEDMNGSRILLTTR-----NDEVACYAGVENSFLRSMFQODSWSLFFKSAFSSSEA 330  
DB 658 LSFPEDEGNR--SRIVVITRLEKGEQVYKCH--IDPYSL--PFLITTESCKILQKVKOKED 712  
QY 331 LPEFETVQKQALDECHGRLPIVIVVAGLLSKRTIEDMKTVAK--VKSEFTNDPDERCS 389  
DB 713 CPPELDQVSGVNAEKCKGRLPIVIVVAGIIKKRKMESWMDLRDSLFDYLDCHSRQYSL 772  
QY 390 RVIGLSYDHLTSLDKTCLAHFGIFPPEDSDIPYKNTLMRSNMAABEFLKIENDLEBEVEKICQ 449  
DB 773 ATMQLSFDNLADLCKPLLYMGFPPEDASINVSALLSLWIAEDFVQ--NIE--SAEDYIM 828

QY 450 ELYDRCILVYKRSRDGFTIRSCKYHDLIYDLCVREVOENEFIM--NDIYLDVSYPEC 506  
DB 829 NLISNVVAVSKREYNG--KIKYCEVHDVVLHFLEKSKREEMVLVAKGHSQPOSFPMQ 887  
QY 507 SYLCMYKQPFKRYVGTDEINCPYGLYRALITPVNKRDLRDHNNMLKTRHSVFSFHLER 566  
DB 888 SRV--SFSLSSEKSKFASKRKCSHOPRLSLIT-----NGASFDI-- 925  
QY 567 IYVYLKSEYVHFKLVLELRHQIDGFEPELIS--LIMRLYLSFS--YGNFVPEPIC 622  
DB 926 --ISLSWVHNRLLKVLVLSHVEYVYNSAVLKPLNHLKYLGRATYFY--FD--RES 978  
QY 623 RLMMNQTFIVQFRSDIILFAEIEWELMOLRLKPLRFYLPDQSGSVYGRHIDFS--- 679  
DB 979 HLPHELTIVENDRS--VWLPQCFWETEDLRH-----DISDAEPKQGLFEBSKRS 1028  
QY 680 -NIGRT-----SYLSPRCCKREYIMGIONYKKGISGNKDYKSFSDSGLPNNIL 727  
DB 1029 ENLRILKNTVGFPIRDADVLSRRC-----TNLQQLHIEFSIDEADSFCLTEN-- 1077  
QY 728 VYLQLEILISLVSDYSLPVIISAKAPATLKKLERTYLSMSYDIIAELPYLEVL 787  
DB 1078 --LTOLQKHLSTERHSVL-----SRLQLPNSLKKLVLSNTCIE--NLTSFLEGLPSELYI 1129  
QY 788 KLMD-----DACCGEEMHPIVMGFNRLKILLIKYSFLKFKATNDNFPVLERMIRS 839  
DB 1130 QLRDIYFPHQSKWCXGD-----ITFHKLKLKLVQDLISRNDVSESEFPLETIIIR 1183  
QY 840 CNLKEPIEFADHITLQLEIELEKCPK--LGESARIQRE--QEDLGNPVDVRI 891  
DB 1184 CNLEIEPIFNADVPTLQIKILHCKKSLDSDSAVRKIKDVEENEGNDRIDLI 1237

## RESULT 15

ID 09SA09 PRELIMINARY; PRT: 1206 AA.

AC 09SA09;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE DISEASE RESISTANCE GENE HOMOLOG Mt-COPY2.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; eusterids I; Solanales; Solanaceae; Solanum.  
NCBI\_TaxID=4081;  
OX [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CV. MOTELLE;  
RA MEDLINE=98374252; PubMed=9707547;  
RA Rossi M., Goggin F.L., Milligan S.B., Kaloshian I., Ullman D.E.,  
RA Williamson V.M.;  
RT "The nematode resistance gene M1 of tomato confers resistance against  
RT the potato aphid."  
RT Proc. Natl. Acad. Sci. U.S.A. 95:9750-9754(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. MOTELLE;  
RA Bodeau J.P., Kaloshian I., Milligan S., Williamson V.M.;  
RT "Isolation and large-scale sequencing of bacterial artificial  
RT chromosomes (BACs) spanning the tomato M1 nematode-resistance  
RT locus."  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U81378; AAC32252.1;  
DR InterPro: IPR000767; Disease\_resist.  
DR InterPro: IPR002182; NB-ARC.  
DR Pfam: PF00931; NB-ARC.  
DR PRINTS: PRO0364; DISEASRESIST.  
SQ SEQUENCE 1206 AA; 138667 MW; 09AB9BC8CF444649 CRC64;

Query Match 17.7%; Score 834.5; DB 10; Length 1206;

Best Local Similarity 29.6%; Pred. No. 1.7e-47;  
Matches 289; Conservative 148; Mismatches 315; Indels 223; Gaps 41.

Search completed: September 12, 2002, 14:07:40  
Job time: 603 sec

QY	13	ISLTLFNSPMOJSLCDHREELCALRECVSSLEFVAKNEFKNNFVGMT-----PFEV66
Db	347	LNDLDSNMSYISL---KEEL-----ELVOSLELFINSF-----FGMAAQGLIKYIMAR 394
QY	67	VHEVSAAEYTO---LALTYV-----LGNSQOKKARRRRQSLQOAVEDMDHIKE 118
Db	395	VLDAVLEADVDIDSIIIVBNGNGLHILFSLPIITTIKKIKLKEELSTADENIPKRGILTVN 454
QY	119	STRIODCKOVAKESLVAHDFSSSTNDILKYNNWNGDDORCOLLEDLTYSGEKVIYP 178
Db	455	SPK-----KPERKSLTTD-----KI---IVGFEENILIKRLT---SGRADLVIS 496
QY	179	IYMGIGIKTTIAKVVYVDESSILCFPDVHAAVATISQOHKKEILLGLHSTIKMDRVKM 238
Db	497	IYMGPSGQTTIATVYVNDKSVSRHFDLRAVCYDQGYDDKK--LDDTIFSOVSGSDS--NL 554
QY	239	IGEAELDAVLOKSLKRRKRYIIIVLDDIMSCVWDGVRCPFLDENAGSRILLTIRNDEVAC 298
Db	555	SENIDVADKLKROLFGKRYLIIVDDVMDTTLTDLBTLTRPF--EAKGSRILLTIREVYL 613
QY	299	YAGVENESLIRSMODESMFLKSAFSEALPYEFETVQKQIADCHGLPLTIVVAG 358
Db	614	HOKLMTDPLDLIRLPRDESMELKEKRTFGNESCDELLDGEKIEAENCKGLPYADOLING 673
QY	359	IL--KSKRTIEDMTYKADVKSVTNDPBCRSRYGLSYDHLTSDIKTLHPIRE 415
Db	674	VLAGKEKRSV--WLEVOSSLSSTILNSPEV--VAKVETELSDYDPHHLKPCLLHFSMWK 730
QY	416	DSODIFVKNLMSMAEGFLKLENDLEG--EVEKC--LOELVDRCLVYKSKSRDGTKIRSC 472
Db	731	DPLPLIYLLTYLGAEGFEV--KTEMKIGEEVAKIYMDLISSLVICFNEIGD---ILNF 786
QY	472	KYHDIYDLCREVORENIPI-----NMIDIVDYSTYE 505
Db	787	QIHDIYHDFCLKARKENLPRIRISSAPSDLLPRQITIDYDEEBEHRGALFWPFDSSNKR 846
QY	506	CSYLOCMYKOPFKRYVGTDEINYCPLYRALLTPVNRQLRDHNMMILKRTHSVFSHLE 565
Db	847	HSGKALYSL---RING-----QLDDSVSD-----AFHLR 873
QY	566	PLYVYLKSEVYHFKLIVYELRHQI---DGFREILISLMLAYLSL-----FSYCN 614
Db	874	-----HLKRIKRLDLEPSLIWVNSOLINELQMLNHELYELRIQVAYLPRPFSFN 922
QY	615	FDVPELICRLNNIOTFYVORERSDIIFAEIEIMLEQMLRLKLPRLYLPDCSGSGVDGR 674
Db	923	-----LWNETSLFVSN--KGSIIVLPRILDYKLVL-----SVGACS 959
QY	675	HLDPNSIOTIYSLSPROCTKEVINGIONVAKLG---ISGNKDYKFSRSGLPNNILVYO 731
Db	960	FPDMDADDSILIAMD--TK-----LENLILBELLIYSTKDTMNIK--RFPN---LQ 1005
QY	732	QLEILISLISVDY-----LDPYIISAKA-----PAT 759
Db	1006	VLOFELKESMDSYSTEQWHPFKLOLCTELETFLCVGFKSSNMTNHGSSVATNRBMDHPFSN 1065
QY	760	LKLLKLEFTYISMSYLDITIELPNTLEYLKMADACGGEWHPYVWG---FNRKLLILK 815
Db	1066	LKELLILDFPLTSSLSSTIKRLPRLPLEMLISLDYITIOGEEWN--NGEDTFENLKFLMLR 1122
QY	816	YSLFKEMKATNDNPFVLERLIMISCKNLKEIPTEFADITLLOLIELRECPRLIGESARI 875
Db	1123	LTLTSLKWEVGESEPPNLEKLQECGLTEIRIPSPFDIYSLAKFIKYK--SPQLEDSALKI 1181
QY	876	OKBOEDL--GNPNVUY 889
Db	1182	KKIAEDMRGNGELOT 1196



•  
•  
•  
•

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 22:23:56 ; Search time 10435.2 Seconds  
(without alignments)  
5450.611 Million cell updates/sec

Title: US-09-864-680-4

Perfect score: 2718  
Sequence: 1 atggtcctcagcaagtggtgc.....ctgattcagagaacattag 2718

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sy:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	2718	100.0	2718	6	AX076883	AX076883 Sequence
2	2718	100.0	3099	6	AX076881	AX076881 Sequence
3	2718	100.0	3099	8	AF202179	AF202179 Capsicum
4	2685.6	98.8	31491	6	AX076880	AX076880 Sequence
5	275.6	10.1	3201	6	AX012619	AX012619 Sequence
6	272.8	10.0	3254	6	STU2494449	STU2494449 Solanum t
7	272.8	10.0	3683	6	AX133916	AX133916 Sequence
8	272.8	10.0	10331	8	AF195939	AF195939 Solanum t
9	272.8	10.0	187352	8	AF265664	AF265664 Solanum t
10	272.4	10.0	3229	6	AX012617	AX012617 Sequence
11	272.4	10.0	3229	6	AX012618	AX012618 Sequence
12	272.4	10.0	3229	6	SAC249448	SAC249448 Solanum a
13	271.6	10.0	3220	6	AX012614	AX012614 Sequence
14	271.6	10.0	5820	6	AX012606	AX012606 Sequence
15	271.6	10.0	18284	8	STU011801	STU011801 Solanum t
16	271.2	10.0	3146	8	AF266747	AF266747 Solanum t
17	271.2	10.0	3254	6	AX012615	AX012615 Sequence
18	269.6	9.9	3066	6	AX012608	AX012608 Sequence
19	269.6	9.9	3213	6	AX012616	AX012616 Sequence
20	268	9.9	3064	6	AX133920	AX133920 Sequence
21	266.4	9.8	2880	6	AX133915	AX133915 Sequence
22	266	9.8	2885	6	AX133917	AX133917 Sequence
23	264.8	9.7	3283	6	AX133918	AX133918 Sequence
24	256.8	9.4	2680	6	AX133919	AX133919 Sequence
25	221.8	8.2	2629	8	AF266746	AF266746 Solanum t
26	195.8	7.2	35250	8	AY007366	AY007366 Lycopersi
27	180.6	6.6	59465	8	AY007367	AY007367 Lycopersi
28	172.2	6.3	5475	6	AR029637	AR029637 Sequence
29	172.2	6.3	5475	6	AR157373	AR157373 Sequence
30	171.4	6.3	678	8	AF404421	AF404421 Lycopersi
31	170	6.3	10968	6	AR029638	AR029638 Sequence
32	170	6.3	10968	6	AR157372	AR157372 Sequence
33	170	6.3	10968	6	LEU65391	LEU65391 Lycopersi
34	170	6.3	59202	8	AF220603	AF220603 Lycopersi
35	170	6.3	60831	8	AF220602	AF220602 Lycopersi
36	164.2	6.0	5134	6	AR085492	AR085492 Sequence
37	161.8	6.0	95845	8	AF411807	AF411807 Lycopersi
38	149.2	5.5	3849	8	AF091048	AF091048 Lycopersi
39	149.2	5.5	3997	6	AR110592	AR110592 Sequence
40	149.2	5.5	3997	8	AF039681	AF039681 Lycopersi
41	149.2	5.5	9870	6	A79336	A79336 Sequence 14
42	149.2	5.5	9870	6	BD003214	BD003214 Tolerance
43	149.2	5.5	51952	6	AR110591	AR110591 Sequence
44	149.2	5.5	51953	6	LEU81378	LEU81378 Lycopersi
45	147.6	5.4	3982	6	AR110593	AR110593 Sequence

#### ALIGNMENTS

RESULT 1  
LOCUS AX076883 2718 bp DNA  
DEFINITION Sequence 4 from Patent WO0107635.  
ACCESSION AX076883  
VERSION AX076883.1 GI:13121544  
KEYWORDS  
SOURCE Capsicum annuum.  
ORGANISM Capsicum annuum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.

REFERENCE 1 (bases 1 to 2718)  
AUTHORS Staskiewicz,B.J., Dahlbeck,D. and Tai,T.H.  
TITLE Bst2 resistance gene  
JOURNAL Patent: WO 0107635-A 4 01-FEB-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
FEATURES  
source 1..2718  
/organism="Capsicum annuum"  
/db\_xref="taxon:4072"  
1..2718  
/note="unnamed protein product"

		/codon_start=1 /protein_id="CAC32383.1" /db_xref="GI:13121545" /translation="MAHASYASLMRTESLITFNSPMQISCDHREELCALREKVSLS EVPKNEKNVGEEMTDEVEVREVAASAEYITQLRTEVTIGENKSQKKRRRR OSLOQVEDMDHIMKESTKIQDKGQVSKESVINDFSSSTMDILKYNMVGDDQK QLLEDLTRYSGEPRVIPVIMGGIGITTYLAKEVYNDESILCFEDVHNAATISQHNK KEILGLHSTIKMDRVMKIGAEELADMRQSKRRRYITLVDLIMSCWGVGRNC FPEEDNAGSRHLLITTRNDEVACVAGVENSILSMSPDQDSMSLSPNVAAPSPALPYE FETVGRQIADCECHLPLTYVYAGLLSKRTIEDPKTYAKDVASFPTNDPDEKSVL GLSDHLSDLTKTLHFHIFPEDSDIPVANKRSMABEFLKLENDLGEVEKQOE LVDRCLVLSKRSRDEGTRISKCVHDLIDLCVREYRENIETMDIVLDSVPSY LCMKQPKFRVYDEINCPYGLYRALLPVROLDHNNMLKRTSVSEFHEIP LYYLKSEVVFHKLKLYELRHRQIDGPREILSLRLSTFSGNEDVEICRL MNLQTFVORESDIIFAEIWEIMOLRHLKLPRELPDPCSGSVKGRHLDENLSNO TYSLSRCKTEKVIQNVKRLIGSNDDQKSPRSDGLPNVLYILOETLSLS VDYSLPVIITSSAKAPATIKRLKERTYSMSYLDIIEALPHEVLKLMDDCCGE MHPVAKFNRKLILIKYSPFLKFWKATNDFPVLERLMTKSCNLEIPIEFADHITL QLLEKRCPRKLESARIQEKEDLGNPNVDVIRISNPLKESDSDEEH"	
BASE COUNT	851 a 454 c 623 g 790 t		
ORIGIN			
Query Match	100.0%;	Score 2718;	DB 6; Length 2718;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 2718; Conservative	0; Mismatches	0; Indels	0; Gaps 0;
Qy 1	atggctacatgcaatgctgctctctatgagaacaatagatcctcttgacatcaat	60	
Db 1	ATGGCTACATGCAATGCTGCTCTCTATGAGAACATAGAAATCTCTTGACATTC	60	
Qy 61	tgcgcagatgcaatctctacccctgacacagagaagaactcttgagctctcg	120	
Db 61	TGCGCGATGCAATCTATCCTGTGATCAGAGAAAGACTTTCGCTCTCGTGA	120	
Qy 121	gttagtccctggaagatattgttgaagaactcttgagaacaacatgtctt	180	
Db 121	GTTAGTCCCTGGAGATATTGTTCAGAACTTTCGAAAAACAATGTTTTGGG	180	
Qy 181	acggattctgaagtagaagtagaagtagaagtagaagtagaagtagaagtag	240	
Db 181	ACGGATTCTGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAATTCATCACT	240	
Qy 241	agactaagaagtagaagtagaagtagaagtagaagtagaagtagaagtaga	300	
Db 241	AGACTAAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAG	300	
Qy 301	tttcgtaaaagcctgcaacaagtagcagagagacatgacatctctgaaag	360	
Db 301	TTTCGTCAAAGCCTGCACAACAGTAGCAGAGACATGATCATCTTGGAAG	360	
Qy 361	aagatccaagaataaagaacaagtagaagtagaagtagaagtagaagtaga	420	
Db 361	AAGATCCAAGATAAAGAAACAAGTAGAAGTAGAAGTAGAAGTAGAAGTAG	420	
Qy 421	tcaacaacagatatttgaagtagaagtagaagtagaagtagaagtagaag	480	
Db 421	TCAACAACAGATATTGGAAGTTAAAGAACATATGTTGACGTATGATGAT	480	
Qy 481	caagtgttagaagtagaagtagaagtagaagtagaagtagaagtagaagtag	540	
Db 481	CAGTGTGTAAGATCTGACTAGAGCTACTCTGGGAAACCAAGTCACTCCG	540	
Qy 541	gggatggagagcagtagaacaacacttagcaagaagaatttcaaatgta	600	
Db 541	GGGATGGAGAGCATAGGTAACAACACTTAGCAAAAAGATTTTACATGATCA	600	
Qy 601	ctatgcgctttagatgtagcagctggctaccatctcaacagcagcaacaa	660	
Db 601	CTATGCCGCTTTGATGTTGATGCTGGGCTACATATCTCAACGACCAACA	660	
Qy 661	atttgcgtggcctctgcattccaacaataatgtagaagggttaagatg	720	
Db 661	ATTTGCTGGGCTTCTGCATTTCCAAATCAAAATGATGACAGGTTAAGAT	720	
Qy 721	gaagcagagctagcagacatgtagacagaaagttttaaagagaagagtag	780	
Db 721	GAAGCAGAGCTAGCAGACATGTTTACAGAAAAGTTTAAAGAAAAGAGT	780	
Qy 781	ttgagtagatctggaggtttagaagtaggagtagagcagatgcttcca	840	
Db 781	TTGAGTAGATCTGGAGTGTGAGAGTGGGATGGGCTGACAGATGCTTT	840	
Qy 841	gacaatgcaagtagcgaatctgtagaagtagaagtagaagtagaagtag	900	
Db 841	GACAATGCAAGGCTGGAATCTGTTGACTACCCGTAATGATGAAGTAG	900	
Qy 901	gagtagagaattttctcttggagtagaagcttccatgtagaagtagaag	960	
Db 901	GAGTAGAGATTTTCTTTGCGGATGACCTTCATGATCAAGATGAGAT	960	
Qy 961	ttcaaaagtagcagcatcttcaagtagaagtagaagtagaagtagaagtag	1020	
Db 961	TTCAAAAGTAGCAGCATTTTCAAGTAGAAGTAGAAGTAGAAGTAGAAG	1020	
Qy 1021	caaatcgcaagtagaagtagcaggtttaccacacactatgtagtgg	1080	
Db 1021	CAAAATGCAAGTAGAAGTAGCAGGTTACCACTAATTTGTGTGCTG	1080	
Qy 1081	aaatcctaagaagtagaagtagaagtagaagtagaagtagaagtagaagtag	1140	
Db 1081	AAATCTAAAGAGCAATAGAAAGTTGGAAGACTGTTGCTAAAGATG	1140	
Qy 1141	acaatgtagcagtagaagtagaagtagaagtagaagtagaagtagaagtaga	1200	
Db 1141	ACAAATGATCTGATGAAGTAGAAGTTTCACTGTGGTGTGATGATG	1200	
Qy 1201	agcgatcctaagaagtagaagtagaagtagaagtagaagtagaagtagaagtag	1260	
Db 1201	AGCGATCTTAAAGACATGCTTCTGCAATTTTCCGAAAGACATGAT	1260	
Qy 1261	gtgaagaattctgtagaagtagaagtagaagtagaagtagaagtagaagtaga	1320	
Db 1261	GTGAAGAATTCTGATGATGATGATGATGATGATGATGATGATGATGAT	1320	
Qy 1321	gaagtagaagtagaagtagaagtagaagtagaagtagaagtagaagtagaagtag	1380	
Db 1321	GAAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAG	1380	
Qy 1381	aagtagaagtagaagtagaagtagaagtagaagtagaagtagaagtagaagtag	1440	
Db 1381	AAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAG	1440	
Qy 1441	ctgtgtagaagtagaagtagaagtagaagtagaagtagaagtagaagtagaagtag	1500	
Db 1441	CTGTGCTGAGAGAGTTTAAAGGAGAACATTTTATCATGAAAGCAAT	1500	
Qy 1501	gtatcatatcagaagtagaagtagaagtagaagtagaagtagaagtagaagtaga	1560	
Db 1501	GATCATATCCAGAAAGTTGATATCTGTATGATTAAGAACGACCTTTAA	1560	
Qy 1561	actgtgtagaagtagaagtagaagtagaagtagaagtagaagtagaagtagaagtag	1620	
Db 1561	ACTGTGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1620	
Qy 1621	aatcgcagtagaagtagaagtagaagtagaagtagaagtagaagtagaagtaga	1680	
Db 1621	AATGCTGATGAGATCATGACAAACAATCTTTGAAACGAACCAAT	1680	
Qy 1681	tccttcatctgagccttlatatgtagtctcaaatcagaagtagaagtagaagtaga	1740	
Db 1681	TCTTTCACTTGAACCTTTAATTAATTAATTAATTAATTAATTAATTAATTA	1740	
Qy 1741	ctcaaaagtagcagtagaagtagaagtagaagtagaagtagaagtagaagtagaagtag	1800	
Db 1741	CTCAAAAGTCTTGAGACTGAGACAGACAGATGATGATGATGATGATGATGAT	1800	



```

QY 1801 ctcatcgtgtgagtgacctatcgttccagctatggaattcgaatgacctccagaa 1860
    |||
Db 1801 CTATCTGCTGTGAGTACCATCATCTTGTAGCTATGGAATTTCCATGTAACCTCCAGAA 1860
QY 1861 atttcagatgatacgtcgcacatcctcgttccaaacggttcgatacagatatata 1920
    |||
Db 1861 ATTTCAGAGGTATGGAATCGCAGACATTCATTGTTCAACGGTTTCATCAGATATATATA 1920
QY 1921 atttcgtcgaagaatttcgggaactaagcaattgaagcattcaactcgcagattc 1980
    |||
Db 1921 ATTTCGTCGAGGAATTTGGGAATCAATCAATTAAGGATCTTAACGCCAGATTT 1980
QY 1981 tatttcagagattgcacaaatgatactgttgacaagaagagagcattgatttcaaac 2040
    |||
Db 1981 TATTTCGCAAGATTGCCAGATGATCTGTGACAAAGGAAGCACTTGGAATTTTCAAC 2040
QY 2041 ttacaactatcttctactgtctccacgttctgcaacgaaggagtataatgagatt 2100
    |||
Db 2041 TTACCAACTATTCTTACTGTCTCCACGTTGTTGCACGAGAGGATTATATGSGGATT 2100
QY 2101 cagaatgcacaaataatgagaatcagtggaataaagagatataaaagtttcgggac 2160
    |||
Db 2101 CAGAAATGCTAAAAAATTAGGAATCAGTGAATAAGGATGACTATAAAGTTTCCGGAC 2160
QY 2161 tctggagctcccaacaactctgtctatctgcaacaactgaactgaatgattatact 2220
    |||
Db 2161 TCTGGGCTTCCCAACAATCTGTCTATCTGACCAACTTAATAATGAGTCTTATATCT 2220
QY 2221 gtgatataagcctcttcgcagtgatcattcaagtcaaaagccttccagcaacgctc 2280
    |||
Db 2221 GTTGATATTATGCTTTTGGCAGTGATCATTTCAAGTCCAAAGCTTTTCCAGCAACGCTC 2280
QY 2281 aagaagctgaagcttggaagaactatctaagctgtgcatacttggacatcagctgag 2340
    |||
Db 2281 AAGAAGCTGGAAGTGGAAAAAACAATTAATCTAAGCTGTGCATATCTGGACATCATAGCTGAG 2340
QY 2341 ttgccaactctgaagtgctggaagctgatagtagagcctgtgtgtgaagaatgcat 2400
    |||
Db 2341 TTGCTTAACCTTGAAGTGTGGAAGCTGATGATGACGCTTGTGTGTAAGAATGGCAT 2400
QY 2401 ccaattgtatggaatttaacgattgaagccttctgtaataataatgatttctcgaag 2460
    |||
Db 2401 CCAATTGTTATGGGATTATATCATTTGAACCTTTTGTCTAATTAATTAATTTTCTCAAG 2460
QY 2461 ttctggaagcacaatgacaatttctcgtccttgagcgccctcatgattagaagttgc 2520
    |||
Db 2461 TTCTGGAAGGCCACAATGATCAATTTTCCGTGCTTGAGCGCCTCATGATTAGAAGTTGC 2520
QY 2521 aaaaattgaagaagatacccatgtgattgctgcagataataacacacacagcctgattgag 2580
    |||
Db 2521 AAAAAATTTGAAGAAGATACCCATTTGAGTTGGCATATACACACACTACAGCTGATTGAG 2580
QY 2581 ttaagaagatgtctcctccaaacttgggaaactcgtcgcagaaattcgaagaagaaga 2640
    |||
Db 2581 TTAAGAAGATGTCTCTCCCAACTTGGGGAATCTGCTGCAGATTCAGAAAGAAACAAGAA 2640
QY 2641 gacctggaagaacacccctgtgagttcgtatcacaatccattgaagagagtgattct 2700
    |||
Db 2641 GACCTGGGAACCAACCCGTGAGTGTTCGATCTCAAAATCATTTGAAGGAGAGTGAATTC 2700
QY 2701 gattcagaagaacattag 2718
    |||
Db 2701 GATTCAAGAACAATTAG 2718

```

```

RESULT 2
LOCUS AX076881 3099 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 2 from Patent WO0107635.
ACCESSION AX076881
VERSION AX076881.1 GI:13121542
KEYWORDS

```

```

SOURCE Capsicum annuum.
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
REFERENCE
AUTHORS Staskiewicz, B.J., Dahlbeck, D. and Tai, T.H.
TITLE Bsg2 resistance gene
JOURNAL Patent: WO 0107635-A 2 01-FEB-2001.
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES
source
location/Qualifiers
1..3099
/organism="Capsicum annuum"
/db_xref="taxon:4072"
93..2810
/note="unnamed protein product"
CDS
/codon_start=1
/protein_id="CAC32382.1"
/db_xref="GI:13121543"
/translation="MAHASYASIMRTIESILTFNSPMOSISCDHREELALREKVSSTL
EYVKNPEKNNVGEMTDEPEVREVASAEYTIQURLITGVIGENKSOKKARRRR
QSLQOYAEEDMDHIMKESTIKQDGKQVSKSLVHDFSSSTNDILKAKNNVGDQDK
QLEEDLFRSYSGEPKVIPIVGMGIGIKTTLAKVEYNDESILCFEDVHAMATTISQHNK
KEILLGLILSTIKMDRVRKMGIGAEELADMLQKSLKRRYLIYDDIISCVMDGVRC
FPEDNAGSRILITTRNDEVACVAVENSLRMSFMDQESNELFKSAFSSALPYE
FETVGKQIADDECHGLPLTIYVYAGILKSKRTIEDMKTVAKDVSEFTYNDDEGRSRLY
GLSYDHLTSDTKCLILFRGTFPPDSDI PKNLMRSMABGFLLENDLBEVEKCLQE
LVDRCLAVLSKRSRDSGTJRSCEVHDIYDLQVREVORENTFLMNDIVLVSTPECSY
LCMYKMQPKPRVYDEINCYGPLYRALPLPVRORLHDHNNMLKRTSHVFSEHLEP
LYVLKSEVVFHLEKLYELRHRQIDGFPREILSLMLRLSLSEYGNFVPEICPL
MNLQETIVOREFRDIIIFAEIWEIMOLMRKLKLPREFLPCPSGVSDGRLHPSNQ
TISYLSPRCCTKEKVIQNGVKKLISGNDKDVKSRRSDSLPNVLYIQLLELISLS
VDYSLPVIITSSKAPPAIILKILKERTYISMSYLDIILALPNLEPKLMDACGEE
WHPITVGFNKLKILIKISFLKFWKATNDFPVLERMLRSCNKLKLEIPLFADIIHL
OLIEURECEPKLIESAARIQKEDEDGNPNVDVIRISNPILKESDSDEEH"
BASE COUNT 970 a 514 c 693 g 922 t
ORIGIN
Query Match 100.0%; Score 2718; DB 6; Length 3099;
Best local Similarity 100.0%; Pred. No. 0;
Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atggctatgcaagtggtgcttctctatgagaacatagatctctcttgacaattcaat 60
    |||
Db 93 ATGGCTATGCAAGTGTGCTCTCTTATGAGAAACAATGATATCTCTTGACATTTCAAT 152
QY 61 tgcgcgaatgcacatctcatcctgtgacacagaagaacttgcgctcctcgtgaaaaa 120
    |||
Db 153 TCGCCGATGCANCTCATCTCTGTGATCAGAGAAACAATTCGCGCTTCGCGMAAAA 212
QY 121 gtagttccctggaagatttgcagaacttggaaaaaacaatglttttgggaaatg 180
    |||
Db 213 GTTAGTCCCTGGAAGATTTTGTCAAGAACTTTGAGAAAAACAATGTTTGGGGAATG 272
QY 181 acgattttgaagtgaagtggaagaagttgcgaagtctgtgaatacaaatccaactg 240
    |||
Db 273 ACGGATTTTGAAGTAGAGGTAAGAGAAAGTTGCAAGTCTGCTGTAATACACAAATCACTG 332
QY 241 agactaacgaactgtacgtggggaataaagaacagaaaaaaagcgcgctggaag 300
    |||
Db 333 AGACTAACGAGAACTGTACTGGGAGAAATTAAGAACCCAGAAAAAAGCGCGCTGGAAG 392
QY 301 ttctgtaaaagctgcacaaagtagcagagacatgatactcgtgaagaagtgaca 360
    |||
Db 393 TTCTGTCAAAGCCTGCAACAAGTAGCAGAGACATGATCATATCTGAAAGAGTGCACA 452
QY 361 aagatccaagataaagaaacaagatacaagaatacatgtgttaatgattttcaagt 420
    |||
Db 453 AAGATCCAAGATAAAGAAACAAGATTCACAAGAAACAATGCTGTCATGATTTTCAAGT 512
QY 421 tcacaaacacatatttgaagcttaagaacaacatagttggaagtgatgaagaaga 480
    |||

```







QY	61	tcgccagtcgaatcctctctctctgtgatacagagaagaacttgcctcttcgttgaaaa	120
Db	1540	tcgccagtcgaatcctctctctgtgatacagagaagaacttgcctctctgttgaaaa	1599
QY	121	gttagtctcccttgaaagtatttgtcaagaacttgaagaaaaaatgttcttgggaatg	180
Db	1600	gttagtctcccttgaaagtatttgtcaagaacttgaagaaaaaatgttcttgggaatg	1659
QY	181	acggaatttgaagttaggtaagagaagttgcgaatgtcgtctgaatatacaaatcaactg	240
Db	1660	acggaatttgaagttaggtaagagaagttgcgaatgtcgtctgaatatacaaatcaactg	1719
QY	241	agacataacggagactgttactggagaagaaataaaagccagaaaaaaagcggtcgaag	300
Db	1720	agacataacggagactgttactggagaagaaataaaagccagaaaaaaagcggtcgaag	1779
QY	301	tttcgtccaagccttccaagaagtagcagagacatgcatcatatctgaaagaagtcgaca	360
Db	1780	tttcgtccaagccttccaagaagtagcagagacatgcatcatatctgaaagaagtcgaca	1839
QY	361	aagatccaaagataaaggaaaaaagaatatacaaggaatcatgttcatgatttttaagt	420
Db	1840	aagatccaaagataaaggaaaaaagaatatacaaggaatcatgttcatgatttttaagt	1899
QY	421	tcaacaaacgatattttgaaagttaaagaacatatgttggacgttgatgacaaagaa	480
Db	1900	tcaacaaacgatattttgaaagttaaagaacatatgttggacgttgatgacaaagaa	1959
QY	481	cagttgttagaagaatctgcactagaagctactctgggaaacccaagtcacccgattg	540
Db	1960	cagttgttagaagaatctgcactagaagctactctgggaaacccaagtcacccgattg	2019
QY	541	ggagatggagagataggtgaacaaacaccttagcaaaagaagttacataagataaat	600
Db	2020	ggagatggagagataggtgaacaaacaccttagcaaaagaagttacataagataaat	2079
QY	601	ctatgccttcttgatgttcatcgtctgggtacacatatctcaacagacacaaagaa	660
Db	2080	ctatgccttcttgatgttcatcgtctgggtacacatatctcaacagacacaaagaa	2139
QY	661	atttgcgtgggcctctctgcattccacacaaatcaaatgtagacaggttagatgattgt	720
Db	2140	atttgcgtgggcctctctgcattccacacaaatcaaatgtagacaggttagatgattgt	2199
QY	721	gaagcagagctagcagacatgttacaagaagtttaagaagaagaaggttaactaatgtc	780
Db	2200	gaagcagagctagcagacatgttacaagaagtttaagaagaagaaggttaactaatgtc	2259
QY	781	ttgagatgatatcttgagatgttgaagttgtagatggcgttgtagacgagtcttccaactg	840
Db	2260	ttgagatgatatcttgagatgttgaagttgtagatggcgttgtagacgagtcttccaactg	2319
QY	841	gacaatgcagggagatgcgaatactgttgaactaccgtaatagtagaagtagctgtatgct	900
Db	2320	gacaatgcagggagatgcgaatactgttgaactaccgtaatagtagaagtagctgtatgct	2379
QY	901	ggtgtagagaatcttctcttgagatgagcttcatgagatcaagatbagagttggaactt	960
Db	2380	ggtgtagagaatcttctcttgagatgagcttcatgagatcaagatbagagttggaactt	2439
QY	961	ttcaaaagtgcagcatcttccaagtgaagcatatacatatgattcgagagcttggaaag	1020
Db	2440	ttcaaaagtgcagcatcttccaagtgaagcatatacatatgattcgagagcttggaaag	2499
QY	1021	caaatgcagatgaatgtcagcggttaccacataactatgtcgtggttgcagggctctc	1080
Db	2500	caaatgcagatgaatgtcagcggttaccacataactatgtcgtggttgcagggctctc	2559
QY	1081	aaatcaaaagacatagaagattggaanaactgttgcctaagaagtccaagtcattcgctc	1140
Db	2560	aaatcaaaagacatagaagattggaanaactgttgcctaagaagtccaagtcattcgctc	2619

```

Db 3700 GTTGATATAGGCTTTTGGCAATGATCATTTCAAGTGCAGAAAGCTTTTCCAGCAACGCTC 3759
Qy 2281 aagaagttgaagttggaagaactatcgaagctggtcatatactggaacataagctgag 2340
Db 3760 AAGAAGTTGAAGTTGGAAGAACTATTCAGCTGGTCACTACTTGGACATCATACCTGAG 3819
Qy 2341 ttgcttaacctgagtgctgctgaagctgatagtatgagctgctgtgtgtgtgtgaagaatgagat 2400
Db 3820 TTGCTTAACCTTGAAGTGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3879
Qy 2401 ccaattgtatgagttatcattcattgaagcttctgtaataataatgattctcag 2460
Db 3880 CCAATTGTATGAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3939
Qy 2461 ttctggaagcacaataatgataatttccctgtccttgagcgccctcattagaaatgtgc 2520
Db 3940 TTCTGGAAGCACAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3999
Qy 2521 aaaaattgaagagatagccattgattgttgaagatatacagactcagctgattgag 2580
Db 4000 AAAAAATTGAAAGATGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4059
Qy 2581 ttaagagatgtctccccaacttggaatctgctgacgaaatcagaagaagaaga 2640
Db 4060 TTAAGAGATGTCTCCCAACTTGGGAATGCTGTCGACGAAATTCAGAAAGAACAGAA 4119
Qy 2641 gacctggaagaacacctgtgagtgctgctatcctaactcaatgaagaaga 2692
Db 4120 GACCTCGAAGAACACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4171

```

## RESULT 5

```

AX012619 AX012619 3201 bp DNA linear PAT 07-SEP-2000
LOCUS AX012619
DEFINITION Sequence 14 from Patent WO954490.
ACCESSION AX012619
VERSION AX012619.1 GI:9998603
KEYWORDS
SOURCE
ORGANISM Solanum juzepczukii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; easterids I; Solanales; Solanaceae; Solanum.

```

```

REFERENCE 1 (bases 1 to 3201)
AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.
TITLE Plant-derived resistance gene
JOURNAL Patent: WO 95/4490-A 14 28-OCT-1999;
BAUDCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA
KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)

```

```

FEATURES
source 1..3201
location/Qualifiers
/organism="Solanum juzepczukii"
/db_xref="taxon:136614"

```

```

BASE COUNT 953 a 556 c 682 g 1010 t
ORIGIN

```

```

Query Match 10.1%: Score 275.6; DB 6; Length 3201;
Best Local Similarity 55.1%: Pred. No. 2.8e-54;
Matches 730; Conservative 0; Mismatches 549; Indels 45; Gaps 8;

```

```

Qy 166 gtcttggaagaatgagcatttgaagtagagtgaggaagttgcaagtgctgaa 225
Db 176 GATCATGAGAGTGAACATCTTGAAGTGAATCTTAGAGTAGCATACACACAGAA 235
Qy 226 taacaatcaactgagactaagaaactgactggaagaataaagaagcagaanaa 285
Db 236 GATACGTTGACTCGGAATCAAGAAGTGTCTTTAGACAGAAATTTGAGGAAAGAAAC 295
Qy 286 aaggcgctgcgaagtttgcataaagcctgcacaagtagcagaagaatgatcatc 345
Db 296 AGGCGTATGTGGAGATTTTTCGTTTGCAACAGCACTAGAAATGCAATTCACACC 355

```

```

Qy 346 tggaaagatcgacaagaatccaagataaaggaanaaagtatcaagaagatcatggtt 405
Db 356 GTGAAACGTTGAGTGGCAACATGAGACATGAAAGATTTAAACACCAACTACTCA 415
Qy 406 catgatttcaagttcaacaacagatatttgaagttgaagacaatatggttgagct 465
Db 416 CTTCATGATTACCTGACC---ATGCTTTGACACAGCTGAGAAATTAATGTTGGCCG 472
Qy 466 gatgataaaggaagaacagttgttaagaatcagactagaagaactctcgtggaaaccaa 525
Db 473 GAAATTAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
Qy 526 gtaacccagttgctggagatggagagatagatgaanaaaccttgaagaagaattac 585
Db 530 GTTCTCTCAATCGAGGAGTGGAGGATGATGAGGAAACCACTTTGGCTACAAACTCTAT 589
Qy 586 aatgataatcaatctcagtcgcttctgatactcagcctgggctacatatacacaag 645
Db 590 AGTATCTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
Qy 646 cacaacaaaggaagaatttgcgtggccttcgcatccaatcaaatgataagcag 705
Db 650 TATTGTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 706
Qy 706 gtaagaatgattgtgagcagagcagacatgttacaagaagaagttaaagagaag 765
Db 707 -----GATCAACTAGCGGACCGACTGCAAAAGCATCTGAAAGCAG 748
Qy 766 aggtactaaatgtcgtgataatcagagatgtgagatgtgagatgtgagatgtgagatgtgagat 825
Db 749 AGATACCTGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 808
Qy 826 tgcttccaactgaagaacatgcagagagtcgaatctgtgactccgtaagatgaa 885
Db 809 TGTTTCCA---GACTGTTTAAAGGAGGAGGAGATGATGATGATGATGATGATGATGATGATGAT 865
Qy 886 gtaactgataatgtcgtgataatcagagatgtgagatgtgagatgtgagatgtgagatgtgagat 945
Db 866 GTGCTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 925
Qy 946 gagaatgtgagatcttcaagaagtcgaacttcaagaagaag---catacacaatgag 1002
Db 926 GAAATGTGGAATTTACACCAAAAGATCTTGAAGAAAGATGATGATGATGATGATGATGATGAT 985
Qy 1003 ttgagacttctggaagaagaacatgcagagatgtgagatgtgagatgtgagatgtgagatgtgagat 1062
Db 986 TTGAAATATTTGGGAACAAATTTGCAATTAATGAGGAGATGATGATGATGATGATGATGATGAT 1045
Qy 1063 gtggttcgaaggtctt---caactaaaggaagaagaatgtgagaagaatgtgagatgtgagat 1119
Db 1046 GTGATGCTGAGACTCTCTCCAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1105
Qy 1120 aaagaatcagatcattcgtcacaagaatgagatgagagaagatgagatgagatgagatgagat 1179
Db 1106 GAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1165
Qy 1180 ttgattagatcactgacatgacagatcacaagaatgagatgagatgagatgagatgagatgagat 1239
Db 1166 TTGAGTTACATCATCTGCTTCTGACCTTAAACCGTGTGTTTGTGATTTTGAATTTTC 1225
Qy 1240 ccaagaagacagtatattcagtgagaagaatgtgagatgagatgagatgagatgagatgagat 1299
Db 1226 GCAGATATGAGACGATTTCTGTAACATAAATGTTGAGTATGAGCTGAGAGGGGTTT 1285
Qy 1300 ctga-----agttggaagaatgtgagagagaggtgtgagaaggtgtgagaaggt 1353
Db 1286 TTGATGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1345
Qy 1354 gtcatagatgctcagtcctcgtcagcagaagaagatgagatgagagaagaatgagatgagatgagat 1413
Db 1346 GTAGATGAGAGTCAATTTCTATCCACAAATTTGAGTTTGTATGAG---GAAATATGAGAAAG 1402

```









Db 1199 CGTGTTCCTGATATTTGCAATTTTCACAGAGATAAAGATTTCTGTAATGACTTG 1258  
 QY 1274 tggatcatgagatgctgagaggtcctga-----agtggaaatgatttgaagag 1327  
 Db 1259 TTGAGTATGCGCTGTAAGAGGATTTTGAATGAGAGAGGAAAAAGCATTAAGAGAG 1318  
 QY 1328 aggttgaagagcttgcagaagcttgcataatgctcctgcctgcagaagaa 1387  
 Db 1319 TGGCAACAACATGATTAAGCAACTTATAGTACAGCTTAATTTTATCCACAAATTTTA 1378  
 QY 1388 gtccagatggacacaaatagatcagtaagctcagatcagtaataatgacctgag 1447  
 Db 1379 GTTTTCGTGGAACAATGAGAAAG---TTGTGGAATGATGATGATGACCGCTGACTGCTT 1435  
 QY 1448 tggagagaagttcaagaagagagacatttta 1477  
 Db 1436 TGAAGGAGAGCTCGAACAATGATTTGTGGA 1465

RESULT 8  
 AF195939 10331 bp DNA linear PLN 31-OCT-1999  
 LOCUS Solanum tuberosum disease resistance protein Gpa2 gene, complete  
 DEFINITION cds.  
 ACCESSION AF195939  
 VERSION AF195939.1 GI:6164968  
 KEYWORDS potato.  
 SOURCE Solanum tuberosum  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 10331)  
 AUTHORS Van der Vossen, E.A.G.  
 TITLES Direct Submission  
 JOURNAL Submitted (19-OCT-1999) Genomics, CPRO, Droeveendaalsesteeg 1,  
 Wageningen 6708 PB, The Netherlands

FEATURES  
 source location/Qualifiers  
 1..10331  
 /organism="Solanum tuberosum"  
 /db\_xref="taxon:4113"  
 /chromosome="12"  
 /clone="BAC 111"  
 /sub\_clone="pBINRG2"  
 /note="introgressed from Solanum tuberosum ssp. andigena"  
 join(4876..7586,7824..>7851)  
 /product="disease resistance protein Gpa2"  
 join(4876..7586,7824..7851)  
 /note="Lz-NBS-LRR protein: confers disease resistance to  
 potato cyst nematode Globodera pallida Pa2-D383"  
 /codon\_start=1  
 /product="disease resistance protein Gpa2"  
 /protein\_id="AF04603.1"  
 /db\_xref="GI:6164969"  
 /translation="MAYAAVTSIMRTIHOSMELTGDLQFYERKLSIRALIEKSCNI  
 MGHHEGLILEVEIIIVATTEEMDVSESNVLAIVNGKRSKSGEIPVEVLEALG  
 IDSTVKOMATSDSMKDIKPTSLVSLPEHVEYGEENINWGENEEMALDLIAGG  
 RELEVSIYMGIGITTLAAKLSIDPTIMSRDIAKATVSEQVSRVNLGLSLT  
 SDEPVLADOLQKILKGRVIVIDITWTEAMDIKICFPDONGSRILLTRNVE  
 VAEYASSGKPPHMRMLNPFDESNWNLHKIKIFEKGSYSEFENIGQIADKCGELAY  
 ITLIALGKISKITLDEMONTAVNSVSTDEAKCMRYALSYHLSHSLPCFLY  
 FAFIAFERDIYVKIYELMAVEGFLNEEGSKIIEVAETCINELVDSIHNVEFD  
 GTEORGMHDTREICLEARANNPNVNRKSDQNSCAQSMGCSKRSRISIHNEE  
 ELWVCNSENASHITITICRKYTLSEFLKVRVLDLGLTFIPSGVSLHLRLIS  
 LRNPRLQQRGSKKEAVPSIIDIPLSISLCYLQFKLYHPPNCPYPTLPELITM  
 LPRKLCGMNVLRSHEPPENLVLSLQCLINLRVCTGSLRFLPNKLKLELVG  
 KEDFRNHKLDYFRYLYOLEKLAFTSYSSACFLKNTAPIGSTPDDPFOEMETLH  
 EHSRATAPTDYPTLPPDCEPQNLKSLTFPSGDFPLAKDLISVGLPKLEVLQ  
 SHNAFGEEMVEVEGEPHLKFLIDISIVIRWASSDHPPYLERLEISDCPYLDSIP  
 RDPADITTLALDIFRCQGSVNSAKQIQQDDINSGSSIIEVTRILIRNGAFVY"

BASE COUNT 3150 a 1342 c 1924 g 3714 t 1 others

Query Match 10.0% Score 272.8; DB 8; Length 10331;  
 Best Local Similarity 54.7% Pred. No. 1.2e-53;  
 Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

QY 140 ttgtcaagaacttggagaaacaatgcttcttggggaatgaagatttgaagtagag 199  
 Db 4988 TGGAGAAATCCTGCAATTAATATGSGCGATCATGAGGGTTAAACATCTTGGAGTTGAAA 5047  
 QY 200 taagaagaagttgcaagtgctgtaatacacaatcacaatcagatcagaagaaagctgac 259  
 Db 5048 TCATAGAGAGTACATACACAACAAGATATGTTGACTCCGAATCAAGAATGTTTWT 5107  
 QY 260 tgggagaaataaagaagccagaanaaaggcgctgcaagtttcgtcaaaagccgac 319  
 Db 5108 TAGCAGCGAATGTGGGAAAAGCAAGGCTATGCTGGGGAATTTTTCCTTGGAGAC 5167  
 QY 320 aagtagcagagatgataatcagtaagaagtcgacaaagatccaaagataaaggaa 379  
 Db 5168 AAGCACTAGATGATGATTCACACCGTGAACGTGATGGCAACATCGACACGATCA 5227  
 QY 380 aacaagatcaagaagaatcattggttcaatgatttccaagttcaacaagatatttga 439  
 Db 5228 AAGATCTAAACCAACAACCTAGCTCATTGTCAGTTTACTGAAAC---ATGATGTTGAGC 5284  
 QY 440 aggttaagaacaatatggttggacgtgataatgaagaacaagttgttaagaatctga 499  
 Db 5285 AGCCGAGAAATATATGATGTTGGCGTGAATGAAATTTGAATGATGCTGATCAACTTG 5344  
 QY 500 ctgaagctactctcgggaacccaagatccagatctgcggatggagagcaatgta 559  
 Db 5345 CTAGACG---AGCAAGGGAACATAGAAAGTGTCTCAATGTAAGGATGGAGGACATCGGGA 5401  
 QY 560 aaacaacctgaagaaagaagttcaacaatgaatcaatcattcattccgtttgattgctc 619  
 Db 5402 AAACAACCTTGGCTGCAAAACCTATAGTATGCTTACATTAATGCTGATTTGATATTC 5461  
 QY 620 atgcttggtcattacatatctcaacagcaacaacaagaagaatttcttggtcccttcgc 679  
 Db 5462 GTGGAAAAGCAACGTGTTACAAAGATATGTTGTGAGAAAAGTACTCTAGGCTCTTCTTT 5521  
 QY 680 attcacacaatcaaatgataagcaggttaagatgattgtaagcagatcagaagaca 739  
 Db 5522 CTTTGACACAGTGAAGCAACCTATATATC-----AGCTAGCGGAC 5560  
 QY 740 tgttacgaagaagttlaagaagaagaaggtacttaattgtcttggatgatactcggagtt 799  
 Db 5561 AACTGCAAAACATCTGAAAGCAGAGATATCTGTGATGATGATGATGATGATGATGATG 5620  
 QY 800 gtgaagtggtgagatggtgagatgagatgcttccaacatgaagaagaatgcaagagtgaa 859  
 Db 5621 CAGAGCTTGGGATGATTAATAACTATGTTCCCA---GACTGCGATTAATGAGCAACA 5677  
 QY 860 tactgttgaactaccgtaaatgataagtagcttgaatcgtggtgtaagaagatttctt 919  
 Db 5678 TACCTCGACATACGCGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 5737  
 QY 920 tgcgagatgagcttcaatgataagaatgagatgagatgagatgagatgagatgagat 979  
 Db 5738 ATCAACATGCGGCTCATGATTAATGACGAAGATGGAATTTACTACACAAAAGATCTTTG 5797  
 QY 980 caagtgaag---caatacacaatgagatgagatgagatgagatgagatgagatgagat 1036  
 Db 5798 AAAAAGAGGTTCTTATTTCTCTAATAATTTGAAAATTTGGGAAACAAATTCATTAATAT 5857  
 QY 1037 gtccaggttaccactaactatgtcgtgtgtgagaggtcct---caactctaaagaa 1093  
 Db 5858 GTGAGGGGTACCTCTGACATTAATCTTGAATGCTGAGCTCTCTCCAAAATCGATTAATA 5917  
 QY 1094 caataagaagattgaaacaatgcttgaagaatgcaatgataatgataatgataatgata 1153  
 Db 5918 CATTGATGATGATGCAAAATGTTGCGGAGATGATGATGATGATGATGATGATGATGATG 5977



Db 150224 TCGCGAACAACATGTATTAACGAACTTGTAGATAGAAGTCTATTCTATCCACAATGTGA 150165  
 QY 1388 gtcgagatggaacaaatagatcatgtaagttcatgataatattgacctgtg 1447  
 Db 150164 GTTTTGATGGGAAACACAGAG--ATGTGAATGCATGATGTGACCCGTGACTCTGT 150108  
 QY 1448 tgagagaattcaaaaggagaacatttta 1477  
 Db 150107 TGAGGGAACCTCGAACAACATGAATTTTGTGA 150078

RESULT 10  
 LOCUS AX012617 3229 bp DNA linear PAT 06-SEP-2000  
 DEFINITION Sequence 12 from Patent W09954490.  
 ACCESSION AX012617  
 VERSION AX012617.1 GI:9998601  
 KEYWORDS  
 SOURCE potato.  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; easterids I; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 3229)  
 AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
 TITLE Plant-derived resistance gene  
 JOURNAL Patent: WO 9854490-A 12 28-OCT-1999;  
 BAUDCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA  
 KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)  
 FEATURES  
 source 1..3229  
 location/Qualifiers  
 /organism="Solanum tuberosum"  
 /db\_xref="taxon:4113"  
 BASE COUNT 952 a 571 c 686 g 1020 t  
 ORIGIN

Query Match 10.0%; Score 272.4; DB 6; Length 3229;  
 Best Local Similarity 55.0%; Pred. No. 1.6e-53;  
 Matches 728; Conservative 0; Mismatches 531; Indels 45; Gaps 8;

QY 166 gttttgggaaatgacgagatttgaagtagaagtagaagttgacagttgctgta 225  
 Db 176 GATCATGAGGAGTAAACATCTTGGAGTGAATCTTAGAGTAGACATACACAAAGAA 235  
 QY 226 tacacaatcaactgagactaacaggaactgactcgtgagagaataaataaagcagaanaa 285  
 Db 236 GATATGGTTGACCTCGAATCAAGAGTGTCTTTTAGCACAGAAATTTGGAGGAAAGAAAC 295  
 QY 286 aagggcgtcgaaagtttcgtcaaaagcctgcacaagtagacagagagacatgatactc 345  
 Db 296 AGGGCTATGTGGAGATTTTTCGTCTTTGGAAACAAGCACTGAAATGCAATTATTCACAC 355  
 QY 346 tggaaagagtcgacaaagatccaaagataaaggaacaaagtaaccaagaatcatgtgt 405  
 Db 356 GTGAACAAGTGGATGCAACATCGACAGCATGAAGAATCTTAACCAACAACCTAGCTCA 415  
 QY 406 catgattttcaagtccaacaagataatttgaaggttaagaataaataatgttgaagt 465  
 Db 416 CTTGTCACTTACCTGAC--ATGCTTTTGGACGCTGAGAAATATAATGTTGGCCGT 472  
 QY 466 gatgataaagaacagttgttagaagatcgcactagaagactactctggggaacccaa 525  
 Db 473 GAAATATGAATTTGAGATGATGCTGATCACTTGTTAGAGAGGAA---GGAACTAGAA 529  
 QY 526 gtcatccgattgtcggatgggagcatagttaaacaacattagcaaaagaatttac 585  
 Db 530 GTTGCTCAATCGTAGGATGGAGGTATCGGAAACAACATTTGGCTACAAACCTAT 589  
 QY 586 aatgataatcaatctatgcctgtttagatgtcatgctggcgccacacatactcaag 645  
 Db 590 AGTGATCCTTACATTATGTCTGATTTGATATTCGCAAAAAGCAACTGTTTCAACAAG 649

QY 646 cacaacaaagaaatttgcctggccttcgcatccacaaatcaaatgataagcag 705  
 Db 650 TATTGTGTAGAAATTTACTCTAGGCTTCTTCTTTGACAAAGTATGAACCTGAT--- 706  
 QY 706 gthaagatgattggtgaagcagaagctagacaaatgttcaagaanaagttaaagagaag 765  
 Db 707 -----CATCAACTAGCGACCGCACTCGCAAAAGCATGTGAAGGACAG 748  
 QY 766 aggtactaatgtcttgatgatactcgtgaggtgtggaagtgtggaagcgtgagagca 825  
 Db 749 AGATACCTTGATGCTATGATGACATATGACATACAAAAGCTTGGAGTGTATTAACAA 808  
 QY 826 tgccttcaacagcaagcagatgcagagagtcgaataactgttgactcccgtaatgata 885  
 Db 809 TGTCTTCCCA---GACTGTATTAAGGAGACAGAAATCTCTGACTCTCTGGAATGTGGAA 865  
 QY 886 gtagctgttaagctgtgtgtagaagaatttctcttgcgagtagagcttcaatgataagat 945  
 Db 866 GTGGCTGAATATGCTAGTTCAAGTAAGCCTCATCATCATGCGCCTCATGAATTTTGA 925  
 QY 946 gaggatgagctcttcaaaagtcagcatlttcaagtgaag---cattacatatgag 1002  
 Db 926 GAAAGTTGAAATTTACTACACAAAAGATCTTGAAGAAAGAGTTCTTATTTCTCTGAA 985  
 QY 1003 ttcgagactgttggaaagaacatgcagatgaatgtcaggggtgtaccactaatattgc 1062  
 Db 986 TTTGAAATATTTGGGAAACAAATTTGCATTAATTTGGAGAGTATCTCTAGCAATTA 1045  
 QY 1063 gtggttcagaggtctc---caatctaaagagacaataagaagattggaanaactgtgtc 1119  
 Db 1046 GTGATGCTGAGACTTCTCTCAAAAATCATGTAACAAATGATGATGAGGCAAAATGTGCG 1105  
 QY 1120 aaagatgtcaatcatctgtcaaatgataatgataatgataagcagatgttcaagttgtg 1179  
 Db 1106 GAGAAATGTAAGTTCGTGTGTAAGCACAGATCTTGAAGCAAAATGATGAGAGTGTGCT 1165  
 QY 1180 ttgagtagatcagatcagctgcaagcagatcacaacatgtcttcgtattcgaatttt 1239  
 Db 1166 TTGAGTTACCATCACTTGTCTCTCACTTAACCGTGTCTTCTATATTTTGCATTTTC 1225  
 QY 1240 ccaagaagacagtatactcagttgaagaattgtatgatactatgatactgaggggttc 1299  
 Db 1226 GCAGAGATGAGACGATTTCTGTAACATACTTGTGAGTTATGAGCTGTAGAGGGGTT 1285  
 QY 1300 ctga-----agttgaaataatgatttgaagagaggttgaagaagtgttgcagaagct 1353  
 Db 1286 TTGAATGAAGAAGAGGAAAGAAACATGAAGAGGTGCAAGAACATGATTAACCGAGCTT 1345  
 QY 1354 gtcgataagatgtcagttcgtcagcaagagaagctgcagatggaacaaatagatca 1413  
 Db 1346 GTAGATAGAGCTATTTCTATCCACAATTTGAGTTTGTGATG---GAAATAGAAAT 1402  
 QY 1414 tgtaagttcatgatactaatatataagcctgtgtcgtgagaagtttcaaggagaacatt 1473  
 Db 1403 TGTGAATCATGATGATGACCCGTGAACCTGTGTGAGGGAAGCTCGAACAACATGAATTT 1462  
 QY 1474 ttta 1477  
 Db 1463 GTAA 1466

RESULT 11  
 LOCUS AX012618 3229 bp DNA linear PAT 06-SEP-2000  
 DEFINITION Sequence 13 from Patent W09954490.  
 ACCESSION AX012618  
 VERSION AX012618.1 GI:9998602  
 KEYWORDS  
 SOURCE potato.  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;





RESULT 13  
 AX012614 3220 bp DNA Linear PAT 06-SEP-2000  
 LOCUS Sequence 9 from Patent WO954490.  
 DEFINITION AX012614  
 ACCESSION AX012614  
 VERSION AX012614.1 GI:9998598  
 KEYWORDS  
 SOURCE potato.  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 3220)  
 AUTHOR Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
 TITLE Plant-derived resistance gene  
 JOURNAL Patent: WO 954490-A 9 28-OCT-1999;  
 BAUCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFFID (GB); KANYUKA  
 KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)  
 FEATURES  
 source  
 Location/Qualifiers  
 1..3220  
 /organism="Solanum tuberosum"  
 /db\_xref="taxon:4113"  
 BASE COUNT 951 a 568 c 688 g 1013 t  
 ORIGIN  
 Query Match 10.0%; Score 271.6; DB 6; Length 3220;  
 Best Local Similarity 48.9%; Pred. No. 2,4e-53;  
 Matches 1296; Conservative 0; Mismatches 1249; Indels 105; Gaps 17;

QY 800 gtgaagtgtggaatgacgagatgcttcccaactgaagaacaatgcaggaagtcgaa 859  
 DB 782 CAGAAAGCTTGGATGATATAAAACATGTTTCCCA---GACTGTTTAAATGGAAGCA 838  
 QY 860 taactgtacaccglaaataagaaagtagctgttaactgtgtgtagaagaatttctt 919  
 DB 839 TACTCTGACTACTCGGAATGCGAAGTGGCTCAATATGCTATGAGTAAAGCCCTCC 898  
 QY 920 tgcgagatgaactcaatgagatcaagatgagaatgtgagctcttcaaaagtcaagat 979  
 DB 899 ATCAGATGCCCTCAGCAATGATTTGAGCAAAAGTTGGAATTTACTACACAAAAAGATCTT 958  
 QY 980 caagtgaag---attacacatgagatgcgagctgtgtggaagaacatgcgaatgat 1036  
 DB 959 AAAAAGAGGTTCTTTTCTCTGAAATTTGAAATTTGGAAACAAATTTGATTAAT 1018  
 QY 1037 gtacggttaccactaactatgtctgtgtgcaaggctct---caaatcaaaaga 1093  
 DB 1019 GTGAGGATTTACCTTAGCAATTTACTGATTTGCTGACTTCTCTCCAAATGGGTCAAA 1078  
 QY 1094 caatgaagaatgtgaaactgtgtctaaagaatgcaatgcatcgtcacaaatgctc 1153  
 DB 1079 GATTAGATGATGGCAAAAGATTTGGGAAATGTAAAGTTGGCTTACACAGATCTCTG 1138  
 QY 1154 atgaagatgttcaatgctgtgtgtgtgtgagttacatgcaactgaacgagtcctaaa 1213  
 DB 1139 AAGCAAAATGATGAGATGATGTTGCTTGAATTTCCATCATCTGCTTCTCACTTAAC 1198  
 QY 1214 catgtctctgcatcttcggaattttccagaagaacagtgatattccagtgaagaatt 1273  
 DB 1199 CGTGTTCCTGATTTTTCGAATTTTTCACAGAGATGAAACAGATTTCTGTAATGAAC 1258  
 QY 1274 tgaagatcagatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1327  
 DB 1259 TTGAGTTATGCGCTGTGAGAGGATTTTGAATGAAGAAAGGAAAGCAATGAAAGG 1318  
 QY 1328 aggtgaagaagtgtgtgcaagactgtgtgtagatgtgtgtgtgtgtgtgtgtgtgt 1387  
 DB 1319 TGSCAACAAATGATTAATGAAGAACTTATGATGAGAGCTTAATTTTCACTCCAAAT 1378  
 QY 1388 gtgcgaatggaacaaatlaagatcaatgaaatgcaatgcaatgcaatgcaatgca 1447  
 DB 1379 GTTTCGTGGAACATGAAAG---TTGTGATCATGATGATGATGATGATGATGATG 1435  
 QY 1448 tgaagaagaatlaaaggaggaacatttta---taatgaagacatgtgtgtgtgtgt 1504  
 DB 1436 TGAAGGAAGCTGGAACATGAAATTTTGAATGTTATGACAGAAAGATGATCAAAAT 1495  
 QY 1505 catatcagaatgttcaatctctgtatgataaataatgcagcccttaagcgtgtgact 1564  
 DB 1496 CATGTGCACAAATCAATGACAGCTTCTTTAAGAGTGAAGTGGATGCAATTCATAAG 1555  
 QY 1565 gtgatagaatlaatgaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1612  
 DB 1556 TGAAGAAATTTGCTGTGTGCTTAACAGTGAAGCTCATATATATATATATATAT 1615  
 QY 1613 -----ccctgttaaatgcagctgtgagagatgcaatgcaatgcaatgcaatgca 1660  
 DB 1616 TCGAATGCTCACACTGGAATGCTTTTCAAGCTTGAAGATGATTAATCTTGGTTTGA 1675  
 QY 1661 aacgaaccatctgttctctcttcttcttcttcttcttcttcttcttcttcttct 1720  
 DB 1676 ATACATGGCGCAATTTTCCACAGTGAAGATCTTCTTAATCATTTGAGATACATCT 1735  
 QY 1721 aggtgttcaatlaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1771  
 DB 1736 TCGGTTTAAATCTTGTGATTAACAGATGATCAAGATCAAGAAAGCTGTTCCATCA 1795  
 QY 1772 ttgactgttccctcagagatacgaacccatctgtgtgtgtgtgtgtgtgtgtgtgt 1819  
 DB 1796 TAAATGACATTCCTCTATGAGATATCAAGCTTATGCTATGCTCAAACTTTTAACT 1855



QY 1820 tatcatgttcagctatggaatttcgattccaccagaatttcaggttgaatc 1879  
 1856 ttccatattccagattatpattccattatpattccatcaggaattttgacattcccaat 1915  
 QY 1880 tccagacattcattgtaacagtttcagatataataattttgctgaagaatt 1939  
 1916 ttaggacgctgtgtatggctggaatttctgcggcgtatgacctatcagagacat 1975  
 QY 1940 ggaacataatgaattt--aagcattcattacagccagatttatttcagagattgc 1996  
 1976 tggatttgaataattgcaattgacctcattcattgaaaccccgatgtttacaggct 2035  
 QY 1997 caagtgatctttgcaagaagagcatttgatttccaacta--caactattct 2055  
 2036 ttttttagctattttcccaattttaaagagttgcaagtatttgccgccaagacctttc 2095  
 QY 2056 tactgtccacagctgtgacaggaaggtattatgaggttcaagaatgcaaaaa 2115  
 2096 gcaattgccaagacctgtatgatttttgcgacttatatcagctcgaagaattgacatttc 2155  
 QY 2116 ttaggaatcagtggaataagatgactataaagtttcggagactcgggctccaac 2175  
 2156 gtttatatttccatpattgctgttcttcttcttcttcttcttcttcttcttcttct 2215  
 QY 2176 aattctgtatctgcaagaacttgaaatatgagcttatatctgtt----gattata 2230  
 2216 aagattctctgagctttcagacggaattttgcaaaaagagatttttgcggggaactg 2275  
 QY 2231 gcttttcgagtgatcatttcaagtgcaaaaagcttttcgaagaagctcgaagaattga 2290  
 2276 cacttcacacttatttacttacttacttacttacttacttacttacttacttacttact 2335  
 QY 2291 agttt--ggaagaacttactaagctgtcactacttgacatcatagctgagttgcta 2347  
 2336 ctttttggggagaaattctgtgtgcatgagagattttgagcattgttgaaatttacc 2395  
 QY 2348 acccttgagtgctgaagctgagatgagatgagctgtgtgtgtgaagaatgagcaccattg 2407  
 2396 aacttcagagcttatttacttacttacttacttacttacttacttacttacttacttact 2455  
 QY 2408 ttatgagatttactgattgaagcttttgtaataataatgatttctcgaattcctga 2467  
 2456 aggaagaggttttcttacttacttacttacttacttacttacttacttacttacttact 2515  
 QY 2468 aagcacaactgacaatttctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 2527  
 2516 gacctgt 2575  
 QY 2528 tgaagaagatcaccattgattgagatgagatgagatgagatgagatgagatgagatgag 2587  
 2576 tggatttcaattccctcgaagattttgcaagatttgaacacactgacttattgatttgaatt 2635  
 QY 2588 aggttcctcccaacttggggaattcgtcgaagaatttgaagaagaagaagaagacctg 2647  
 2636 acgtgcaacaaattgtttggaatttccgccaagaagaatttgaagaagaagaagaacct 2695  
 QY 2648 gaaacaacctgt 2707  
 2696 atggaagcttctatcgagctgctatcgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2755  
 QY 2708 aagaacattat 2717  
 2756 tacaacata 2765

ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; eusterids I; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 5820)  
 AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
 TITLE Plant-derived resistance gene  
 JOURNAL Patent: WO 9954490-A 1 28-OCT-1999;  
 BAULCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFFID (GB); KANYUKA  
 KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)  
 FEATURES  
 source 1..5820  
 Location/Qualifiers  
 /organism="Solanum tuberosum"  
 /db\_xref="taxon:4113"  
 BASE COUNT 1776 a 996 c 1111 g 1937 t  
 ORIGIN  
 Query Match 10.0%; Score 271.6; DB 6; Length 5820;  
 Best Local Similarity 48.9%; Pred. No. 2,3e-53;  
 Matches 1296; Conservative 0; Mismatches 1249; Indels 105; Gaps 17;  
 QY 140 tttgcaagaacttggaaaacaaatgttttggggaatgacgagatttgaagtagag 199  
 2361 tggagaaattctcgaattatpattggcgatcatgaggggttgaacattcttgaaattgaaa 2420  
 QY 200 taagagaagttgcaagtgctgtcgtgaataaccattcaactgagactaaggaactgac 259  
 2421 tctgtaggggtgagatgacacacagaaagatggtgtgctggaatvcaagaattgttttt 2480  
 QY 260 tgggagaataataaagccagaaaagagcgctgcgaagtttcgtcgaagccctgaac 319  
 2481 tagcacagaaatttggagaaagaaagagcgctgtatgtggagattttttgctctggaac 2540  
 QY 320 aagtagcagagagacatgacatatacttgaagaagtcgacaaagatccagaataaagaa 379  
 2541 aagcactgagaaatgattgatttccacggtgaacggtgagatgagcgaacatcgacatga 2600  
 QY 380 aacaagtataaaggaatcattgttcaatttcaatttcaacaaagatatttga 439  
 2601 aagatttcaaaac 2657  
 QY 440 aggttaagaacaataatgttggagcgtgagatgacaaagaaagatttgaagaatcga 499  
 2658 agcccgagaaatpattatggttgcgcgtgaataatgatttggagatgactggaatcactg 2717  
 QY 500 ctgaagctactcctggggaaccccaagtcacccgatttcgagatgagagagacagta 559  
 2718 ctgagag--AGGAAGGAACTAGAAAGTTGTCATCGTAGAGGAGGAGCATCGGGA 2774  
 QY 560 aacaacattagcaaaagaaagtttaccatgattgaatcaattctatgctgttgaagttc 619  
 2775 AAACAACTTTGGCTACAAACTCTATAGTGAATCGTGCATTAATGTCTCGATTGATATTC 2834  
 QY 620 atgcctggtacacatactcaacagacacacacacacacacacacacacacacacacacac 679  
 2835 gtgcgaaagcaactgtttcacaacagatgtgtgcaaaatgctgctgagccctgtttt 2894  
 QY 680 attcacaatcaaaatgagatgacagggtttaagatgattgttgaagcagagctagcagaca 739  
 2895 ctttgacacagatgac 2933  
 QY 740 tgttacaagaagtttaagaagaagaggtactaattgttcttgatgattgagaggt 799  
 2934 GACTGCAAAAGCATCTGAAGGCGAGAGATCTGTGATGATGATGATGATGATGATGATGAT 2993  
 QY 800 gtgaagtgtgagtggttgaagcagcttcccaactgaagaagaatgcaagcagagagagaa 859  
 2994 CAGAGCTTGGAGATGATTAATAACTATGTTCCCA---GACTGTATTAAGGAAGCAAGAA 3050  
 QY 860 tactgttgaactaccgtaatgagatgagatgagctgttctgctgtgtgagagatttctc 919  
 3051 TACTCTGACTACTCGGAAGTGTGGAAGTGTGGAATGCTGATGCTGATGCTGATGCTGATGCT 3110

RESULT 14  
 LOCUS AX012606 5820 bp DNA linear PAT 06-SEP-2000  
 DEFINITION Sequence 1 from Patent WO9544490.  
 ACCESSION AX012606  
 VERSION AX012606.1 GI:9998596  
 KEYWORDS potato.







Oy	1505	catatccagaatggtcatatctctctgatagtataaaatgcagcccttaagcggtgacg	1564
Dd	13308	catgtgcacaaatccatgcacgcttcccttttaaaagtcgaagtcgagatcagaatccataaag	13367
Oy	1565	gtatgtaaatlaatatgltccctatggtccttaataagggtctctcta-----	1612
Dd	13368	tggaaagattggcgttgctgtgttaacacagtagagccatctattttatcattgtgctgagat	13427
Oy	1613	-----ccctgtaaatcgtcaagtgtgagagatcatgtcaacacaca--atcctttga	1660
Dd	13428	tccgaatgcgtcacatcgggaattgtcttttcaaaccttgaagagctctgacatcttggtttga	13487
Oy	1661	aacgaaccatctgctttctctctttcactcctgaagccttatalatgattctcctaactcag	1720
Dd	13488	atfaccatggccaaatttttccacagtgagagactttctcctaattcattgagatfaccctfcttt	13547
Oy	1721	aggctgtctcttccaatacttaccaaagctctggagctgaga-----cacagacaga	1771
Dd	13548	tgcgttttaattccttgctctttacacacagatatacagaagtcgaanaagcgtgttcctctatcaca	13607

Oy	2528	tgtaaagatgaccatttgagtcttgcagaatacaacaactcagctgataggtaaag	2587
Dd	14388	TGGATTCAATCCCTCGAGATTTTGCAGATATACCACACTGAGCTTATGTATGATATGATT	14447
Oy	2588	agttccctcccnaactltggggaatlgtctgcacgaattcagaaaacaaagaacctcg	2647
Dd	14448	ACTGTCAAACAATGTGTGTGAATTCGCCGAAAGCANAATTAACACAGCATTCAGACAACT	14507
Oy	2648	gaaacaacccctgtgtagtcgtatatccaatccaattgaaggagaagtcatctcgattcsg	2707
Dd	14508	ATGGAACCTTGATCGAGGTCCTAACHGNCATCTTTGTAGAAGACATCTCTTCCTGCTT	14567
Oy	2708	aagaaacata 2717	
Dd	14568	TRACAACAATA 14577	

Search completed: September 11, 2002, 22:27:22  
Job time: 38713 sec

```
Search completed: September 11, 2002, 22:27:22
Job time: 38713 sec
```

Job time: 38713 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 22:37:03 ; Search time 881.41 Seconds

(without alignments)  
5294.441 Million cell updates/sec

Title: US-09-864-680-4

Perfect score: 2718  
Sequence: 1 atggtcatgcaagtgtgc.....ctgattcagaagaacattag 2718

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq\_032802.\*  
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2718	100.0	2718	22	AAAF63303
2	2718	100.0	3099	22	AAAD10204
3	2718	100.0	3099	22	AAAF63302
4	2685.6	98.8	31491	22	AAAD10203
5	2685.6	98.8	31491	22	AAAF63301
6	272.8	10.0	2739	21	AAZ50262
7	272.8	10.0	2817	21	AAZ50652
8	272.8	10.0	3683	22	AA503713
9	272.8	10.0	10329	21	AAZ50264

10	272.8	10.0	10329	21	AAZ50653
11	271.6	10.0	5820	20	AAZ37153
12	269.6	9.9	3066	20	AAZ37154
13	268	9.9	3014	22	AAZ503715
14	266.4	9.8	2880	22	AAZ503717
15	266	9.8	2885	22	AAZ503719
16	264.8	9.7	3283	22	AAZ503716
17	256.8	9.4	2679	22	AAZ503718
18	172.2	6.3	5475	19	AAV17777
19	170	6.3	10968	19	AAV17789
20	149.2	5.5	3997	19	AAV26082
21	149.2	5.5	9870	19	AAV13935
22	149.2	5.5	9870	19	AAV16457
23	149.2	5.5	51952	19	AAV26084
24	147.6	5.4	3982	19	AAV26083
25	132.2	4.9	23670	24	ABA97077
26	119	4.4	3909	24	ABA97078
27	103.4	3.8	534	21	AAZ51888
28	95.2	3.5	540	21	AAZ51891
29	94.4	3.5	3801	21	AAZ59332
30	94.4	3.5	6658	18	AAZ79882
31	92.2	3.4	532	21	AAZ51889
32	88.8	3.3	517	21	AAZ51884
33	83.6	3.1	4465	17	AAZ42135
34	81.4	3.0	477	21	AAZ51880
35	76	2.8	472	21	AAZ51876
36	74	2.7	644	21	AAZ51886
37	72.2	2.7	2862	21	AAZ58295
38	70.4	2.6	647	21	AAZ59959
39	66.6	2.5	489	21	AAZ51874
40	62.8	2.3	1028	21	AAZ59956
41	59.2	2.2	2954	21	AAZ58294
42	59.2	2.2	6760	21	AAZ58293
43	56	2.1	4948	17	AAZ42134
44	50.4	1.9	5910	19	AAZ6798
45	48.2	1.8	548	21	AAA40001

#### ALIGNMENTS

RESULT 1  
ID AAF63303 standard; cDNA; 2718 BP.  
AC AAF63303;  
XX 02-MAY-2001 (first entry)  
XX  
DE Pepper Bs2 open reading frame sequence.  
XX Bs2; pepper: pathogen resistant; Xanthomonas campestris pv vesicatoria;  
KW Kcv; bacterial spot disease; transgenic plant; crop: fruit; flower; ss.  
XX  
OS Capsicum annuum.  
XX  
PN W0200107635-A1.  
XX  
PD 01-FEB-2001.  
XX  
PF 23-DEC-1999; 99WO-US30891.  
XX  
PR 23-JUL-1999; 99US-0360186.  
XX  
(REGC ) UNIV CALIFORNIA.  
PA Staskawicz BJ, Dahlbeck D, Tai TH.  
PI  
XX  
XX WPI: 2001-168560/17.  
DR P-FSDB; AAB72198.  
XX  
XX Novel Bs2 polypeptide from Capsicum annuum for producing transgenic  
PT plants having resistance to bacterial spot disease caused by

Genomic DNA encodi  
DNA sequence of BA  
Partial nucleotide  
DNA encoding Rx 72  
DNA encoding Rx 19  
DNA encoding Rx 32  
DNA encoding Rx 39  
DNA encoding Rx 7,  
Tomato Prf cDNA.  
Tomato Prf genomic  
Tomato Prf resist  
Tomato Mi resist  
Wild tomato Mi res  
Tomato pest resist  
Tomato pest resist  
Tomato Hero gene c  
Tomato Hero gene A  
N. tabacum Class I  
N. tabacum Class I  
Nucleotide sequenc  
Tomato immunity 2  
N. tabacum Class I  
N. tabacum Class I  
I2C-2 gene encodin  
N. tabacum Enh8 ge  
N. tabacum Enh4 ge  
N. tabacum Class I  
Sorghum resistance  
Rice disease resis  
N. tabacum Enh2 ge  
Rice disease resis  
Sorghum resistance  
Sorghum resistance  
I2C-1 gene encodin  
Rice bacterial lea  
Rice disease resis

PT Xanthomonas campestris pv vesicatoria (Xcv) -  
 XX  
 PS Claim 3; Page 64-68; 72zp; English.

XX This invention relates to the amino acid sequence of the Bs2 protein  
 CC isolated from  *Capsicum annuum*  (pepper). The protein and DNA sequences of  
 CC Bs2 can be used to confer resistance to the plant pathogen  *Xanthomonas*   
 CC  *campestris*  pv  *vesicatoria*  (Xcv) which causes bacterial spot disease. Bs2  
 CC DNA and protein sequences are useful for producing transgenic plants such  
 CC as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola,  
 CC cowpea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton,  
 CC cassava and walnut, having resistance to  *X. campestris* . The protein and  
 CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
 CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
 CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
 CC carnations and roses having resistance to  *X. campestris* . The present  
 CC sequence represents the open reading frame of Bs2.

XX Sequence 2718 BP; 851 A; 454 C; 623 G; 790 T; 0 other;

# Query Match

100.0%; Score 2718; DB 22; Length 2718;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggtctatgcaagtgtgtgtctcttattgagaacaatagaatctcttgaattcaat 60  
 DB 1 atggtctatgcaagtgtgtgtctcttattgagaacaatagaatctcttgaattcaat 60  
 QY 61 tgcgcgatgcaatctctctctgctgatacagagaagaacttgcgtcttcgtgaaaaa 120  
 DB 61 tgcgcgatgcaatctctctctgctgatacagagaagaacttgcgtcttcgtgaaaaa 120  
 QY 121 gttatgtccctcggaaagtatttgcagaacttgcagaacaaatgcttttggggaatg 180  
 DB 121 gttatgtccctcggaaagtatttgcagaacttgcagaacaaatgcttttggggaatg 180  
 QY 181 acggattttgaaagtgaaggaagaattgcaagtgctgtcgtgaatacaattcaatg 240  
 DB 181 acggattttgaaagtgaaggaagaattgcaagtgctgtcgtgaatacaattcaatg 240  
 QY 241 agacttaacagaaactgtactcgtggaagaataaagaacccagaacaaagcgctgcgaag 300  
 DB 241 agacttaacagaaactgtactcgtggaagaataaagaacccagaacaaagcgctgcgaag 300  
 QY 301 ttctgtcaaacgctgcacaagaatgacagagacatgatactatctgtaaaagatcgaca 360  
 DB 301 ttctgtcaaacgctgcacaagaatgacagagacatgatactatctgtaaaagatcgaca 360  
 QY 361 aagatccaagaagctgcacaagaatgacagagacatgatactatctgtaaaagatcgaca 420  
 DB 361 aagatccaagaagctgcacaagaatgacagagacatgatactatctgtaaaagatcgaca 420  
 QY 421 tcaacaacagatatttgaaggttaagaacaataatggttgcagtgatcaacaagaagaa 480  
 DB 421 tcaacaacagatatttgaaggttaagaacaataatggttgcagtgatcaacaagaagaa 480  
 QY 481 caggtttgaagaatctgtaagaactcgtggaacccagaagatcccccgttttc 540  
 DB 481 caggtttgaagaatctgtaagaactcgtggaacccagaagatcccccgttttc 540  
 QY 541 gggatgggagacatagttaaaacaaacttagcaaaaagatttacaatgatatcaatt 600  
 DB 541 gggatgggagacatagttaaaacaaacttagcaaaaagatttacaatgatatcaatt 600  
 QY 601 ctatgcgctttgagttcaatgctcgtggtaccatactcacaacgacacacaaaaggaa 660  
 DB 601 ctatgcgctttgagttcaatgctcgtggtaccatactcacaacgacacacaaaaggaa 660  
 QY 661 atttgcgtggtccttcgatacccaaatcaaatgagatgacagggttaagaatgattgt 720  
 DB 661 atttgcgtggtccttcgatacccaaatcaaatgagatgacagggttaagaatgattgt 720

QY 721 gaagcagagctagcagacatggttacagaaaaagtttaagaagaagagctactaatgtc 780  
 DB 721 gaagcagagctagcagacatggttacagaaaaagtttaagaagaagagctactaatgtc 780  
 QY 781 ttgatgatatactcggaggttggtaagtgtggaatgagtgagacagatgcttccaactgaa 840  
 DB 781 ttgatgatatactcggaggttggtaagtgtggaatgagtgagacagatgcttccaactgaa 840  
 QY 841 gacaatgcaaggagctgatactcgttgaactaccgtaaatgagaatgaaatctgtatgtc 900  
 DB 841 gacaatgcaaggagctgatactcgttgaactaccgtaaatgagaatgaaatctgtatgtc 900  
 QY 901 ggtcgaagaatttctcttgcgtgagcttcatactgataccaatagaaggttgaagctc 960  
 DB 901 ggtcgaagaatttctcttgcgtgagcttcatactgataccaatagaaggttgaagctc 960  
 QY 961 ttcaaaagtgcagacatttccaagtgaagcattacacatgagttcagactgttggaag 1020  
 DB 961 ttcaaaagtgcagacatttccaagtgaagcattacacatgagttcagactgttggaag 1020  
 QY 1021 caaatcgcaatgaaatgtaacggttacacactactatggttgcgttgcagggcttcc 1080  
 DB 1021 caaatcgcaatgaaatgtaacggttacacactactatggttgcgttgcagggcttcc 1080  
 QY 1081 aaatctaagaaggaacataagaatctgaaacactgttgcataaagatgccaagtatcgtc 1140  
 DB 1081 aaatctaagaaggaacataagaatctgaaacactgttgcataaagatgccaagtatcgtc 1140  
 QY 1141 acaaatgatactcgtatgaaacgagtccaagtgctggttgggttgaatgatacacttgaca 1200  
 DB 1141 acaaatgatactcgtatgaaacgagtccaagtgctggttgggttgaatgatacacttgaca 1200  
 QY 1201 agcgatctaaacaatgctcgtcgtcgtatggaattttccagaagaacagtgatattcca 1260  
 DB 1201 agcgatctaaacaatgctcgtcgtcgtatggaattttccagaagaacagtgatattcca 1260  
 QY 1261 gtcgaagaatttgaatgatactgagatgagctgagaggttccctgaagtgcgaataatgtctg 1320  
 DB 1261 gtcgaagaatttgaatgatactgagatgagctgagaggttccctgaagtgcgaataatgtctg 1320  
 QY 1321 gaaggaagaagttgagaaggttttgcagaagcttgcgtatgataatgatactcgtcgaac 1380  
 DB 1321 gaaggaagaagttgagaaggttttgcagaagcttgcgtatgataatgatactcgtcgaac 1380  
 QY 1381 aaggaagaagctgagatgagaaacaaatattgatactgataaggttgcataatataatgaa 1440  
 DB 1381 aaggaagaagctgagatgagaaacaaatattgatactgataaggttgcataatataatgaa 1440  
 QY 1441 ctgtgcgtgagaagaagttcaaaaggagaaacattttatcaatgaaagatgtgtttttc 1500  
 DB 1441 ctgtgcgtgagaagaagttcaaaaggagaaacattttatcaatgaaagatgtgtttttc 1500  
 QY 1501 gtaacataccagaatgttcatatctcgtatgtatataaaatgaaatgaaagcccttaagcggtg 1560  
 DB 1501 gtaacataccagaatgttcatatctcgtatgtatataaaatgaaatgaaagcccttaagcggtg 1560  
 QY 1561 actgtgtatgaaatataatgtgtccctatggtccttataatgaggtccttaccctgtga 1620  
 DB 1561 actgtgtatgaaatataatgtgtccctatggtccttataatgaggtccttaccctgtga 1620  
 QY 1621 aatcgtcaagttgagaaggtatgatactcgtatgtatataaaatgaaatgaaagcccttaagcggtg 1680  
 DB 1621 aatcgtcaagttgagaaggtatgatactcgtatgtatataaaatgaaatgaaagcccttaagcggtg 1680  
 QY 1681 tctttcatcttgagccttataatgtatcgttccaatcaagaaggtgttcaattccaatga 1740  
 DB 1681 tctttcatcttgagccttataatgtatcgttccaatcaagaaggtgttcaattccaatga 1740  
 QY 1741 ctcaaaagtcttgagcctgagacacagacagatgagttgttccctcgagagatacctaagc 1800  
 DB 1741 ctcaaaagtcttgagcctgagacacagacagatgagttgttccctcgagagatacctaagc 1800  
 QY 1801 ctcaatcgtgttgaggtatcccatcatgttcaagctatgaggaatttcgatacctccaagaa 1860

```

Db 1801 ctcactggttgaggtactactatctgttcagctcagtggaatttcgagttaccctccaa 1860
Qy 1861 attgcaggtatggaatctgcagacatctatgttcaacggtttcgatcagataata 1920
Db 1861 attgcaggtatggaatctgcagacatctatgttcaacggtttcgatcagataata 1920
Qy 1921 attttgctgagaaatttggaactaatgcaatgaagcctcttaactcgcagattt 1980
Db 1921 attttgctgagaaatttggaactaatgcaatgaagcctcttaactcgcagattt 1980
Qy 1991 tatitgcaaggttgcagaggtatctgttgcacaaaggaaggaagcacttgattttcaaac 2040
Db 1991 tatitgcaaggttgcagaggtatctgttgcacaaaggaaggaagcacttgattttcaaac 2040
Qy 2041 ttacaactatttcttacttgcctcagcgttggtgcacgaaggaaggtattatgggatt 2100
Db 2041 ttacaactatttcttacttgcctcagcgttggtgcacgaaggaaggtattatgggatt 2100
Qy 2101 cagaatgtcaaaaatttggaatcagtggaataaggaatgactataaaagtttcgggac 2160
Db 2101 cagaatgtcaaaaatttggaatcagtggaataaggaatgactataaaagtttcgggac 2160
Qy 2161 tctgggcttcccaacaatctgtctatctgcagcaacttgaataatttggtctatct 2220
Db 2161 tctgggcttcccaacaatctgtctatctgcagcaacttgaataatttggtctatct 2220
Qy 2221 gttgattatagccttttgccagtgatcatctcaagtgcacaaagccttccagcaacgctc 2280
Db 2221 gttgattatagccttttgccagtgatcatctcaagtgcacaaagccttccagcaacgctc 2280
Qy 2281 aagaagttggaatttggaagaaactatctcaagctgttcaacttgacactagaagctgag 2340
Db 2281 aagaagttggaatttggaagaaactatctcaagctgttcaacttgacactagaagctgag 2340
Qy 2341 ttgctaaaccttgagtgctgagcgtgatgatgagcgttgtgtggtgaagaatgcat 2400
Db 2341 ttgctaaaccttgagtgctgagcgtgatgatgagcgttgtgtggtgaagaatgcat 2400
Qy 2401 ccaattgtatggatttaatcagatggaagccttgcgtaataataatagttttcgaag 2460
Db 2401 ccaattgtatggatttaatcagatggaagccttgcgtaataataatagttttcgaag 2460
Qy 2461 ttctggaagccacaatgacaatttctcctgcctgagcgcctcagcttagaagttgc 2520
Db 2461 ttctggaagccacaatgacaatttctcctgcctgagcgcctcagcttagaagttgc 2520
Qy 2521 aaaaatttgaagagatacccatgtgagtttcagatatcacacatacagctgattgag 2580
Db 2521 aaaaatttgaagagatacccatgtgagtttcagatatcacacatacagctgattgag 2580
Qy 2581 ttaagagagtgctcctcccaacttggggaatctgtctgcagaaattcagaagaagaaga 2640
Db 2581 ttaagagagtgctcctcccaacttggggaatctgtctgcagaaattcagaagaagaaga 2640
Qy 2641 gacctcggaacaacccctgagatgttcgtatctcaaatccatctgaagagagtgattct 2700
Db 2641 gacctcggaacaacccctgagatgttcgtatctcaaatccatctgaagagagtgattct 2700
Qy 2701 gattcagaagaacattag 2718
Db 2701 gattcagaagaacattag 2718

```

```

RESULT 2
AADI0204
ID AADI0204 standard; cDNA; 3099 BP.
XX
AC AADI0204;
XX
DT 24-Sep-2001 (first entry)
XX
DE Pepper Bs2 cDNA.

```

```

XX
KW Bs2 gene; pepper; resistance gene; plant pathogen; virulence gene;
KW bacterial spot disease; Xanthomonas campestris pv. vesicatoria;
KW AvrBs2; hypersensitive response; transgenic plant; tomato; tobacco;
KW rice; corn; wheat; ss.
XX
OS Capsicum annuum.
XX
FH Key Location/Qualifiers
FT CDS 93..2810
FT /tag=a
FT /product="Bs2 protein"
FT /note="This region is claimed as SEQ ID NO:4
FT in claim 7"
XX
PN US6262343-B1.
XX
PD 17-Jul-2001.
XX
PE 23-Jul-1999; 99US-0360186.
XX
PR 23-Jul-1998; 98US-0093957.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Staskawicz BJ, Dahlbeck D, Tai TH;
XX
DR WPI: 2001-450496/48.
DR P-PSDB: AA05409.
XX
PT Nucleic acid molecules encoding Bs2 protein, useful for producing
PT transgenic plants having resistance to the plant pathogen Xanthomonas
PT campestris -
XX
PS Claim 7; Column 49-56; 37pp; English.
XX
CC The present sequence is Bs2 cDNA from pepper. The Bs2 gene is shown
CC to confer resistance to plant pathogen
CC Xanthomonas campestris pv. vesicatoria which causes bacterial spot
CC disease. The Bs2 protein has Bs2 biological activity, i.e., when
CC co-expressed in a plant with a X. campestris AvrBs2 gene product,
CC it produces a localised hypersensitive response. The protein
CC includes a nucleotide binding motif and leucine rich repeats of the
CC type found in other plant resistance genes. The Bs2 nucleic acid
CC molecule is useful for producing transgenic plants such as pepper,
CC tomato, tobacco, broccoli, cauliflower, cabbage, cowpea, grape, canola,
CC bean, soybean, rice, corn, wheat, barley, citrus, cotton, cassava and
CC walnut, that are resistant to plant pathogen Xanthomonas campestris.
CC The transgenic plants produced using Bs2 molecule develop a
CC hypersensitive response to the pathogen at the site of inoculation and
CC show an enhanced resistance to systemic infection. The Bs2 nucleic acid
CC molecule is also useful as polymerase chain reaction (PCR) primers for
CC amplifying portions of Bs2 nucleic acid molecule, as sequencing primers
CC to verify the authenticity of an amplified molecule, and as
CC hybridisation probes.
XX
SQ Sequence 3099 BP; 970 A; 514 C; 693 G; 922 T; 0 other;

```

```

Query Match 100.0%; Score 2718; DB 22; Length 3099;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 atggcctatgcaagtggtgcttctctatagaacaatagaatctcttgacatcaat 60
Db 93 atggcctatgcaagtggtgcttctctatagaacaatagaatctcttgacatcaat 152
Qy 61 tgcgcgatgcaatctctatctctgtatcacagagaagaacttggcgtctctgtgaaaa 120
Db 153 tgcgcgatgcaatctctatctctgtatcacagagaagaacttggcgtctctgtgaaaa 212
Qy 121 gttagttccttggaagatttgcagaacttgcagaagaacaatggttttggaagt 180

```

Db 213 gtiatgccctggaagtattcttgcaagaacttgagaaaaaacaatgttttggggaatg 272  
QY 181 acggattttggaagtagaagtagaagattgcaagtgtgtgtgatacacaaattccaactg 240  
Db 273 acggattttggaagtagaagtagaagattgcaagtgtgtgtgatacacaaattccaactg 332  
QY 241 agactcaacagaactgttactgtggaagaataaagccggaanaaaagcgcgctcgaaag 300  
Db 333 agactcaacagaactgttactgtggaagaataaagccggaanaaaagcgcgctcgaaag 392  
QY 301 ttctgtcaaaagccgcaacaaagtagcagaagacatgatacatctcgtgaagagtcgaca 360  
Db 393 ttctgtcaaaagccgcaacaaagtagcagaagacatgatacatctcgtgaagagtcgaca 452  
QY 361 aagatccaagaataaaggaaacaagatccaagaagatcattgttcaatgttttcaagt 420  
Db 453 aagatccaagaataaaggaaacaagatccaagaagatcattgttcaatgttttcaagt 512  
QY 421 tcaacaaacgaatatttgaaaggttaagaacaatatggttggaagtgatcaacaagaagaa 480  
Db 513 tcaacaaacgaatatttgaaaggttaagaacaatatggttggaagtgatcaacaagaagaa 572  
QY 481 cagttgttagaagaactgtgactagaagactactctggaaccccaagatcccgatgtgc 540  
Db 573 cagttgttagaagaactgtgactagaagactactctggaaccccaagatcccgatgtgc 632  
QY 541 gggaatggagagcataggttaaaacaacacttagcaaaagaagtttaacaatgatacaat 600  
Db 633 gggaatggagagcataggttaaaacaacacttagcaaaagaagtttaacaatgatacaat 692  
QY 601 ctatgacggttttgatgttcatatgctgtggtgtaacaatctcaacagcaacaaanaagaa 660  
Db 693 ctatgacggttttgatgttcatatgctgtggtgtaacaatctcaacagcaacaaanaagaa 752  
QY 661 attttgtgagccctctgcgcatctccacaatcaaaatgatacagaggttaagatgttgc 720  
Db 753 attttgtgagccctctgcgcatctccacaatcaaaatgatacagaggttaagatgttgc 812  
QY 721 gaagcagaagctagcagacatgttacaagaaagtttaagaagaagagtaactaatgttc 780  
Db 813 gaagcagaagctagcagacatgttacaagaaagtttaagaagaagagtaactaatgttc 872  
QY 781 ttgataatactgagatgttgaaagtgttggaatggcggtgagaagatgcttccaactgaa 840  
Db 873 ttgataatactgagatgttgaaagtgttggaatggcggtgagaagatgcttccaactgaa 932  
QY 841 gacaaatgcagggagtcgaatactgttgaaccacgtaatatgaagtagcttttatgtc 900  
Db 933 gacaaatgcagggagtcgaatactgttgaaccacgtaatatgaagtagcttttatgtc 992  
QY 901 ggtgtagaagaatttctctgcggaatgagcttcaatgatacagaatgagatggaagtcct 960  
Db 993 ggtgtagaagaatttctctgcggaatgagcttcaatgatacagaatgagatggaagtcct 1052  
QY 961 ttcaaaagtcagacattttaagtgaaagcatctacatagatgagttcgagactgttgaaag 1020  
Db 1053 ttcaaaagtcagacattttaagtgaaagcatctacatagatgagttcgagactgttgaaag 1112  
QY 1021 caaatcgcaagatgaaatgcaacgggttaaccataactattgtgtgttcagggctctcc 1080  
Db 1113 caaatcgcaagatgaaatgcaacgggttaaccataactattgtgtgttcagggctctcc 1172  
QY 1081 aaatctaaagaagcaatagagaattggaaacactgttgtaaaagatgcaagtcattcgtc 1140  
Db 1173 aaatctaaagaagcaatagagaattggaaacactgttgtaaaagatgcaagtcattcgtc 1232  
QY 1141 acaaatgatctgatgaagaatgttcaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200  
Db 1233 acaaatgatctgatgaagaatgttcaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1292  
QY 1201 agcgatctaaacacatgtctctgcattctcggaatttccggaagaagagatatttcca 1260  
Db 1293 agcgatctaaacacatgtctctgcattctcggaatttccggaagaagagatatttcca 1352

---

QY 1261 gtaagaatatttgatgatacagatgctgaggggttccctgaagtgtgaaaaatgatttg 1320  
Db 1353 gtaagaatatttgatgatacagatgctgaggggttccctgaagtgtgaaaaatgatttg 1412  
QY 1321 gaaggaagagttgagaagatgtttgcagaagctgtctgataagatgtcttccctgaac 1380  
Db 1413 gaaggaagagttgagaagatgtttgcagaagctgtctgataagatgtcttccctgaac 1472  
QY 1381 aagaagaatgcagatggaacaaaaattagatcaatgttaaggttcatgatctaatatagac 1440  
Db 1473 aagaagaatgcagatggaacaaaaattagatcaatgttaaggttcatgatctaatatagac 1532  
QY 1441 ctgtgcgtgaggaagttcaaaagggaacattttatcatatgaagacatgttcttgac 1500  
Db 1533 ctgtgcgtgaggaagttcaaaagggaacattttatcatatgaagacatgttcttgac 1592  
QY 1501 gtaataacccagaaatgtcatatactctgtcatgataaaatgacgaccttaagcgctg 1560  
Db 1593 gtaataacccagaaatgtcatatactctgtcatgataaaatgacgaccttaagcgctg 1652  
QY 1561 actgtgtatgaataatattatgttccctatggttcttataaggctctcttaaccctgta 1620  
Db 1653 actgtgtatgaataatattatgttccctatggttcttataaggctctcttaaccctgta 1712  
QY 1621 aatcgatcagttgagagatcatgacaacaacaaactctttgaaacggaacccattctgttc 1680  
Db 1713 aatcgatcagttgagagatcatgacaacaacaaactctttgaaacggaacccattctgttc 1772  
QY 1681 tctttcatcttgagccttatatatgttctcaaatccagaaaggtgtgtcatctcaaat 1740  
Db 1773 tctttcatcttgagccttatatatgttctcaaatccagaaaggtgtgtcatctcaaat 1832  
QY 1741 ctcaaaagcttcttgagctgagacagacaagaatgtgtgttccctcgagagatataagc 1800  
Db 1833 ctcaaaagcttcttgagctgagacagacaagaatgtgtgttccctcgagagatataagc 1892  
QY 1801 ctcatctgtttaggttaacctatcatctgttcaagctatggaatctcgatgtacccccaagaa 1860  
Db 1893 ctcatctgtttaggttaacctatcatctgttcaagctatggaatctcgatgtacccccaagaa 1952  
QY 1861 atttcaggttatggaatctgcagacatcatgttctcaagcggttcgcatacataata 1920  
Db 1953 atttcaggttatggaatctgcagacatcatgttctcaagcggttcgcatacataata 2012  
QY 1921 attttgtcgaagaaatttgggaacttaatgcaatgaagcacttaaacctccaagatt 1980  
Db 2013 attttgtcgaagaaatttgggaacttaatgcaatgaagcacttaaacctccaagatt 2072  
QY 1981 tatttgcagatttgcacaaatgagatctgttgcaaaaggaagagcttgatcttccaac 2040  
Db 2073 tatttgcagatttgcacaaatgagatctgttgcaaaaggaagagcttgatcttccaac 2132  
QY 2041 ttacaactatttcttacttcttccacgctgtgtgcacgaaagaggtataatgaggatt 2100  
Db 2133 ttacaactatttcttacttcttccacgctgtgtgtgcacgaaagaggtataatgaggatt 2192  
QY 2101 cagaatgttcaaaaaattaggaatcagttggaataagaatgataaaagtttcgggac 2160  
Db 2193 cagaatgttcaaaaaattaggaatcagttggaataagaatgataaaagtttcgggac 2252  
QY 2161 tctgggtcccaacaaactgtctatctctgcagcaacttgtaaatatgagcttatct 2220  
Db 2253 tctgggtcccaacaaactgtctatctctgcagcaacttgtaaatatgagcttatct 2312  
QY 2221 gttgattatagccttttgcagatgatacttcaagtgtcaaaagcttccagcaacgctc 2280  
Db 2313 gttgattatagccttttgcagatgatacttcaagtgtcaaaagcttccagcaacgctc 2372  
QY 2281 aagaagttgaagttggaagaacttatctaagctgtgtcatatctgtggaacatcatagcgag 2340  
Db 2373 aagaagttgaagttggaagaacttatctaagctgtgtcatatctgtggaacatcatagcgag 2432



OY 2341 ttgcctaaccttgagtgctgaagctgatagtgacgtgtgtgtgtgaagaatgcat 2400  
 |||||||  
 Db 2433 ttgcttaaccttgagtgctgaagctgatagtgacgtgtgtgtgtgaagaatgcat 2492  
 OY 2401 ccaattgtatgtgagtttaacatgataagctttgtcctaataatagttttctcaag 2460  
 |||||||  
 Db 2493 ccaattgtatgtgagtttaacatgataagctttgtcctaataatagttttctcaag 2552  
 OY 2461 ttctggaaagccacaagaatcttctctctgtgagcgccatcatattagaagtgc 2520  
 |||||||  
 Db 2553 ttctggaaagccacaagaatcttctctctgtgagcgccatcatattagaagtgc 2612  
 OY 2521 aaaattgtgaagagataccatgtgatttgagataacacacactacagctgattga 2580  
 |||||||  
 Db 2613 aaaattgtgaagagataccatgtgatttgagataacacacactacagctgattga 2672  
 OY 2581 ttaagaagtgctctccccaataattggtggaatctgtgcagagatcagaanaaacaaga 2640  
 |||||||  
 Db 2673 ttaagaagtgctctccccaataattggtggaatctgtgcagagatcagaanaaacaaga 2732  
 OY 2641 gacctcgaaacaacccgtgtgattgtcgtatcacaatccattgaagagagtgattct 2700  
 |||||||  
 Db 2733 gacctcgaaacaacccgtgtgattgtcgtatcacaatccattgaagagagtgattct 2792  
 OY 2701 gattcagaagaacattag 2718  
 |||||||  
 Db 2793 gattcagaagaacattag 2810

## RESULT 3

AA63302 standard; CDNA; 3099 BP.

ID AAF63302;

AC AAF63302;

XX 02-MAY-2001 (first entry)

DE Pepper Bs2 cDNA sequence.

XX Bs2; pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;

XX Xcv; bacterial spot disease; transgenic plant; crop; fruit; flower; ss.

XX Capsicum annuum.

XX WO200107635-A1.

XX 01-FEB-2001.

XX 23-DEC-1999; 99WO-US30891.

XX 23-JUL-1999; 99US-0360186.

XX (REGC ) UNIV CALIFORNIA.

XX Staskawicz BJ, Dahlbeck D, Tai TH;

XX WPI; 2001-168560/17.

XX P-PsDB; AAB72198.

XX Novel Bs2 polypeptide from Capsicum annuum for producing transgenic

XX plants having resistance to bacterial spot disease caused by

XX Xanthomonas campestris pv vesicatoria (Xcv) -

XX Claim 3; Page 57-61; 72pp; English.

CC This invention relates to the amino acid sequence of the Bs2 protein  
 CC isolated from Capsicum annuum (pepper). The protein and DNA sequences of  
 CC Bs2 can be used to confer resistance to the plant pathogen Xanthomonas  
 CC campestris pv vesicatoria (Xcv) which causes bacterial spot disease. Bs2  
 CC DNA and protein sequences are useful for producing transgenic plants such  
 CC as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola,  
 CC cowpea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton,  
 CC cassava and walnut, having resistance to X. campestris. The protein and

CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
 CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
 CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
 CC carnations and roses having resistance to X. campestris. The present  
 CC sequence represents cDNA encoding Bs2.

SQ Sequence 3099 BP; 970 A; 514 C; 693 G; 922 T; 0 other;

Query Match 100.0%; Score 2718; DB 22; Length 3099;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2718; Conservative

OY 1 atggcttcacgacgaagtgctgctctctctatgagacaatagaaatctcttgacatcaat 60  
 |||||||  
 Db 93 atggcttcacgacgaagtgctgctctctctctatgagacaatagaaatctcttgacatcaat 152  
 OY 61 tcgacgatgcaatctctatcctgtgtatcacagagaagaacttgctctctgtgaaaaa 120  
 |||||||  
 Db 153 tcgacgatgcaatctctatcctgtgtatcacagagaagaacttgctctctgtgaaaaa 212  
 OY 121 gttagttcccttggaagtattttgcaagaacttgagaaaaacaatgttttggggaatg 180  
 |||||||  
 Db 213 gttagttcccttggaagtattttgcaagaacttgagaaaaacaatgttttggggaatg 272  
 OY 181 acgagatttgaagtagaggtgaagagaagtgcaagtgctgtgatacacaatccaactg 240  
 |||||||  
 Db 273 acgagatttgaagtagaggtgaagagaagtgcaagtgctgtgatacacaatccaactg 332  
 OY 241 agactaacaggaactgtactggaagaataaagccagaanaaagagcgctgcgaag 300  
 |||||||  
 Db 333 agactaacaggaactgtactggaagaataaagccagaanaaagagcgctgcgaag 392  
 OY 301 ttctgtcaagcgctgcaacaagtagcagagagacatgatactctgaaagagtcgaca 360  
 |||||||  
 Db 393 ttctgtcaagcgctgcaacaagtagcagagagacatgatactctgaaagagtcgaca 452  
 OY 361 aagatccaagaataaaggaacaagaatccaagaagaatcattgttcaatgtttcaagt 420  
 |||||||  
 Db 453 aagatccaagaataaaggaacaagaatccaagaagaatcattgttcaatgtttcaagt 512  
 OY 421 tcaacaaacgatattttgaaggttaagaacaataatgttgagctgtatgatacaagaaa 480  
 |||||||  
 Db 513 tcaacaaacgatattttgaaggttaagaacaataatgttgagctgtatgatacaagaaa 572  
 OY 481 caattgttagaagatctgactagaagctactctgtgggaacccaagatcccgatgtgc 540  
 |||||||  
 Db 573 caattgttagaagatctgactagaagctactctgtgggaacccaagatcccgatgtgc 632  
 OY 541 gggaatggagagcataggtlaaacaacaccttagcaaaaagatttcaatgtatgaatcaat 600  
 |||||||  
 Db 633 gggaatggagagcataggtlaaacaacaccttagcaaaaagatttcaatgtatgaatcaat 692  
 OY 601 ctatgcgctttttagtttctatgctgtgctgctacatctcacaacagcaacaanaagaaa 660  
 |||||||  
 Db 693 ctatgcgctttttagtttctatgctgtgctgctacatctcacaacagcaacaanaagaaa 752  
 OY 661 atttgcctggcctctctgcatccacaatcaaatgtgatgcaggttaagatattgtgt 720  
 |||||||  
 Db 753 atttgcctggcctctctgcatccacaatcaaatgtgatgcaggttaagatattgtgt 812  
 OY 721 gaagcagaagctagacagcatgtttacagaaaagtttaagagaanaaggtacttaatttc 780  
 |||||||  
 Db 813 gaagcagaagctagacagcatgtttacagaaaagtttaagagaanaaggtacttaatttc 872  
 OY 781 ttgatgatctctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 840  
 |||||||  
 Db 873 ttgatgatctctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 932  
 OY 841 gacaatcagagagatcgaatactgtttgactaccctgaatgataatgataatgataatg 900  
 |||||||  
 Db 933 gacaatcagagagatcgaatactgtttgactaccctgaatgataatgataatgataatg 992

QY	901	gtgtaggaattttctcttcgcgatgtgccttcatagtatcoaaagabagagtttgagctc	960
Db	993	ggttcagaagaattctctcttcgcgatgagctcttcatagtatcoaaagabagagtttgagctc	1052
QY	961	ttcaaaagtgcagatttccaagtgcgaacattaccatatgtgttcgcagactgttgaaag	1050
Db	1053	ttcaaaagtgcagatttccaagtgcgaacattaccatatgtgttcgcagactgttgaaag	1112
QY	1021	caatcgagaattgatatgtccaaggtttaccataactatgtcgtggttcgaaggtcttc	1080
Db	1113	caaatcgagaattgatatgtccaaggtttaccataactatgtcgtggttcgaaggtcttc	1172
QY	1081	aaatctaaaggacaataagaaagatttggaacactgttcctaaagtgtccaagtcttc	1140
Db	1173	aaatctaaaggacaataagaaagatttggaacactgttcctaaagtgtccaagtcttc	1232
QY	1141	acaaatgactctgtatgcgaacgtatccagctgtgttcgtggtgagttacgaaccattgaca	1200
Db	1233	acaaatgactctgtatgcgaacgtatccagctgtgttcgtggtgagttacgaaccattgaca	1292
QY	1201	agcagatcctaaacacgtctcttcgtcatttcggaaattttccagaagacagtgtatccca	1260
Db	1293	agcagatcctaaacacacgtctcttcgtcatttcggaaattttccagaagacagtgtatccca	1352
QY	1261	gtgaagaatttgatgcagatcatggaatgcgtgcgaaggtcttcgtgaagtgtggaataattg	1320
Db	1353	gtgaagaatttgatgcagatcatggaatgcgtgcgaaggtcttcgtgaagtgtggaataattg	1412
QY	1321	gaagaagaagtttgagaagttttgcgaagactgttcgatatgatagtctcagccctgcagc	1380
Db	1413	gaagaagaagtttgagaagttttgcgaagactgttcgatatgatagtctcagccctgcagc	1472
QY	1381	aagaagaagctgcagatgcgaacaaaataatagatcatgtaagttcatgatcctatataagac	1440
Db	1473	aagaagaagctgcagatgcgaacaaaataatagatcatgtaagttcatgatcctatataagac	1532
QY	1441	ctgtgcgttgagagaaggttccaagaagggaacaaatttatcatgcgaacatgttcttgac	1500
Db	1533	ctgtgcgttgagagaaggttccaagaagggaacaaatttatcatgcgaacatgttcttgac	1592
QY	1501	gtatcatatccagaatgattatctcctgtatgatatataaaatgcagcccttaagcgcgtg	1560
Db	1593	gtatcatatccagaatgattatctcctgtatgatatataaaatgcagcccttaagcgcgtg	1652
QY	1561	actcgtgatagaataattatattatgtccctatggtccttatagaggtccttctaccctgtga	1620
Db	1653	actcgtgatagaataattatattatgtccctatggtccttatagaggtccttctaccctgtga	1712
QY	1621	aatcgtcagattgcagagatcatgcgaacaaacaaactctttgaacgaaacccattcgttttc	1680
Db	1713	aatcgtcagattgcagagatcatgcgaacaaacaaactctttgaacgaaacccattcgttttc	1772
QY	1681	tcttttcatcctgcagcccttatattatgttctcoaaatcgagaggtgttcatlccaatga	1740
Db	1773	tcttttcatcctgcagcccttatattatgttctcoaaatcgagaggtgttcatlccaatga	1832
QY	1741	ctcaaaagctcttgagactgcagacacagaacagatattgtttccctcgcgaagatactaagc	1800
Db	1833	ctcaaaagctcttgagactgcagacacagaacagatattgtttccctcgcgaagatactaagc	1892
QY	1801	ctcaatcgtgtgaagttaccatcatgttcacgctatgtaggaattctcgatgtacctcoagaa	1860
Db	1893	ctcaatcgtgtgaagttaccatcatgttcacgctatgtaggaattctcgatgtacctcoagaa	1952
QY	1861	atttcgagaattgagaatctgcagacattcatattgttccaacggtttcgcatacagataaata	1920
Db	1953	atttcgagaattgagaatctgcagacattcatattgttccaacggtttcgcatacagataaata	2012
QY	1921	attttgtcgaagaaatttgtagaacataatgcataaagacattcaaatcgcagattt	1980
Db	2013	attttgtcgaagaaatttgtagaacataatgcataaagacattcaaatcgcagattt	2072
QY	1981	tatttcgcaagattgcaccaagtgcagctgtgtgacaaaggaaggaactgtgattttccaac	2040

Db	2073	tattgcagatgtgccaaagtgaacgtcttgacaagaaggaaacttgattttccaac	2133
Qy	2041	ttcaaacatttcttacttgtcctccaaagtgtgttcgacgaagggttaataagggat	2100
Db	2133	ttccaaccttcttctaacttgctcccaagtggtgtcgacgaaggaggtttaataagggat	2192
Qy	2101	cagaatgcgcanaaaatlagnaatcagtlgbataaagaataaccataaaggtttcggac	2160
Db	2193	cagaatgcgcanaaaatlagnaatcagtlgbataaagaataaccataaaggtttcggac	2255
Qy	2161	tctgggcttcccacaacatcttgtctatctctgcagcaacttgaatatgtgcttatct	2220
Db	2253	tctgggcttcccacaacatcttgtctatctctgcagcaacttgaatatgtgcttatct	2312
Qy	2221	gttgatataagcctttgcsagtgatcatcttccaagtgcgaagaacgtttccagcaagtc	2280
Db	2213	gttgatataagcctttgcsagtgatcatcttccaagtgcgaagaacgtttccagcaagtc	2372
Qy	2281	aagaagtgtgaagtctgynaagaactctaagctggtlcalacttgyacatacatagtctag	2340
Db	2373	aagaagtgtgaagtctgynaagaactctaagctggtlcalacttgyacatacatagtctag	2432
Qy	2341	ttgcctcaaccttgaagtgtcgaagctgaatgtagaagcctgttgtgtgtgaagaatgcat	2400
Db	2433	ttgcctcaaccttgaagtgtcgaagctgaatgtagaagcctgttgtgtgtgaagaatgcat	2492
Qy	2401	ccaatgtltatvggaatttaatcgatlgaaagcctttgctaattaataatagtttctcaag	2460
Db	2493	ccaatgtltatvggaatttaatcgatlgaaagcctttgctaattaataatagtttctcaag	2552
Qy	2461	ttctggaagccacacaatgtaaattttcctgttccttgtagcgctcctatgataagaattgc	2520
Db	2553	ttctggaagccacacaatgtaaattttcctgttccttgtagcgctcctatgataagaattgc	2612
Qy	2521	aaaaatttgaagaagatacccatgagtttgcagatacacacacatacagctgattgag	2580
Db	2613	aaaaatttgaagaagatacccatgagtttgcagatacacacacatacagctgattgag	2672
Qy	2581	ttaaagaaggtctcctcccaacttgggaaatctgcctgcacgaattcagaagaagaacaa	2640
Db	2673	ttaaagaaggtctcctcccaacttgggaaatctgcctgcacgaattcagaagaagaacaa	2732
Qy	2641	gacctcgyaaaacaacctgtggaatgttcgatctcaatccatgaaagagtgattct	2700
Db	2733	gacctcgyaaaacaacctgtggaatgttcgatctcaatccatgaaagagtgattct	2792
Qy	2701	gattcaagaagaactag 2718	
Db	2793	gattcaagaagaactag 2810	
<b>RESULT 4</b>			
AADI0203			
XX	ID	AADI0203 standard; DNA; 31491 BP.	
AC	XX	AADI0203;	
XX	DT	24-SEP-2001 (first entry)	
XX	DE	Pepper Bs2 gene.	
XX	KM	Bs2 gene; pepper; resistance gene; plant pathogen; virulence gene;	
KW	KM	bacterial spot disease; Xanthomonas campestris pv. vesicatoria;	
KW	KW	AVBs2; hypersensitive response; transgenic plant; tomato; tobacco;	
OS	XX	rice; corn; wheat; ds.	
XX	XX	Capsicum annuum.	
EH	Key	Location/Qualifiers	
FT	promoter	I..502	
FT	exon	/tag= a 503...554	

```

FT      /tag= b
FT      /number= 1
FT      /note= "This region contains a portion of
FT      5', untranslated region (5' UTR)."
FT      555..1439
FT      intron
FT      /tag= c
FT      /number= 1
FT      /note= "The 5' untranslated region (5' UTR)
FT      continues in this region"
FT      1440..4162
FT      exon
FT      /tag= d
FT      /number= 2
FT      /note= "The region 1440-1479 contains 5' UTR which
FT      is followed by the coding region"
FT      1480..31219
FT      CDS
FT      /tag= e
FT      /product= "Bs2 protein"
FT      4163..31184
FT      intron
FT      /tag= f
FT      /number= 2
FT      31185..31216
FT      exon
FT      /tag= g
FT      /number= 3
FT      31220..31491
FT      3'UTR
FT      /tag= h

PN      US6262343-B1.
XX      17-JUL-2001.
XX      23-JUL-1999; 99US-0360186.
XX      23-JUL-1998; 98US-0093957.
XX      (REBC ) UNIV CALIFORNIA.
PA      Staskawicz BJ, Dahlbeck D, Tai TH;
PI      WPI: 2001-450496/48.
DR      P-PSDB; AAB05409.
XX      Nucleic acid molecules encoding Bs2 protein, useful for producing
PT      transgenic plants having resistance to the plant pathogen Xanthomonas
PT      campestris -
XX      Claim 7: Column 21-50; 37pp; English.
XX      The present sequence is Bs2 gene from pepper. The Bs2 gene is shown
CC      to confer resistance to plant pathogen
CC      Xanthomonas campestris pv. vesicatoria which causes bacterial spot
CC      disease. The Bs2 protein has Bs2 biological activity, i.e., when
CC      co-expressed in a plant with a X. campestris AVRBs2 gene product,
CC      it produces a localised hypersensitive response. The protein
CC      includes a nucleotide binding motif and leucine rich repeats of the
CC      type found in other plant resistance genes. The Bs2 nucleic acid
CC      molecule is useful for producing transgenic plants such as pepper,
CC      tomato, tobacco, broccoli, cauliflower, cabbage, corn, grape, canola,
CC      bean, soybean, rice, corn, wheat, barley, citrus, cotton, cassava and
CC      walnut, that are resistant to plant pathogen Xanthomonas campestris.
CC      The transgenic plants produced using Bs2 molecule develop a
CC      hypersensitive response to the pathogen at the site of inoculation and
CC      show an enhanced resistance to systemic infection. The Bs2 nucleic acid
CC      molecule is also useful as polymerase chain reaction (PCR) primers for
CC      amplifying portions of Bs2 nucleic acid molecule, as sequencing primers
CC      to verify the authenticity of an amplified molecule, and as
CC      hybridisation probes.
XX      Sequence 31491 BP; 9652 A; 6344 C; 5992 G; 9503 T; 0 other;

```

```

Query Match      98.8%; Score 2685.6; DB 22; Length 31491;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2688; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1 atggtcattgcaagctgtgcttctctatagacacataagaatctcttgcattcaat 60
      |||||||
DB      1480 atggctcagcaagctgtgcttctctctatagagacataagaatctcttgcattcaat 1539
QY      61 tcgcgatgcacatctctatctctgtgatacagaagaagaacttgcgctctctgtgaaaaa 120
      |||||||
DB      1540 tcgcgatgcacatctctatctctgtgatacagaagaagaacttgcgctctctgtgaaaaa 1599
QY      121 gttagttccctggaagtattgtccaagaactttgaaaaaaaacaatgttttggggaatg 180
      |||||||
DB      1600 gttagttccctggaagtattgtccaagaactttgaaaaaaaacaatgttttggggaatg 1659
QY      181 acggatttgaagtaaggttaagaagaagtgttcgaagctgtcctaacaacataccaactc 240
      |||||||
DB      1660 acggatttgaagtaaggttaagaagaagtgttcgaagctgtcctaacaacataccaactc 1719
QY      241 agactaacaggaactgttactgaggagaaaaataaagccagaaaaaaaaggcgtcgaaag 300
      |||||||
DB      1720 agactaacaggaactgttactgaggagaaaaataaagccagaaaaaaaaggcgtcgaaag 1779
QY      301 ttctgtcaaaagcctgtcaacaagtagcagaggaatgatactctggaagaagctcgaca 360
      |||||||
DB      1780 ttctgtcaaaagcctgtcaacaagtagcagaggaatgatactctggaagaagctcgaca 1839
QY      361 aagatccagaataaaggaaacaagaatcaaaaggaatcattgttcatgtatttccaagt 420
      |||||||
DB      1840 aagatccagaataaaggaaacaagaatcaaaaggaatcattgttcatgtatttccaagt 1899
QY      421 tcaacaaacgataatttgaaaggttaagaacaataatgttggagcgtatgatacaagaagaa 480
      |||||||
DB      1900 tcaacaaacgataatttgaaaggttaagaacaataatgttggagcgtatgatacaagaagaa 1959
QY      481 cagttgttagaagatctgtgataagtaactctcgggggaacccaagaatcccgattgtc 540
      |||||||
DB      1960 cagttgttagaagatctgtgataagtaactctcgggggaacccaagaatcccgattgtc 2019
QY      541 gggatggaggcagtagtaaaaaacaaccttagcaaaagaagtttaacaatgtatgaatcaat 600
      |||||||
DB      2020 gggatggaggcagtagtaaaaaacaaccttagcaaaagaagtttaacaatgtatgaatcaat 2079
QY      601 ctatgcgcttttgatgttcaatgcctgtggtctacacatatctcaacagacaacaaaaaggaa 660
      |||||||
DB      2080 ctatgcgcttttgatgttcaatgcctgtggtctacacatatctcaacagacaacaaaaaggaa 2139
QY      661 atttgctggccttctgtgattccacaatcaaatgtatgacgggttaagatgtgt 720
      |||||||
DB      2140 atttgctggccttctgtgattccacaatcaaatgtatgacgggttaagatgtgt 2199
QY      721 gaagcagagctagcagacatgtttacagaaaaagtttaagaagaagaagttactaatgttc 780
      |||||||
DB      2200 gaagcagagctagcagacatgtttacagaaaaagtttaagaagaagaagttactaatgttc 2259
QY      781 ttggatgatatctggaagctgtgaaagtgtggaatgagcgtgtgagacgatcttccaactgaa 840
      |||||||
DB      2260 ttggatgatatctggaagctgtgaaagtgtggaatgagcgtgtgagacgatcttccaactgaa 2319
QY      841 ggcacagcgggaagtgtaactgttgataccggaatgaatgaatgaatgtttatgtc 900
      |||||||
DB      2320 gacaaagcgggaagtgtaactgttgataccggaatgaatgaatgaatgtttatgtc 2379
QY      901 ggtgtgaagaattttctcttgcgagatgacttcatatgatcaagaatagagttgaattct 960
      |||||||
DB      2380 ggtgtgaagaattttctcttgcgagatgacttcatatgatcaagaatagagttgaattct 2439
QY      961 ttcaaaagtgcagcatttccaagtgaagcatcaacatgatagttcgaagctgttgaagaag 1020
      |||||||
DB      2440 ttcaaaagtgcagcatttccaagtgaagcatcaacatgatagttcgaagctgttgaagaag 2499
QY      1021 caaatgcagatgaatgttaacgggttaaccataactatgtcgtgttcaagggtcttc 1080
      |||||||
DB      2500 caaatgcagatgaatgttaacgggttaaccataactatgtcgtgttcaagggtcttc 2559

```



isolated from  *Capsicum annuum*  (pepper). The protein and DNA sequences of Bsr2 can be used to confer resistance to the plant pathogen  *Xanthomonas campestris pv vesicatoria*  (Xcv) which causes bacterial spot disease. Bsr2 DNA and protein sequences are useful for producing transgenic plants such as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola, corn, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton, cassava and walnut, having resistance to  *X. campestris* . The protein and DNA molecule are also useful for producing transgenic alfalfa, flax, sunflower, safflower, brassica, peanut, clover, lettuce, cucurbit, potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots, carnations and roses having resistance to  *X. campestris* . The present sequence represents the Bsr2 gene of the invention.

Sequence 31491 BP; 9652 A; 6345 C; 5992 G; 9502 T; 0 other;

Query Match 98.8%; Score 2685.6; DB 22; Length 31491;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2688; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 1 atggtctatgcaagtggtgctctctttagaacaatagaatctcttgcattcaat 60
DB 1480 atggtctatgcaagtggtgctctctttagaacaatagaatctcttgcattcaat 1539
QY 61 tcgacgatgcaatctctatcctctgtatcacagaaagaacttgcgctcttcgtgaaaa 120
DB 1540 tcgacgatgcaatctctatcctctgtatcacagaaagaacttgcgctcttcgtgaaaa 1599
QY 121 gttatgtccctggaagtatttgcaagaacttgaagaaacaatgttttggggaatg 180
DB 1600 gttatgtccctggaagtatttgcaagaacttgaagaaacaatgttttggggaatg 1659
QY 181 agggatttgaagtgaagtaagaagaagtgtcaagtcgtcgtgaataccaattcaacg 240
DB 1660 agggatttgaagtgaagtaagaagaagtgtcaagtcgtcgtgaataccaattcaacg 1719
QY 241 aagactaacaggaactgtactctggagaaaaataaagccagaaaaaaagcgctgcaag 300
DB 1720 aagactaacaggaactgtactctggagaaaaataaagccagaaaaaaagcgctgcaag 1779
QY 301 ttctgtcaaacctcgcaacaagtagcagagagacatgacatatactcgtgaagaagtcgaca 360
DB 1780 ttctgtcaaacctcgcaacaagtagcagagagacatgacatatactcgtgaagaagtcgaca 1839
QY 361 aagatccaagataaaggaanaacaagatatacaagaatcttgcataatattttcaagt 420
DB 1840 aagatccaagataaaggaanaacaagatatacaagaatcttgcataatattttcaagt 1899
QY 421 tcaacaacaagatatttgaaggttlaagaaacaatatgttgcacgttgatgatacaagaa 480
DB 1900 tcaacaacaagatatttgaaggttlaagaaacaatatgttgcacgttgatgatacaagaa 1959
QY 481 caagtgttagaagatcgtagtaagtaactcttggggaacccaagtcaccgattgtc 540
DB 1960 caagtgttagaagatcgtagtaagtaactcttggggaacccaagtcaccgattgtc 2019
QY 541 gggatggggagataggttaaaaaaacattagcaaaaagaagtttacaatgatgaat 600
DB 2020 gggatggggagataggttaaaaaaacattagcaaaaagaagtttacaatgatgaat 2079
QY 601 ctatgcgcttctgatttcatatgcctctggtctacacatactccaacagcacaacaaaaggaa 660
DB 2080 ctatgcgcttctgatttcatatgcctctggtctacacatactccaacagcacaacaaaaggaa 2139
QY 661 atttgcgtggcctctcgtaccatccacaatcaaatatgatgacagggtttagatgtgt 720
DB 2140 atttgcgtggcctctcgtaccatccacaatcaaatatgatgacagggtttagatgtgt 2199
QY 721 gaagcagagactagcagacatgtttacagaaaagtttaagaagaagggtactaatgttc 780
DB 2200 gaagcagagactagcagacatgtttacagaaaagtttaagaagaagggtactaatgttc 2259
QY 781 ttgatgatatacttgaggtgtgaggtgtgaggtgtgagacgacttccaactgaa 840
```

```
DB 2260 ttgatgatatacttgaggtgtgaggtgtgaggtgtgagacgacttccaactgaa 2319
QY 841 gacaatgcagggagtgcaactgttgaactaccgtaagtatgaaagtgtatgct 900
DB 2320 gacaatgcagggagtgcaactgttgaactaccgtaagtatgaaagtgtatgct 2379
QY 901 ggtgtgagaattttcttcttgagagcttcatatgacaaatagaaggttgaaact 960
DB 2380 ggtgtgagaattttcttcttgagagcttcatatgacaaatagaaggttgaaact 2439
QY 961 ttcaaaagtcagcagcatcttcaagtgagaatcacaatagatctgagagactgttgaag 1020
DB 2440 ttcaaaagtcagcagcatcttcaagtgagaatcacaatagatctgagagactgttgaag 2499
QY 1021 caaatgcagatgaatgtacaggggttaccacataactatgtcgtgttcagggctctc 1080
DB 2500 caaatgcagatgaatgtacaggggttaccacataactatgtcgtgttcagggctctc 2559
QY 1081 aatctcaaaaggaacaatagaagatggaaaactgtgtcctaaagatgcaatcactcgtc 1140
DB 2560 aatctcaaaaggaacaatagaagatggaaaactgtgtcctaaagatgcaatcactcgtc 2619
QY 1141 acaaatgatccctgatatgaacgatttcaacgtgtgtcgtgtgtgtgattacgataccttgaca 1200
DB 2620 acaaatgatccctgatatgaacgatttcaacgtgtgtcgtgtgtgtgattacgataccttgaca 2679
QY 1201 agcgcataaaaacaatgctcttcgtacatccgaaattttccagaagaacagtgatatcca 1260
DB 2680 agcgcataaaaacaatgctcttcgtacatccgaaattttccagaagaacagtgatatcca 2739
QY 1261 gtgaagaatttgaatgagatcatgagctgaggggttccctgaagtgtggaanaatgattg 1320
DB 2740 gtgaagaatttgaatgagatcatgagctgaggggttccctgaagtgtggaanaatgattg 2799
QY 1321 gaaggaaggttgaagaagtttgcagaagctgtcogataagatgtcagtcctcgtcagc 1380
DB 2800 gaaggaaggttgaagaagtttgcagaagctgtcogataagatgtcagtcctcgtcagc 2859
QY 1381 aagaagaagctcagagatgagcaaaaatagaatcgtatgaagttcatatcatatagac 1440
DB 2860 aagaagaagctcagagatgagcaaaaatagaatcgtatgaagttcatatcatatagac 2919
QY 1441 ctgtcgtgagagaagttccaagaagggaacattttatcatctgaacagacattgttctgac 1500
DB 2920 ctgtcgtgagagaagttccaagaagggaacattttatcatctgaacagacattgttctgac 2979
QY 1501 gtatcatccagaatgttcatatctctgtatgtataaataatgcagcccttaagcgctg 1560
DB 2980 gtatcatccagaatgttcatatctctgtatgtataaataatgcagcccttaagcgctg 3039
QY 1561 actggtgagaaatattatattgttccctatggtcttataagggtctcttctacccctgta 1620
DB 3040 actggtgagaaatattatattgttccctatggtcttataagggtctcttctacccctgta 3099
QY 1621 aatcgtcagttgagagatcatgacaacaacaacacttcttgaagaaacccacttgttttc 1680
DB 3100 aatcgtcagttgagagatcatgacaacaacaacacttcttgaagaaacccacttgttttc 3159
QY 1681 tctttcatcttgaagccttataatattgttccaatcagaaggtgttcaattccaatta 1740
DB 3160 tctttcatcttgaagccttataatattgttccaatcagaaggtgttcaattccaatta 3219
QY 1741 ctcaaaagcttcttgagctcgtgacacagacagatgaggtttccctcgaagataactaagc 1800
DB 3220 ctcaaaagcttcttgagctcgtgacacagacagatgaggtttccctcgaagataactaagc 3279
QY 1801 ctcatctggttgaagtaaccatcatgttgcagatagtggaatttcgatacctccagaa 1860
DB 3280 ctcatctggttgaagtaaccatcatgttgcagatagtggaatttcgatacctccagaa 3339
QY 1861 atttgcaggttgaagatctgcagacatcaattgttccaacggtttcogataagataata 1920
```

```

Db 3340 atttcaggtatggaatctgcagacattcattgttcaacggttttcgatacagataa 3399
Oy 1921 attttgtcgaagaatttggaaactaatgcataaagcacttaactgcccagatt 1980
Db 3400 attttgcgaagaatttggaaactaatgcataaagcacttaactgcccagatt 3459
Oy 1981 tatttcgaagattggccaaagtgcattgttgcacaagaaggcacttgattttcaaac 2040
Db 3460 tatttcgaagattggccaaagtgcattgttgcacaagaaggcacttgattttcaaac 3519
Oy 2041 ttacaactatttcttactgtctccacgttgttgcacgaaggaggtattatgggatt 2100
Db 3520 ttacaactatttcttactgtctccacgttgttgcacgaaggaggtattatgggatt 3579
Oy 2101 cagaatgcacaanaattggaatcagtcgaaataagatgataaagttttcgggac 2160
Db 3560 cagaatgcacaanaattggaatcagtcgaaataagatgataaagttttcgggac 3639
Oy 2161 tctgggctcccaaatctgtctatctgcagcaacttgaataattgattctatct 2220
Db 3640 tctgggctcccaaatctgtctatctgcagcaacttgaataattgattctatct 3699
Oy 2221 gtgtattatagccttttcgcagtgatcatttcaagtcgacaagctttccagcagctc 2280
Db 3700 gtgtattatagccttttcgcagtgatcatttcaagtcgacaagctttccagcagctc 3759
Oy 2281 aagaagttgaagttggaagaactatctaaagctgtcatatttgatactagctag 2340
Db 3760 aagaagttgaagttggaagaactatctaaagctgtcatatttgatactagctag 3819
Oy 2341 ttgcctaaacttgagtgctgaagctgatagtgacgctgtgttgcgtgaagaatgagat 2400
Db 3820 ttgcctaaacttgagtgctgaagctgatagtgacgctgtgttgcgtgaagaatgagat 3879
Oy 2401 ccaattgtatggagtttaactgcattgaagcttttgcctaataatatagtttttcaag 2460
Db 3880 ccaattgtatggagtttaactgcattgaagcttttgcctaataatatagtttttcaag 3939
Oy 2461 ttctggaagccacaacatgcaaatcttctccttgagcgccctatgattgaagttgc 2520
Db 3940 ttctggaagccacaacatgcaaatcttctccttgagcgccctatgattgaagttgc 3999
Oy 2521 aaaaattggaagagatacccatgtgatttgcagatatatacacacatacagctgattgag 2580
Db 4000 aaaaattggaagagatacccatgtgatttgcagatatatacacacatacagctgattgag 4059
Oy 2581 ttaagagagtgctccccaacttggggaatctgctgcacgaattcagaagaacaaagaa 2640
Db 4060 ttaagagagtgctccccaacttggggaatctgctgcacgaattcagaagaacaaagaa 4119
Oy 2641 gacctcgaacaacacccgtgtgattcgtatcctaattcattgaaagaga 2692
Db 4120 gacctcgaacaacacccgtgtgattcgtatcctaattcattgaaagata 4171

```

RESULT 6  
AAZ50262  
ID AAZ50262 standard; DNA; 2739 BP.

XX AC AAZ50262;  
XX XX 18-MAY-2000 (first entry)  
XX XX  
DE Coding region of potato Gpa2 resistance gene.  
XX  
KW Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p;  
KW marker; IPM4; IIR; Potato Cyst Nematode; PCN; Globodera; nematode;  
KW nematode resistance; detection; diagnosis; ds.  
XX OS Solanum tuberosum.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2739

```

FT /*tag= a  
FT /product= "Potato Gpa2 polypeptide"  
FT /function= "Confers resistance to phytopathogenic  
FT nematodes of the Globodera genus"  
PN WO200006754-A2.  
XX PD 10-FEB-2000.  
XX PR 30-JUL-1999; 99WO-NL00491.  
XX PR 31-JUL-1998; 98WO-NL00445.  
PA (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.  
PA (UWVA-) LANDBOUMUNIVERSITEIT WAGENINGEN.  
PI Van Der Vossen EAG, Van Der Voort JNAMR, Lankhorst RMK, Bakker J;  
PI Stiekema WJ;  
XX WP1; 2000-183132/16.  
DR P-PSDB; AAY44818.  
PT New isolated Gpa2 nematode resistance gene from potato, useful for  
PT producing plants which are resistant to nematodes and polypeptides for  
PT use in nematode compositions  
XX  
PS Claim 62; Fig 3a; 96pp; English.  
CC The present DNA sequence is the coding region of the potato resistance  
CC gene Gpa2, that confers resistance to infection by phytopathogenic  
CC nematode of the Globodera genus. It is mapped to short arm of chromosome  
CC 12 (12p), between the markers IPM4 and IIR. This locus is associated  
CC with resistance to Potato Cyst Nematodes (PCN) like G. pallida and  
CC G. rostochiensis, that invade and damage the roots of solanaceae. It has  
CC nematocidal activity. A recombinant DNA sequence comprising the Gpa2  
CC gene sequence can be transformed or transfected into plants, to provide  
CC increased resistance to nematodes. The polypeptides can also be used in  
CC nematocidal compositions and for detection and diagnosis of nematode  
CC infections.  
XX  
SQ Sequence 2739 BP; 814 A; 498 C; 600 G; 827 T; 0 other:  
Query Match 10.0%; Score 272.8; DB 21; Length 2739;  
Best Local Similarity 54.7%; Pred. No. 6.5e-63;  
Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;  
Oy 140 ttgtcaagaacttgcgaagaacaaatgttttggggaatgacgagtttgaagtagag 199  
Db 113 tggagaatactcgcataataatggcgatcatgaggggttaacaaacttggaggttgaa 172  
Oy 200 taaaggaagttgcagtgctgtgatacacaaatcgaactgagacttaacagaaactgtac 259  
Db 173 tcaatagaggtatgatacacacaagaagatagtgatcgtggaatcagaagaatgttttt 232  
Oy 260 tggagaataataaagccagaanaaaagcgctgcgaaggttgcgtcaaaagcctgcacac 319  
Db 233 tagcaggaatgtggggaagaagaagcaggtatgtggggagtttttctgccttgagac 292  
Oy 320 aagtcagcagagacatgatatcatcttganaagatgcgacaagttccaagtaagaa 379  
Db 293 aagcactagaatgcattgattccaccgtgaaacagltgacacatgcagacatgaa 352  
Oy 380 aacaagtatcaaggatcatctgttcatttttcaagttcaacaacaagatatcttga 439  
Db 333 aagatctaacaacacaacactgctcactgttcagtttccctggaac--atgattgtgagc 409  
Oy 440 aggttaagaacaatatgtgttgacgttgatgataaaggaacagttgttagaagaatctga 499  
Db 410 agcccgagaataataatgtgttcggtgcgtgaagaatgatttgagatgctgcgtacacttg 469  
Oy 500 ctagaagctactctgvggaaccacaaagtcattccgattgtcggagatggagagcatagta 559

```

Db 470 ctgaag---aggaaggaactagaaggtgtctcaatcgtlaagatggagatcgga 526  
 QY 560 aaaaacattgaagaagatttacaatgaatcaatctatgcttgaatgc 619  
 Db 527 aaaaacattgtctgaagaacacttaagatgaatcttaattgtctgattgataac 586  
 QY 620 atgctgtggtacatcatctcaacagacacaaagaaatttgcgtggtcttcgc 679  
 Db 587 gtgcaaaagcaactgttcaacaagatattgtgtggaatgaatgactccctaggtctt 646  
 QY 680 attcccaatcaaaatggtatgacaggttaagttgtgtggaagagagctagacac 739  
 Db 647 ctttgacaagatgaaccgtatc-----agctagcgacc 685  
 QY 740 tgttacaagaagtttaagaagaaggaaggaacttaattcttgaatgaatctggaat 799  
 Db 686 aactgcaaaagcactcgaagaagcagagatactgtgtagcatgtgacataatgacta 745  
 QY 800 gtgaagtggtgagatgctgagacgatagtcttcaactgaagaacatgacgagatcga 859  
 Db 746 cagaagcttggaatgataaactatgttccca---gactgagataatgagaagacga 802  
 QY 860 tactgttgaactaccgtaagatgaatgaatgctgtatgctgtgtgtagagaatttctt 919  
 Db 803 tactcctgaactcggaaatggtgaagtggtcgaataatgtagctcgaagtaagctcttc 862  
 QY 920 tgcgataagcttcaatgaatgaatgaatgagatgttcaaaagtgcagatctt 979  
 Db 863 atcaatgcgcctcatgaatttgaacgaagttgaatttactacaacaaagacttgc 922  
 QY 980 caagtgaag---catacctatgagttcgaagctgttgaagaagcaatgcagatgaat 1036  
 Db 923 aaaaagaagtttcttctccctgaatttgaataatggaacaaatgcattgaat 982  
 QY 1037 gtacaggttaccacactactgtcgtgttgaagggctct---caaatctaaagga 1093  
 Db 983 gtggaaggttactctcgaacttaacttgaattgtcgtgaactctcctcaaaatcgataa 1042  
 QY 1094 caataagaatgtgaagaactgttgaataagaatgaatcattcgtacaaatgatactgc 1153  
 Db 1043 catgtgagtggtgcaaaatggtgcgagaatgaatgactgtgtgtaagacagatctgc 1102  
 QY 1154 atgaacatgttcaacgtgtctgtgtgtgtgaatgaatgaatgaatgaatgaatgaatga 1213  
 Db 1103 aagaacatgtgaagatgt 1162  
 QY 1214 catgtcttgcattcgaatatttccagaagaacagtgatcagtgagaatttga 1273  
 Db 1163 cgtgttctcgtatttgcgaatttgcagagagtgaaacgatttatgataataactgt 1222  
 QY 1274 tgaatcatgagatgctgaggggttctcga-----agttggaatgatttgaagag 1327  
 Db 1223 ttgagttatgagccgtagaaggggttttgaatgaagaaggaagaaagcagaagaag 1282  
 QY 1328 aggttgaagatgtgttgcagaagatttgcagatgaatgtcagatcctcgtcgaagaag 1387  
 Db 1283 tggcagaacactgtataacgaactgtgaatgaatgaatgaatgaatgaatgaatga 1342  
 QY 1388 gtgcagatgagacaaaattgaatcagtgatgaatgaatgaatgaatgaatgaatgaatga 1447  
 Db 1343 gtttgaatggggaacacag---atgtggaatgcatgagtgacccgtgaactctgt 1399  
 QY 1448 tgaagagaatcagaaggaagaacatttga 1477  
 Db 1400 tgaaggaagctcgaacacatgaatttga 1429

RESULT 7  
 AA250652  
 ID AA250652 standard; DNA; 2817 BP.  
 XX  
 AC AA250652;  
 XX

DT 23-MAY-2000 (first entry)  
 DE Coding region of potato Gpa2 resistance gene.  
 XX  
 XX Resistance; Gpa2; potato; phytopathogenic nematode; chromosome 12p;  
 KW marker; IPM4c; 11R; potato Cyst Nematode; PCN; Globodera; nematode;  
 KW nematode resistance; detection; diagnosis; transgenic plant; ds.  
 OS Solanum tuberosum.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2817  
 FT /tag= a  
 FT /product= "potato Gpa2 polypeptide"  
 FT /function= "Confers resistance to phytopathogenic  
 nematodes of the Globodera genus"  
 PN MO200006753-A1.  
 XX  
 PD 10-FEB-2000.  
 XX  
 XX 31-JUL-1998; 98MO-NL00445.  
 PF 31-JUL-1998; 98MO-NL00445.  
 XX  
 PR 31-JUL-1998; 98MO-NL00445.  
 XX  
 PA (CPRO-) CPRO-DIO CENT PLANTENVEREDELINGS REPROD.  
 PA (UYMA-) LANDBOUMUNIVERSITEIT WAGENINGEN.  
 XX  
 PI Van Der Vossen EAG, Van Der Voort JNMR, Lankhorst RMK, Bakker J;  
 PI Stiekema WJ;  
 XX  
 DR WPI: 2000-195310/17.  
 DR P-PSDB; AA25004.  
 XX  
 PT Recombinant Gpa2 polynucleotide from potato, Solanum tuberosum, useful  
 PT to confer resistance to phytopathic nematodes of the genus Globodera in  
 PT transgenic plants, e.g. resistance to potato cyst nematodes in potatoes  
 PT  
 PS Claim 1; Fig 3a; 96pp; English.  
 XX  
 CC The present DNA sequence is the coding region of the potato resistance  
 CC gene Gpa2, that confers resistance to infection by phytopathogenic  
 CC nematode of the Globodera genus. It is mapped to short arm of chromosome  
 CC 12 (12p), between the markers IPM4c and 11R. This locus is associated  
 CC with resistance to Potato Cyst Nematodes (PCN) like G. pallida and  
 CC G. rostochiensis, that invade and damage the roots of Solanaceae. It has  
 CC nematocidal activity. Recombinant DNA sequence comprising the Gpa2  
 CC gene can be used to produce transgenic plants with increased resistance to  
 CC nematodes. The polypeptides can also be used in nematocidal compositions  
 CC and for detection and diagnosis of nematode infections.  
 XX  
 XX Sequence 2817 BP; 846 A; 503 C; 626 G; 842 T; 0 other;  
 SO

Query Match 10.0%; Score 272.8; DB 21; Length 2817;  
 Best Local Similarity 54.7%; Pred. No. 6.5e-63;  
 Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

QY 140 ttgtcaagaacttgaagaacaaatgttttggggaatgacgatttgaagagag 199  
 Db 113 tggagaatctcgtcaataatgagtgatcagaggggttgaacacttggagattgaa 172  
 QY 200 taaggaagttgcaagtgctgtgatacacaaatcgaactgaactaacaagaactgtac 259  
 Db 173 tcatagagtgatcacacacagaagaatagtgtagctcggaaatcaagaatgttttt 232  
 QY 260 tggagaataataaagccagaacaaagcgctcgaaggttctgtaaacgctcgac 319  
 Db 233 tagcacggaatgtggggaagaagcagggctatgtgggggatttttctgcttggaa 292  
 QY 320 aagtacgagagactgtgatactatctcgtgaagagtgacgaagatccaagataagaa 379



Db 293 aagcactagaatgcatgtatccacggtgaacagtgatgagcaacatcggaacatga 352  
 Qy 380 aacaagatcaagaagatcatgtgtcatgatttttcaagttcaacaacgatatttga 439  
 Db 353 aagatctaaacacaaactagctactgtcagtttaccctgaac--atgatgttgagc 409  
 Qy 440 aggttaagaacaatagtgtgagcgtgagatgaagaagaacagttgttagaagatcga 499  
 Db 410 agccgagaataatagtgtgagcgtgaataatgttagatgtgagcgtgataactgtg 469  
 Qy 500 ctgaaagctactcttgaggaaacccaagatcatcccgatttcgggagtgaggacatga 559  
 Db 470 ctgaaag--aggaaaggaaactagaagttgtctcaactgtaaggatggagacatcgga 526  
 Qy 560 aaacacacttagaagaagaagtttaacatgataatcctatcgccgtttgtgatttc 619  
 Db 527 aaacacacttggtgtaaaactctatagatgacatcttaactgtgctcgtatgtatc 586  
 Qy 620 atgctggtctacacatactcaacagacacaaaaggaaatttgcgtggcctctgc 679  
 Db 587 gtgcaaaagcaactgttccacaagatgtgtgtgagaatgtactcctagcctctctt 646  
 Qy 680 attccacaatcaaaatgtagtgaaggttaagatgtgtgtgaagcagagctagacaga 739  
 Db 647 ctttgacaagtgatgaactgtatc-----agctacgagacc 685  
 Qy 740 tgttacagaagaagtttaagaagaagagttacttaattgtcttgatgatactcgtgatt 799  
 Db 686 aactgcaaaagatctgaaagcagagatactgtgtgacttgatgatactgatactgata 745  
 Qy 800 gtgaaagtgtgagatggtgagagagatgcttccaaactgaagaacaatgcaggagtcga 859  
 Db 746 caagaagcttgaggatgataaaacatgtttccca--gactgcgataatgaaagcagaa 802  
 Qy 860 tactgttgactaccggttaatgtagaagctgtgtatgctggtgtgtagaagattttctt 919  
 Db 803 tactcctgactactcgtgaatgtagaagtgctgataatgactcagatgaagcctctc 862  
 Qy 920 tggagatgagctcatgatacaagaatgagagttgagatccttccaagaatgcagatctt 979  
 Db 863 atcaatcgcctcactgaatttgcgaaggttggaatttactacacaaaagatctttg 922  
 Qy 980 caagtgag--cattaccataatggtcgaagctgtggaagaacaaatgcagatgaat 1036  
 Db 923 aaaaagaaggtcttattcctccgaaatttgaataatgggaacaacaaatgcatlaaat 982  
 Qy 1037 gtcacgggttaacactaattgtcgtgtgagggcctct--caactctaaagga 1093  
 Db 983 gtgaggggttacccttagcaattactgtgtgtgagcctctcctcacaataatcgtlaaa 1042  
 Qy 1094 caatagaagatttgaagaactgttgcataaagatgccaagatcgtcacaatgacatcctg 1153  
 Db 1043 catgtgagatgagatggaanaatgttgcggagaaatgtaagttcgtgtgaagcagacatctg 1102  
 Qy 1154 atgaacgagtgtcactgctgtgtgtgtagatgacgacttgaacagcagatataaa 1213  
 Db 1103 aagcaaatatgataagaggt 1162  
 Qy 1214 catgtcttcatttgcgaatttcccaagaagaacagtgatattccagtgaaagatttga 1273  
 Db 1163 cgtgttctctatttgcgaatttccgaagagtgaaagatttgaataataactgt 1222  
 Qy 1274 tgaatcatgtagtgcgtgaggggtcctga-----agttggaanaatgatttgaagga 1327  
 Db 1223 ttgagttatggccgtgaggggttlttgatgaagaagggggaanaaagatagaagga 1282  
 Qy 1328 aggttgaagaagttgttgcagaagctgtgtagatgattctagccctgttgaagaaga 1387  
 Db 1283 tggcagaagaactgtataacgaactgtgatagaagaagttcaattctacacaatgtga 1342  
 Qy 1388 gtgcgaatggaacaanaaatatgatacatgtaagttcatgataataatgacatctgag 1447  
 Db 1343 gtttctgtggggaacacagag--atgtggaatgcatgtgtgacccgtgaaactctgtt 1399

Qy 1448 tgaagaagttcaagaaggagacatttga 1477  
 Db 1400 tgaaggaaagctcgaacatgatttga 1429  
 RESULT 8  
 AAS03713  
 ID AAS03713 standard; CDNA; 3683 BP.  
 XX AAS03713;  
 XX 29-AUG-2001 (first entry)  
 XX  
 DE DNA encoding Rx 25, a modified resistance protein.  
 XX  
 KW Rx: modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant; ss.  
 OS Solanum tuberosum.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 37..2850  
 FT /\*tag= a  
 FT /product= "Modified resistance protein 25"  
 XX  
 PN W0200129239-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PE 12-OCT-2000; 2000MO-GB03930.  
 XX  
 PR 15-OCT-1999; 99GB-0024483.  
 XX  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 XX  
 PI Bendahmane A, Baulcombe DC;  
 DR WPI: 2001-290924/30.  
 DR P-PADB: AA002143.  
 XX  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 XX  
 PS Disclosure; Page 46-60; 77pp; English.  
 XX  
 CC The sequence represents the coding sequence of Rx clone 25, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 XX  
 SO Sequence 3683 BP; 1149 A; 635 C; 782 G; 1117 T; 0 other;  
 Query Match 10.0%; Score 272.8; DB 22; Length 3683;  
 Best Local Similarity 54.7%; Pred. No. 7.4e-63;  
 Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;  
 Qy 140 tgcagaagacttgaagaacaatgttttggggaatgacggatttgaagtgaagg 199  
 Db 149 tggagaatccctgcataataatgagcgcgacatgaggggttaacaacttggaaagtga 208



QY 200 taagaagaattgcaagtgtctgaaatacacaattcaactgagactgaacaggaactgtac 259  
 DB 209 tctgtaagaagtaacatacacaagaagatactgtgactcgtgaatacaagaattgttctt 268  
 QY 260 tgggaagaataaagccgcgaataaagcgctgcgaaggttctgcaaacgctcgaac 319  
 DB 269 tggcagagatttggaggaagaagcagagctatgtggagatttcttcgtccctggaac 328  
 QY 320 aagtgacagagacatgacatcatalctggaagaagtcgacaagaatccaagataaaggaa 379  
 DB 329 aagcactagaatgactgtctccaccgtgaacaagtgatgacacatcggaacagatga 388  
 QY 380 aacaagatcaagaagaatcatctgttcatgattttccaagttcaacaacgcatatttga 439  
 DB 389 aagatctaaacacacaactagctcgtctgctagttactctg--aactgagttgagc 445  
 QY 440 aggttaagaacaataatgcttgacgtgacgtatcaacaaggaacaggttgttagaagatcga 499  
 DB 446 agcccgagagataataatggttgcgtgcaaatgaaatttgatgactgctcgatcaactcg 505  
 QY 500 ctgaagactactctggggaaccccaagatcccgatctgcggatggagagcatagta 559  
 DB 506 ctgagag--aggaagggagactagaaggttgcatacgtlaaggtggagcgatcgga 562  
 QY 560 aacaacacttagcaaaagaagtttaacatgacatgaatcaattctatgcgttttgatctc 619  
 DB 563 aacaacacttgcatacaaaactctatagtcacgtcgtctatgtctcgttttgatctatc 622  
 QY 620 atgcctggctaccatcatctcaacgacacaacaagaataatttcgcggcgctctgc 679  
 DB 623 gtgcacaagaacactgtttcaacaagatattgtgtgagaattgactccctcagccctctt 682  
 QY 680 attccaacatcaaaatgatacgaaggttaagaatgattggtgaagcagagctagcagaca 739  
 DB 683 ctctgacaagtgatgaacctgat-----gactagctagcgagcc 721  
 QY 740 tcttcagaagaagtttaagaagaagaggtacttaattgtcttgagtgatctgaggt 799  
 DB 722 gactcgaagaagcactcgaagaagcagagactctgtagtcatgacatagta 781  
 QY 800 ggaaggtgtgagatgagcgagagacgtcttccaaactgaagacaatgagggagtcga 859  
 DB 782 cagaagccttgagatataataaactatgttccacgacctataat---ggaagcagaa 838  
 QY 860 tactctgactaccctgaatgataatgataagtagctgttatagtcgtgtagagaatttctt 919  
 DB 839 tactcctgactactcgaatgtggaagtgctgaatatgtgttcaagtaagcctctc 898  
 QY 920 tgcgagtagcttcatgatacgaatgataaggttgagttctttccaagaatgacgacttt 979  
 DB 899 atcacactgacctcagaaatttctgaagaagttgaaatttactaacaacaaagatcttgc 958  
 QY 980 caagtgaaag---cattcacataagttcgaagactgtgaaagacaatcgacagat 1036  
 DB 959 aaaaagaaggttcttattctcctgaatttgaataatatttggaacaacatgtcaat 1018  
 QY 1037 gtcaaggttaccactaactattgtcgtgtgcaaggctctc---caacttaaaagga 1093  
 DB 1019 gtgagagattactactcactgaacttactgtgtgactctctccaatgtgcaaa 1078  
 QY 1094 caatagaagattggaanaactgtctgctaagaagatgcaagcttcgcacaaatgtacccg 1153  
 DB 1079 gatttgatgagtgagcaaaatgtgggaaatgtaagttcgttcgtttagacacagatcccg 1138  
 QY 1154 atgaacgatatgtcacgctgtcgttggttgaatgacatcaacttgacaagcgaactaa 1213  
 DB 1139 aagcaaatgatagtagagaggttgctgtgacatccacttgcttccactaaac 1198  
 QY 1214 catgcttctcgtatttgcgaatttttccagaagacagtgatattccagtggaagaatttga 1273  
 DB 1199 cgtgttctctgatttgcgaatttccacagagatgaacagatttctgtaaatgaaactgtg 1258

QY 1274 tgaatcatgagatgctggaagggttctctga-----agttgaaatgatttgaagag 1327  
 DB 1259 ttgagttatggcctgtgagaggatcttttgaataaagaaggaaagatgagagag 1318  
 QY 1328 aggttgaagaagtgcttgcagaagctgtgcagatgctagctcctcgtcagaagaa 1387  
 DB 1319 tggcacaacatgtataaagaacttatagatagaagcttaatttcatccacaatttta 1378  
 QY 1388 gtccgaatgtgaaacaaaatagatcatgtaagttcatgataatcatatgactgtgc 1447  
 DB 1379 gtttcgttgaaacataagaag---ctgtggaatgatagtgtgaccctggaactcgtt 1435  
 QY 1448 tgaagaagttcaaaaggagacaatttta 1477  
 DB 1436 tgaaggagctcgaacaacatgaaatttctga 1465

RESULT 9  
 AA250264  
 ID AA250264 standard; DNA; 10329 BP.  
 AC AA250264;  
 XX  
 DT 18-MAY-2000 (first entry)  
 XX  
 DE Genomic DNA of potato Gpa2 resistance gene.  
 KW Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p;  
 KW marker; IPM4C; 11LR; Potato Cyst Nematode; PCN; Globodera; nematode;  
 KW nematode resistance; detection; diagnosis; transgenic plant; ds.  
 XX  
 OS Solanum tuberosum.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_signal 1..4874  
 FT /tag= a  
 FT /note= "Gpa2 regulatory region"  
 FT CDS 4875..7850  
 FT /tag= b  
 FT /product= "Potato Gpa2 resistance protein"  
 FT /note= "This region is specifically claimed"  
 FT exon 4875..7850  
 FT /tag= c  
 FT /number= 1  
 FT intron 7586..7822  
 FT /tag= d  
 FT /number= 1  
 FT /note= "Located within the coding region of Gpa2 gene"  
 FT exon 7823..7850  
 FT /tag= e  
 FT /number= 2  
 FT /note= "Includes the stop codon, TGA"  
 FT intron 7942..8053  
 FT /tag= f  
 FT /number= 2  
 FT /note= "Located in the 3' UTR of Gpa2 gene"  
 XX  
 PN WO200006754-A2.  
 XX  
 PD 10-FEB-2000.  
 XX  
 PF 30-JUL-1999; 99WO-NL00491.  
 XX  
 PR 31-JUL-1998; 98WO-NL00445.  
 XX  
 PA (CPR0-) CPR0-DLO CENT PLANTENVEREDELINGS REPROD.  
 PA (UYWA-) LANDBODUWUNIVERSITEIT WAGENINGEN.  
 XX  
 PI Van Der Vossen ENG, Van Der Voort JNMNR, Lankhorst RMK, Bakker J;  
 PI Stiekema WJ;  
 XX  
 DR WPI; 2000-183132/16.  
 DR P-PSDB; AAY4818.



```

FT      /number= 1
FT      7566..7822
FT      /tag= d
FT      /note= "This region is claimed (Claim 13)"
FT      /number= 1
FT      /note= "Located within the coding region of Gpa2 gene"
FT      7823..7941
FT      /tag= e
FT      /number= 2
FT      /tag= f
FT      7942..8053
FT      /tag= f
FT      /number= 2
FT      /note= "This region is claimed (Claim 13)"
XX      WO200006753-A1.
XX      10-FEB-2000.
XX      31-JUL-1998; 98WO-NL00445.
XX      31-JUL-1998; 98WO-NL00445.
XX      31-JUL-1998; 98WO-NL00445.
XX      (CPRO-) CPRO-DLO CENT PLANTENVERDELINGS REPROD.
XX      (UYWA-) LANDBOUDUNIVERSITEIT WAGENINGEN.
XX      Van Der Voosen EAG, Van Der Voort JNMNR, Lankhorst RMK, Bakker J;
XX      Stiekema WJ;
XX      WPI: 2000-195310/17.
XX      P-PSDB: AA145004.
XX      Recombinant Gpa2 polynucleotide from potato, Solanum tuberosum, useful
XX      to confer resistance to phytopathic nematodes of the genus Globodera in
XX      transgenic plants, e.g. resistance to potato cyst nematodes in potatoes
XX      -
XX      Claim 21; Fig 3c; 96pp; English.
XX      The present sequence is the genomic DNA encoding potato Gpa2 resistance
XX      protein. It is inserted in the pBINRGHZ plasmid which is used to
XX      transform host plant cells to produce transgenic plants. Gpa2 confers
XX      resistance to infection by phytopathogenic nematode of the
XX      Globodera genus. It is mapped to short arm of chromosome 12 (12p),
XX      between the markers IPM4c and 111R. This locus is associated
XX      with resistance to potato Cyst Nematodes (PCN) like G. pallida and
XX      G. rostochiensis, that invade and damage the roots of Solanaceae. It has
XX      nematocidal activity. Recombinant DNA sequence comprising the Gpa2
XX      gene can be used to produce transgenic plants with increased resistance to
XX      nematodes. The polypeptides can also be used in nematocidal compositions
XX      and for detection and diagnosis of nematode infections.
XX      Sequence 10329 BP; 3150 A; 1542 C; 1924 G; 3713 T; 0 other;
SQ

```

```

Query Match      10.0%; Score 272.8; DB 21; Length 10329;
Best Local Similarity 54.7%; Pred. No. 1.2e-62;
Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

```

```

QY      140  ttgtcaagaactttgagaaacaatgttttggggaatgacggaattttggaagtagag 199
DB      4987  tggagaatacctgcacataaattggcgacatcagaggttaacaactcttggagattgaa 5046
QY      200  taagaagaattgcaagtgtctgatacacaactccaactgagactgaactgac 259
DB      5047  tcatagaggttagcacaacacagaagatattgttgactcggaatccaagaattgttttt 5106
QY      260  tggggaataataaaagccagaaaaaagcgctcgaaagtttcgtcaaaccttgcac 319
DB      5107  tagcaggaatttggggaaaagaagcagggctatgttggggatttttttcgtcttgcgaac 5166
QY      320  aagtcagagagacatgatatctatctgaaagatcgacaagaatccaagtaagaa 379
DB      5167  aagcactagaatgcattccaccgtgaacacagtgatggtgacaacatcgacacatga 5226

```

```

QY      380  aacaagtatcaaggaatcatcttggttatgatttttaagttaacaacaagatattga 439
DB      5227  aagatcaaaaacacaactagctcacttgcagtttaccgtgaac---atgatttgagc 5283
QY      440  aggttaagaacaatatgtgttgacgtgatgataaagaacagtttttgaagatctga 499
DB      5284  agcccgagaataataatgtgttcgcgtaaaaatgaatttgagatgaatgcgtgaactcg 5343
QY      500  ctagaagctactctcgtgggaaccacaagtcacccgatctgcgagatgtaggaatagta 559
DB      5344  ctagagg---aggaaagggaactagaagttgtcttcacatcgtaaggatgtaggaatcgga 5400
QY      560  aaacaaccttagcacaagaagatttacaatgaatgaatcaattcctacgttttgatctc 619
DB      5401  aaacaacttgcgtgcaaaaactctatagtgatctcattacattatgtctcgaattgatatc 5460
QY      620  atgcctgggtacacatattcacaagacaacaagaagaattttgcttggtcctctgc 679
DB      5461  gtgcagaagaactgtttccacaagagatattgttgagaatgaatgaatcctcctgacctctc 5520
QY      680  attcacaatcaaaatgagatgacaggggttaagaatgattggtgaagcagagctagacaga 739
DB      5521  ctltgacaagtgtgacacctgattatc-----agctagcgagacc 5559
QY      740  tgttacagaanaagtttaagaagaagagagacttaattgtcttgatgatatctgaggt 799
DB      5560  aactgcaaaaagcatctgaaaggcagagatattgtgtgactatgtagacatatgtagacta 5619
QY      800  gtgaagtgtggaatggtcgtagacagatgtcttcacactgaagaacatgcagggatcgaa 859
DB      5620  cagaagcttggagtgatataaaactatgtttccca---gactcgataatgaagacagaa 5676
QY      860  tactgttgcactccgttaatgatgaatgagctgtttagctgtgtgtagagaattttctt 919
DB      5677  tactcctgactactcgtgaatgtggaagtgtgtaataatgtagctcgaagtaagcctctc 5736
QY      920  ttggagatgagcttgcagatgacatgagatgagaggttggtcttttcaaaagtcgacattt 979
DB      5737  atcacatgcgcccacatgaaattttgacgaagatgttggaatttaccacaaaagaactctt 5796
QY      980  caagttaag---cattacacatgaatgcagatgcagactgttggaagaacgaatgcagatga 1036
DB      5797  aaaaagaagttcttattcttcctcgaatttgaataatttgggaacaacatgacttaaa 5856
QY      1037  gtcaaggtttaccactaactattgtcgtgtgtagaggctctc---caacttaaaaga 1093
DB      5857  gtggaaggttacctctcagcaatattactgtatgtctgactctctcacaatcagtaaaa 5916
QY      1094  caatgaagaattggaaaactgttgcctaagaatgtaagatcattcgtcacaaatgactcgt 1153
DB      5917  cattgattgagtggaacaaatgttcgcgagaatgaatgtaatgccttcgtgtgaagcagactctg 5976
QY      1154  atgaacgatgttcaacgtgtgctgtggttgatgatacactgtgaacacgactcaaaaa 1213
DB      5977  aagcaaaatgcattgagagaggttggtcttgatgatacactgtcctctccacttaaac 6036
QY      1214  catgtcttctgcatttcggaattttccagaagacagatgatatctcaagtgaagaatttga 1273
DB      6037  cgtgtttcttgtaatttttgcgaatatttcgcagagatgaacggaatttgaataaataacttg 6096
QY      1274  tgagatcatggaatgtgtgaggggtctcga-----agttggaanaatgttttggagggg 1327
DB      6097  ttgagttatgggcccgtgagggggttttttgaatgaagaagaaggaagaaacatagaagagg 6156
QY      1328  aggttgaagaagtgttgcagaagctgttcgatagatgtctagctcgtcagcaagaagaa 1387
DB      6157  tggcagaacacatgtaaaacgaactgttagatagaagctcaattctacccaacatgtga 6216
QY      1388  gtcagagatggaacaaaataatgaatcatcgtaaagttcatatgataatataatgacctgtg 1447
DB      6217  gttttgatggggaacacacagag---atgtggaatgcatgattgtgacccgtgaactctgtt 6273

```



QY	1037	gtccgcgggttacccactaactatgtcgtgtgttcgaaggctctc---caatctaaagaa	1093
Db	3321	gtggagagattacccttaaccactactgtgattgtctgtgcgtctctctccaaatggttcaa	3290
QY	1094	caataagaagattctggaanaacgtttactaaagttgtcaagtcattctgtccaaatgtactctg	1153
Db	3291	gattagaagatgtgcgaagaatctggggaanaatgtgaagtctgtgtctgtacgaacgtctctg	3350
QY	1154	atgaacgaattgtccacgtgtgtctgggtgtgaagttacgatacctttgacaaagcgatctaaaa	1213
Db	3351	aagcaaatgatgagagtgtgtgcgtttgtgagtttaccatacctactgtctctctccactaaac	3410
QY	1214	catgtctctgcattcttggaatttttccagaagacagtgatcttccagtgaagaatttga	1273
Db	3411	cggtgttctcgtattttgcatttccatttccacagagatggaacagattctctglaattgnaacttg	3470
QY	1274	tgaagatcatgtatggcgtgaagggtgtctctga-----agttgaaatgtatgtgaaagag	1327
Db	3471	ttgagttatgacctgtagaagagatttttgaatgaagaagagggaataagcatagaagag	3530
QY	1328	aggttgagaagagtggtttggaaggcgtgtccagatagatgtctagctcgtgcagcaagaaga	1387
Db	3531	tggcaacacacatgataaacggaactatagatagaagacttaatttccatccaaatttta	3590
QY	1388	gtccgaatgtgacaaanaattagatcatatgtaaagttcattgatctaatatataatgacctgtcg	1447
Db	3591	gtttctcgtgcgaacataagaag---tttgygaatgatgatgtgaacccgtgaactctgtt	3647
QY	1448	tgaagagaattcaaaaggsgaacaatttta-----tccatgaagacattgtcttgcagttat	1504
Db	3648	tgaagggaagctctgnaaacaatgaaattttgtgaaatgtatccagaaagaaagatgatacaaat	3707
QY	1505	catatccagaatgttccatactctgtatgtatataaatagtacgacctttaaagcgcgtgactg	1564
Db	3708	catgtgcacaaatccacagcagcggttctcctttaagagtcgaagtcggatccagaatccataag	3767
QY	1565	gtgaagaaattaatatttgcctctatagtgcttatagggtctctcta-----	1612
Db	3768	tgaagaagattgtcgtgtgtgcgtaaagggtgaagctcaattcatatccatgattgtgtgagat	3827
QY	1613	-----cccttgaatactgcagttgaaagatcatgacaacaaca--atcttttga	1660
Db	3828	togaatgcgtcaacacacggaattgtcttccaagctagtaagagctactgaactctgtttga	3887
QY	1661	aacgaacccaattctgtttctctcttccaacttgaagccttatattatgttccaatcag	1720
Db	3888	atacatgycacaatttttccacagtggaagtaatttctccaattatlttgaagatacctaact	3947
QY	1721	aggttttccaattccaattacccaagaagctcttggagctgaga-----cacagacaga	1771
Db	3948	tgcgttttaactccttgccttcacagcagatatacaagatgcgaagaagcgtgtccctcatcaa	4007
QY	1772	ttgatgtttccctcgagagatactaaagcctcatcgtgtg-----aggtacc	1819
Db	4008	taatagacattccctcatgatatcaagaagcctatgatactctgcaaacattttaaactaac	4067
QY	1820	tatcatgttccagctatagggaatttggatgtatacctccagaatttggaaatttgaagttagatc	1879
Db	4068	ttccatttccagttatcatcccttccatcatccatccaggaatttggagatgcacaat	4127
QY	1880	tgcagacattcatgttccaacggttttcagatcagataataaattttgtctgaaggaattt	1939
Db	4128	tggagagcgcgtgtatgtggctggaattacttgcggagtcagccttacaagaaacagat	4187
QY	1940	gggaacataatgcaatt---aagacatttaacgtgccagattttatttgcgaattgac	1996
Db	4188	tgtgtttgaaanaatttgcatagtccctcaatcaaatgaaacccctggtattgtacagaggtct	4247
QY	1997	caagtgtatcgtttgacaagaaggaagcacttggatttttcaaatla--caactatttct	2055
Db	4248	tttttaagcatatttcccaatttaagaagatgtgcagaagtatttgggtccccaagaagacttcc	4307

[illegible]

XX 28-OCT-1999.  
 PD 16-APR-1999; 99MO-GB01182.  
 XX 16-APR-1998; 98GB-0008083.  
 PR (PLAN-) PLANT BIOSCIENCE LTD.  
 XX  
 PI Bendahmane A, Baulcombe DC, Kanyuka KV;  
 DR WPI, 1999-634006/54.  
 DR P-PSDB; AA52152.  
 XX  
 PT New isolated plant virus resistance gene, used to produce transgenic  
 PT plants with resistance to virus infection  
 XX  
 PS Claim 4; Page 87-90; 124pp; English.  
 CC This is the DNA sequence of the potato Rx gene. The Rx gene is a  
 CC resistance gene which confers extreme resistance against potato virus X  
 CC (PVX). Sequence AA237153 is the Rx gene including introns. The Rx gene  
 CC can be used to create a recombinant vector which encodes the Rx  
 CC resistance polypeptide AY52152, this vector can be used to transform  
 CC plant cells to produce a transgenic plant with resistance to PVX. The Rx  
 CC gene can be used to engineer resistance traits, preferably broad spectrum  
 CC extreme resistance, into plants. The Rx gene can also be activated by  
 CC non-PVX viruses, e.g. Narcissus mosaic virus (NMV), Nandina virus X  
 CC (NVX), Viola mosaic virus (VMV), Cymbidium mosaic virus (CYMV), Poplar  
 CC mosaic virus (PopMV) and white clover mosaic virus (WCLMV). Rx can be  
 CC used to offer specific protection against this group. The Rx gene  
 CC sequence can be used to create antibodies specific for Rx. The antibodies  
 CC can be used to down-regulate Rx activity and also for the detection,  
 CC identification or isolation of Rx or homologues.  
 XX  
 SQ Sequence 3066 BP: 913 A; 533 C; 675 G; 945 T; 0 other;

Query Match 9.9%; Score 269.6; DB 20; Length 3066;  
 Best Local Similarity 54.5%; Pred. No. 4.9e-62;  
 Matches 736; Conservative 0; Mismatches 569; Indels 45; Gaps 8;

QY 140 ttgtcaagaacttggagaaacatgttttgggaaatgacgatttttaagtagagg 199  
 DB 163 tggagaaatcccgcatataaaaggcgatcagaggggttaacaactcttggagattgaaa 222  
 QY 200 taagagaattgcaagtgctgtaatacacaattcaactagactaagcaagaactgtac 259  
 DB 223 tctagaggtagcatcacacacagaagatgtgtgactcggaatcaagaattgtttt 282  
 QY 260 tgggagaaataaagccagaaagaaagcgcgctgcaaggttccgtcaaaagcctgcaac 319  
 DB 283 tagcagaatttggaggaagaaagcaggtatgtgtggagatttttctgctcgagac 342  
 QY 320 aagtagcagagacatgcatatctgtgaagagtcgacaagaatccaaagataagaa 379  
 DB 343 aagcactagatgcatgtatccacccgtgaaacagtgatgacaaatccgacgacatga 402  
 QY 380 aacaagtatcaaggaatcattgttcaatgttttcaagttcaacaacgataatttga 439  
 DB 403 aagatctaaacccaactagctcgtctgcatgttaaccgt---aacatgattgtgagc 459  
 QY 440 aggttaagaacaatatgttggacgtgatagtatcaaaagaaacagtgttagaagatcta 499  
 DB 460 agcccgaaatataatgtgttggccgtgaaatgaatttgaatgtatgtctgataactgt 519  
 QY 500 ctagaagctactctgggaaacccaagtcacccgattgtgagtgagtgagggagctagta 559  
 DB 520 ctagaag---aggaagggaactaagaattgtctcaatcgttagggatgagggacatcgga 576  
 QY 560 aaacaacctatgcaaaagagtttaacaatgaatgaatcaatctatgacggtttgatgttc 619  
 DB 577 aaacaacttggctacaaaactcatatagtgatcgctgattatgtctcgattttgatatctc 636

QY 620 atgcctgggtacacatctcacagccacaacaaagaaatttctggtgaccttcgc 679  
 DB 637 gtgcaaaagcaactgttccacaagagatattgttgagaagatgactcctagcctcttc 696  
 QY 680 attccacatcaaatgtatgacaggttgaagatgattgtgtgaagcagagctagcagaca 739  
 DB 697 ctgtgacaagtgtgaacctgtat-----gatacgttagcggacc 735  
 QY 740 tgttacaagaagtttaagaagaagtagtacttaattgtctgttgatgatatgaggtt 799  
 DB 736 gactgcaaaagcatctgaaagcgagagatattctgtgtagtcatgacatagtgacta 795  
 QY 800 gtgaagttgtgattggtcggtgagacgatttccaaactgaaagacatcgagggatcgaa 859  
 DB 796 cagaagcttggatgatatataaactatgttccacagctgtataat---ggaagcgaa 852  
 QY 860 tactgtgactaacccgtaatagtatgattgttctgctggtgtagaagattttctc 919  
 DB 853 tactctgactaaccccgaaatgagaaatgagctgtaataatgctgagtgaaagctcttc 912  
 QY 920 tgcgattgacttcaatgataagatgagagttgagttcttttcaaaagtcagacatttt 979  
 DB 913 atcaatgctgctcatgatttgaacgaagttggaatttaactacacaaaagatctttg 972  
 QY 980 caagtgaag---attacataatgattcgaagctgttgaagcaaaatcgacagatttt 1036  
 DB 973 aaaaagaagttcttattcttctcgaatttgaataatttggaaacaatattgactaataat 1032  
 QY 1037 gtccaggttaccctactactgttctgtgttgagaggtctc---caattcaaaagga 1093  
 DB 1033 gtggaagattacaccttgcacattactgtgtgtgacttctcctcaaaatgtgtcaca 1092  
 QY 1094 caatagaagattggaacaaactgttgaagaatgcaagtcattcgtacaaatgacatcgt 1153  
 DB 1093 gattagaatgattgccaagaagatttgggaaatgtlaagttcgtcgttgaacagatcccg 1152  
 QY 1154 atgacgatgttcaactgttctgtgtgtgtgattgattgattcattgacaaagcattaaa 1213  
 DB 1153 aagcaaatatcagagaggtgtgtgcttggattacacactgtgcttctcactcaaaaac 1212  
 QY 1214 catgtcttgcatttgcgaattttccagaagaacagtgatattcagtgaaagatttga 1273  
 DB 1213 cgtgttctcgtatttgcgaattttccagaaggaatgaacagatttctgtcaaatgaaactg 1272  
 QY 1274 tggatattgattggtcgtgaaggttccgtga-----agttgaaatattgtgaagag 1327  
 DB 1273 ttgattatggtccgtgaagagatttctgaaatgaagaagaggaagaaacatagaagagg 1332  
 QY 1328 aggttgaagagttgttgaagagctgttcgatatagatgcttgcgtcgaagaaagaa 1387  
 DB 1333 tggcaacaacatgtataaagaactatagatagaagacttaatttccaccacaatttta 1392  
 QY 1388 gtccgatatggaacaaatataatgatactgaagttcaatgataatataatgacgtgtgcg 1447  
 DB 1393 gtttctgttgaacaaatagaag---ttgtgaatgattgattgtgacccgtgaactctgtc 1449  
 QY 1448 tgaagaaatcacaagggagaacatttta 1477  
 DB 1450 tgaagaaagctcgaacaatgaaattttgtga 1479

RESULT 13  
 AAS03715  
 ID AAS03715 standard; cDNA; 3014 BP.  
 XX  
 AC AAS03715;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE DNA encoding Rx 72, a modified resistance protein.  
 XX  
 KW Rx; modified resistance; NBS; LRR; cell death; autoactivator;

KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 plant; ss.  
 OS Solanum tuberosum.  
 OS Synthetic.  
 XX

FT Key Location/Qualifiers  
 FT /\*tag= a  
 FT CDS /product= "Modified resistance protein 72"  
 XX

PN MO200129239-A2.

PD 26-APR-2001.

XX 12-OCT-2000; 2000MO-GB03930.

XX 15-OCT-1999; 99GB-0024483.

XX (PLAN-) PLANT BIOSCIENCE LTD.

XX Bendahmane A, Baulcombe DC;

XX WPI: 2001-290924/30.

XX P-PSDB: AAU02145.

PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 XX

PS Disclosure: Page 46-57; 77pp; English.

XX The sequence represents the coding sequence of Rx Clone 72, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 CC  
 XX

SQ Sequence 3014 BP; 891 A; 555 C; 674 G; 894 T; 0 other;

Query Match 9.9%; Score 268; DB 22; Length 3014;

Best Local Similarity 54.4%; Pred. No. 1.3e-61;

Matches 735; Conservative 0; Mismatches 570; Indels 45; Gaps 8;

QY 140 ttgtcaagaacttggaaacaaatgttttggggaatgacgagatttgaagtgaag 199  
 DB 154 tggagaaatccctgcaatataatgtggcgatcaatgaggtgtaacaacttggagttgaa 213  
 QY 200 taagaaagtgtgcaagtgctgtgaatacaacaattcaactggaactcaacgagacgtgtac 239  
 DB 214 tcgtlaaggtlaagcatcacacacagaagatagttgtaactggaatacaagaatgttttt 273  
 QY 260 tggggaanaataaagccgaanaaaaagcgctggaagtttcgtlcaaacgtcgaac 319  
 DB 274 tggcaagaatttggggaagaagaagcaggtctatgtggagatttttctgctcctggaac 333  
 QY 320 aagtagcagaagacatgcatcatatctggaagaagtcgacaagaatccaagaataaaggaa 379  
 DB 334 aagcactagatgcatgattccacgctgaaacagtgatgagcaacatcggaaagcatga 393  
 QY 380 aagaagtatcaagaagatcttggttcatatttttcaagttcaacaacagcatatttga 439  
 DB 394 aagatctaaaccacaacactagctcgctgttcagtttactctg---aactgagtggtgagc 450

QY 440 aggttaagacaatatgtgtgacgtgatcatcaagaagaaacagtgtttagaagatcga 499  
 DB 451 agcccgagaaataatgtgtgacgtgatcatcaagaagaaacagtgtttagaagatcga 510  
 QY 500 ctagaagctactctggggaaccccaagtcacccgatttgggagatggagcatagta 559  
 DB 511 ctagaag---aggaagggacactagaagatgtgtcactcgtlaagggatggagcatcggga 567  
 QY 560 aacacaccttgaagaagaagattcaatgaatgaatcaatctcattcgttttgaatc 619  
 DB 568 aacacaccttggctaaacactctatgtatgcacgtgcatctatgtctggtttgaatc 627  
 QY 620 atgcttgggtctacatcatcaccagcacacaanaaaggaaatlttgcgtgctctgc 679  
 DB 628 gtgcgaagaacatctttcacaagaagtattgtgtggaatgtactcctagcctctt 687  
 QY 680 attcacaatcaaatatgtagtgaaggttaagaatgttggtagaagcagctagcagaca 739  
 DB 688 ctltgacaagatgtgacgtgtat-----gattcagctagcggacc 726  
 QY 740 tgttacaagaagatttaagaagaaggtacttaattgtctgtgatatcgtgaagt 799  
 DB 727 gactgcaaaagcatctgaaagcaggaagatacttggtagtcatctgtgacatcgtgacta 786  
 QY 800 gtgaagtgtggagatggtgagacgagatgcttccaaactgaagaacatgcaggagtcgaa 859  
 DB 787 cagaagcttggagatgatatataaactatgttccacagactgtataat---ggaagcagaa 843  
 QY 860 tactgttgcactaccgtaatgtagatgtagctgttatgtctgtgtgtagaagatttctt 919  
 DB 844 tactcctgactactcggaaatgtggaagtgtgaaatgtgaaatgtgaaatgtgaaatgtgaa 903  
 QY 920 tgggagtgagctcatggaatcaagatgagaggttgagcttccaaagtgcagacattt 979  
 DB 904 atcactgtgctcactgaatatttgacgaaagttggaatttactcaacaanaagacttgg 963  
 QY 980 caagtgaag---catacatatgagttcgagactgttgaaagcaaatgcagagatgaat 1036  
 DB 964 aaaaagaagttcttattcctcctgaatttgaataatttggaaacaaatgcatcctaanaat 1023  
 QY 1037 gtacaggttaccacactacattgtgtgttgcagagcttc---caactcaaaagaa 1093  
 DB 1024 gtggagatattaccctcagacatattactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1083  
 QY 1094 caataagaattggaanaactgtgtcctaaagatttcaagttcattcgtlcaacaatgactcgt 1153  
 DB 1084 gattagatagtggtgcaagaagatttggggaanaatgtaagttcgtgtgacacagatcgtg 1143  
 QY 1154 atgaacgatgttcaagtggt 1213  
 DB 1144 aagcacaatgcatgagagatgt 1203  
 QY 1214 catgtcttgcattcgtgatttttccagaagaacagtgatattccagtgaagaatttga 1273  
 DB 1204 cgtgttctcgtatttgcacatttccacaaggttgaacagatttccgttaataagaacttg 1263  
 QY 1274 tgaatcatgattgctgtgaggttccctga-----agttggaanaatgatttgaagaag 1327  
 DB 1264 ttgattatgtgctgtgagaggt 1323  
 QY 1328 aggttgaagaatgttgcagaagcgttgcagatgattgtcagttcagttcgttgaagaagaa 1387  
 DB 1324 tggcaacaacatgtatataaagaaacttataagtaagccttaatttcatlccacaatttta 1383  
 QY 1388 gtccgagatggaacaaataattagatcatgtaagttcactgaatcactaataatagcctgtgc 1447  
 DB 1384 gtttctgtgaaacaatgtgaag---ttgtggaatgcatgtatgtgacccgtgaactcgtt 1440  
 QY 1448 tgaagaagttcaaaaggaggaacatttla 1477  
 DB 1441 tgaaggagaagctcgaaacatgaatttltga 1470



```

RESULT 14
AAS03717
ID AAS03717 standard; cDNA; 2880 BP.
XX
AC AAS03717;
XX
DT 29-AUG-2001 (first entry)
XX
DE DNA encoding Rx 193, a modified resistance protein.
XX
KW Rx: modified resistance; NBS; LRR; cell death; autoactivator;
KW nucleotide binding site; leucine rich repeat; pathogen resistance;
KW plant; ss.
XX
OS Solanum tuberosum.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 37..2850
FT /tag= a
FT /product= "Modified resistance protein 193"
XX
XX MO200129239-A2.
XX
XX 26-APR-2001.
XX
XX 12-OCT-2000; 2000MO-GB03930.
XX
XX 15-OCT-1999; 99GB-0024483.
XX
XX (PLAN-) PLANT BIOSCIENCE LTD.
XX
XX Bendahmane A, Baulcombe DC;
XX
XX WPI: 2001-290924/30.
XX
XX P-PSDB: AAU02147.
XX
XX Modifying activation characteristics of plant resistance proteins to
XX produce autoactivator polypeptide capable of activation in absence of
XX elicitor, by introducing modifications in amino acid sequence of
XX protein.
XX
XX Disclosure: Page 46-57; 77pp; English.
XX
XX The sequence represents the coding sequence of Rx clone 193, a modified
XX resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a
XX nucleotide binding site (NBS), leucine rich repeat (LRR), and which
XX mediates cellular response leading to pathogen resistance and/or cell
XX death or dysfunction in response to an elicitor. The Rx was modified by
XX introducing modification to the amino acid sequence to produce an
XX autoactivator polypeptide, capable of activation in absence of an
XX elicitor. Decoupling of resistance response from its natural elicitor is
XX useful for developing novel pathogen resistant plants. The modified
XX resistance proteins are useful for conferring resistance to non-natural
XX agents or stimuli and also for investigating resistance response pathways
XX and protein interactions e.g. with activators and repressors.
XX
XX Sequence 2880 BP; 864 A; 512 C; 641 G; 863 T; 0 other;
XX
Query Match 9.8%; Score 266.4; DB 22; Length 2880;
Best Local Similarity 54.4%; Pred. No. 3,5e-61;
Matches 734; Conservative 0; Mismatches 571; Indels 45; Gaps 8;

```

```

DB 269 tagcaccgaatttggaggaagaagcagggcctatgctgggagatttttcgcccggaaac 328
QY 320 aagtaacagagacatgcatcatalctggaagaagtcgacaagaatccaaagataaagaa 379
DB 329 aagcactagaatgcatctgattccaccgctgaacaagtgatgacataatcgacagcatga 388
QY 380 aacaagtatcaagaagaaatcattggttcattgattttccaagttccaacaacgataattga 439
DB 389 aagatctaaaccacaactagctcgttcgatttaccctg---aactatgtttgagc 445
QY 440 aggttaagaacaaatcgtgttgagcgtgatacgaagaagaaacagttgataagagctga 499
DB 446 agcccgagataataatggttgcgcgtgaaatgaaatgagatgagtcggtcaacttg 505
QY 500 ctagaagctactctggggaaccacaagtcaccgattgctcggaatggagacataagga 559
DB 506 ctagaag---aggaagggactagaaggttgcctcaatcgtaaggatggagacatcgga 562
QY 560 aaacacacttagcaaaaagatttacaatgataatcaatttatacgcggttgatgctc 619
DB 563 aaacacacttagcaaaaacacttaagcgtacgcgtgattatgctcgatttataatc 622
QY 620 atgctgggctacacatatacagcacaacaaagaagaatttgcctgggactctgc 679
DB 623 gtgcacaagcaactgtttcacaagagatgtgtgagaaatgatactccaggactctctt 682
QY 680 attccacaatcaaatgatagtacagggtaagatgattggtgtaagcagaatagacaga 739
DB 683 cttagacaagtatgacactga-----gatacgaatgagcgc 721
QY 740 tgttacagaagaatttaagaagaaggtactaattgtcttgatgatctcgaatt 799
DB 722 gactgcnaaagacatctggaagcagagagatctgtgtgataatgatacatalgagacta 781
QY 800 gtgaagtggtgagatggtcgtagacagatgcttcccaactgaagacaatgcaaggagtcga 859
DB 782 cgaagacttgagatgataataaactatgttccgactgtataat---ggaagcagaa 838
QY 860 tactgtgactaccgtaagtatgataagtagctgtgtatgctggtgttaagaattttctt 919
DB 839 tactcctgactatcctggaatgtggaagtgtgcaatgatagtcagttcgaatgaagccttc 898
QY 920 tgcgatagactcatggtcacaatgataagatgtgagcttcttcaaaagtgcagacttt 979
DB 899 atcacatggtcctcatgatttttgacgaagttgaaatttactacaacaaagatcttg 958
QY 980 caagtgaag---cattacatatgagttcgaagactgttggaagaacaaatcgcaatgaat 1036
DB 959 aaaaagaagttcttattctcctcgtgaatttgaataatattgggaacaaatgcatnaaat 1018
QY 1037 gtcaaggggttaccataactattgtcgtgtgtgacggctct---caacttaaaagga 1093
DB 1019 gtggaggaattaccttaagcaatctactgtgactgtgcgtcctctctccaaatgggtcaa 1078
QY 1094 catagaagatggaaaactgttcttaagaatgtaagatgtaactatcglogicaacaatgactcg 1153
DB 1079 gattagatgagtggaagaagaattggggaatgtaagtgtcgtgtgacgacagactcg 1138
QY 1154 atgaacgatgtcactgctgtggtgtgagttgagttacgactgtaacaagcgatctaaaa 1213
DB 1139 aagcacaatgcatgagagtggtgagttgagttacacactcactcctctccactaaac 1198
QY 1224 catgctctcgtatcttggaatttttccagaagcagtgatattccacgttgaaagtattga 1273
DB 1199 cgtgttcttctgatttgcacttccacagagatgaaacagatttctgtaaatgaacttg 1258
QY 1274 tgaagtcatagtatggtcgaaggttccctga-----ggttgaaatgatttgtaagag 1327
DB 1259 ttgattttggtcctgtagagagatttttgaatgaaagaggggaaaaagcatagaagagg 1318
QY 1328 aggttgagaagtggttgcaagagctgtgcataatgtlctatgctcgttcagcaagagaa 1387

```



Db 1319 tggcaacaacatgataacgaactatagatagaagcttaatttcacacaaatttta 1378  
OY 1388 gtccagatggaacaaattagatcatgtaagttcatgataatataatgactgagc 1447  
Db 1379 gttctcgtggaacataagaag---ttgtggaatgcatgtgtgacccgtgaactcgtt 1435  
OY 1448 tggagaagaagtcgaagggaagacatttta 1477  
Db 1436 tgaagggaagctcgaacataatcttctga 1465

RESULT 15  
AAS03719  
ID AAS03719 standard; cDNA; 2885 BP.  
AC AAS03719;  
XX 29-AUG-2001 (first entry)  
DT  
XX DNA encoding Rx 32, a modified resistance protein.  
DE  
XX Rx; modified resistance; NBS; LRR; cell death; autoactivator;  
KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
KW plant; ss.  
XX  
OS Solanum tuberosum.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 37-2850  
FT /\*tag= a  
FT /product= "Modified resistance protein 32"

PN W0200129239-A2.  
XX 26-APR-2001.  
PD  
PF 12-OCt-2000; 2000WO-GB03930.  
XX  
PR 15-OCt-1999; 99GB-0024483.  
XX  
PA (PLAN-) PLANT BIOSCIENCE LTD.  
XX  
PI Bendahmane A, Baulcombe DC;  
XX  
DR WPI: 2001-290924/30.  
DR P-PSDB; AAU02149.  
XX  
XX Modifying activation characteristics of plant resistance proteins to  
PT produce autoactivator polypeptide capable of activation in absence of  
PT elicitor, by introducing modifications in amino acid sequence of  
FT protein -  
XX  
PS Disclosure: Page 46-57; 77pp; English.  
XX  
XX The sequence represents the coding sequence of Rx clone 32, a modified  
CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
CC mediates cellular response leading to pathogen resistance and/or cell  
CC death or dysfunction in response to an elicitor. The Rx was modified by  
CC introducing modification to the amino acid sequence to produce an  
CC autoactivator polypeptide, capable of activation in absence of an  
CC elicitor. Decoupling of resistance response from its natural elicitor is  
CC useful for developing novel pathogen resistant plants. The modified  
CC resistance proteins are useful for conferring resistance to non-natural  
CC agents or stimuli and also for investigating resistance response pathways  
CC and protein interactions e.g. with activators and repressors.  
XX  
SQ Sequence 2885 BP; 861 A; 514 C; 649 G; 861 T; 0 other;

Query Match 9.8%; Score 266; DB 22; Length 2885;  
Best Local Similarity 54.7%; Pred. No. 4.5e-61;

Matches 724; Conservative 0; Mismatches 555; Indels 45; Gaps 8;  
OY 166 gttttggggaagagcaggtatttgaagtagaggaaggttcaggtcgtcgaa 225  
Db 175 gatactgggggttaacaacatcttggaaattgaatcgtgaagggtgagcctaacacagcagaa 234  
OY 226 tacacattcaacttgaagatacagaagaaactgtactgggagaataaataaagccagaanaa 285  
Db 235 gatactgttgcctcgaaatcaagaatgttttttagacagaattttgaggtgaagaagc 294  
OY 286 aagcgcgtcgaaggtttctgcgaagcctgcacaaagtagcagagagatgatatc 345  
Db 295 aggcgtatgttggaattgttctgcctcggaaacaaactgaatgtatgtatccccc 354  
OY 346 tggagaagatgcacaagaatccagataagaagaacaaagtaacaaagatcatgtgtt 405  
Db 355 gtgaacacagtgatggaacatcgacacgcatgaagaatcctaaacccagaaactgctcg 414  
OY 406 catgattttcaagttcaacaacagataatttgaaggttaagaacataatgttgaagct 465  
Db 415 ctgtcgttttaacctgaa---catgattgtgacgagcccggaataatagtgttgcgt 471  
OY 466 gatgataaaggaaacagttgttagaagatcgtactgaagactactcgtgggaaccacaa 525  
Db 472 gaaatgtaattgagatgtgtgtgatacactgtcctagagagagaa---gggaactagaa 528  
OY 526 gtcatcccgattgtcggatggagagcataggttaacaacaccttagcaaaagaattac 585  
Db 529 gtgtcctcaatcgtatagatgagagcagatcgggaacaaacttgcctacaaactctat 588  
OY 586 aatgataatcaactctatgcgttttgatgtacatgcctgggtacacatcacaag 645  
Db 589 agtgcctcgtgattatgtctcgtatgtatctgtgcgaagaaacactgttccacaagag 648  
OY 646 caacaacaaaggaaatttgcgtgagccttcgtgcacttccacatacaaaatgatatgag 705  
Db 649 tatgtgtgagaagatgactcctcctagagccttctctcttgaacagatgtaagacctgat 705  
OY 706 gttaaagatgtgtgagacagagctagcagacatgttcaagaanaagtttaagaagaag 765  
Db 706 -----gatcagctagagcagcagactgcaaaagcatctgaaagcag 747  
OY 766 aggtacttaattgtcttgaatgatatctgaggtgtgaaagtgtgagatgagcgttgagagca 825  
Db 748 agatacttgtagcatatgacatgacatgacacagaagcttggagatgataaaca 807  
OY 826 tgccttcaacgaagacatgacagagagctgaatactgtgacacccgtaatgtgaa 885  
Db 808 tgtttccca---gactgtataatggaagcagaatacctcctgactactcogaatgtgaa 864  
OY 886 gtagctgttatgctgtgtgtagaagaatttcttcttgcgagatgagcttcatgatacat 945  
Db 865 gtgcctgaatagctcagtagttcagtagcctcctcatcatcagctgcctcatgatttgcac 924  
OY 946 gagagttgagtcctttcaaaagttcagacatttcaagtgaag---cattacatattgag 1002  
Db 925 gaaagttggaatttacttaacaacaaagatcttgaanaaaggagttctatttccctgaa 984  
OY 1003 ttcgagactgttgaagaagaacatcgagatgaatgacaggggttaccacataactatgac 1062  
Db 985 ttggaataatttgggaacaaatattgacataaattgtggaggtattactacttagaatact 1044  
OY 1063 gtgtgtcagggcttct---caaatcaaaagacataatgaagatttgaanaactgttgc 1119  
Db 1045 gtagttgcgtgacttctcccaaaatggttcaaaagatttagatgagtgagcaagaattgg 1104  
OY 1120 aagaatgataatgcttgcctcaaaatgtagtccgtatgagacagatgattcaggtgtgctgg 1179  
Db 1105 gaaaatgtaagtcgtgcgttgcagacagatcccggaagcagatgacatgagtgagtggtg 1164  
OY 1180 ttgaatgatacacttgcgaagcgaatctaaacaaatgcttcttgcatttgcgaattttt 1239  
Db 1165 ttgagttacatcaactgtgcttctcaaccctaaacggttcttctgtatattgcaatttcc 1224

[illegible]

```
Search completed: September 11, 2002, 22:38:45
Job time: 39396 sec
```

GenCore version 4.5  
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 19:26:02 : Search time 6528.21 Seconds  
(without alignments)  
5619.415 Million cell updates/sec

Title: US-09-864-680-4  
Perfect score: 2718  
Sequence: 1 atggcgtatgcaagtgctgc.....ctgattcagaagaacattag 2718

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145.2	5.3	663	10	BI433950 EST536711
2	135.4	5.0	535	10	BM109555 EST557091
3	135.4	5.0	691	10	BI406780
4	135.4	5.0	635	9	AW979731
5	126.2	4.6	669	10	BM411546
6	125.4	4.6	607	10	BE473157
7	122.2	4.5	659	10	BE1934806
8	120.4	4.4	426	10	BE923412
9	119.6	4.4	701	12	AO367206
10	118	4.3	515	10	BI934083
11	118	4.3	639	12	BH14383
12	113	4.2	617	10	BE460726
13	108.4	4.0	756	10	BM408141
14	107.2	3.9	417	9	AW030063
15	105.4	3.9	660	9	AW216532
16	104.8	3.9	524	12	BH142479
17	103.4	3.8	576	9	AT772710

18	102.8	3.8	464	10	BF114223
19	100.6	3.7	579	9	AM034628
20	100.4	3.7	573	10	BM407382
21	100.2	3.7	643	9	AM622905
22	98.8	3.6	558	10	BF053416
23	98	3.6	558	10	BI425924
24	97.2	3.6	593	10	BM110993
25	97	3.6	800	10	BI421945
26	96.4	3.5	779	10	BG596578
27	95.2	3.5	526	9	AM217536
28	94.8	3.5	587	9	AM934420
29	94.4	3.5	323	9	AM933105
30	90.8	3.3	725	9	BI177939
31	90	3.3	339	10	BI176878
32	89.8	3.3	414	9	AW737247
33	88.8	3.3	784	10	BI432945
34	83.8	3.1	604	10	BI179578
35	81.8	3.0	785	10	BM404923
36	81.2	3.0	686	10	BI920482
37	81.2	3.0	692	10	BI920471
38	81.2	3.0	708	10	BI920408
39	80.8	3.0	541	10	BM178803
40	80.8	3.0	606	10	BM405792
41	79.8	2.9	663	10	BG890386
42	79	2.9	471	10	BF054511
43	78.8	2.9	555	9	AM737464
44	78.6	2.9	433	9	AM031596
45	78.4	2.9	396	10	BM409153

#### ALIGNMENTS

RESULT 1  
BI433950  
LOCUS  
DEFINITION  
PCBRK40 5' sequence, mRNA sequence.  
ACCESSION  
BI433950  
VERSION  
BI433950.1  
KEYWORDS  
EST.  
SOURCE  
potato.  
ORGANISM  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE  
1 (bases 1 to 663)  
Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Romling, C.M., Fry, W.E. and Baker, B.  
Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction  
Unpublished (2000)  
JOURNAL  
Contact: Cathy Romning  
The Institute for Genomic Research  
For clone info: please contact Research Genetics, Libraries  
Division tel 1-800-711-6195, email cdna@resgen.com  
Seq primer: MJ3F-R.

FEATURES  
source  
Location/Qualifiers  
1..663  
/organism="Solanum tuberosum"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="PCBRK40"  
/clone\_lib="P. infestans-challenged leaf"  
/tissue\_type="leaf"  
/dev\_stage="6 week old"  
/lab\_host="SOLR"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI; Whole plants were challenged with 450,000 sporangia/ml P. infestans US-1 (DS 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed



LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES															
BI406780	180E06 Mature tuber lambda ZAP Solanum tuberosum	BI406780	BI406780	EST.	potato.	Solanum tuberosum	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.	Nielsen, K.L., Crookshanks, M., Emmersen, J. and Wellinder, K.G.	EST-sequencing of mature potato tuber (Var. Kuras)	Unpublished (2000)	Contact: Karen G. Wellinder Institute for bioteknologi Aalborg University Sohnsgaardsholmsvej 49, 9000 Aalborg, Denmark Tel: +45 96358467 Fax: +45 98141808 Email: kgw@bio.auc.dk Sequenced from the 5' end. High quality sequence stop: 691 POLYA-No.																
2249	tttcagatgcaaaagcttttcacgaacagctcaagaagttgaagttggaagaactatc	120	tttccattgtgtgggtctttccaccgaactgaagaagctgacatttcaaggaactatc	2309	taagctggtcactactgagacatcagatgctgagttgctcaaccttgagtgctgaagctga	180	ttattatgctgacgaacatcgacacattatgacaaagttgacaaagctgacgaagctgac	2369	tgagatgagcgtgtgtgtgtgaaga-----tgccatccaattgttatgtg	240	aaataattttaaagttgtttgctgattgagccttgagaaactgcccgggaagatcagaatg	2414	gatttaacatgattgaagctttgctcaaatataatagttttctcaagttctgaaagcca	300	gatttttcgatttgaattttttgcttcattatgagagagatgagatttttaattcttgaaagc	2474	caaatgacaaatttctgtccttgagcgagcctcatgattgaagttgcaaaaatttgaag	360	ccaaagatttctttcccatgctttgagcggcgttatttataaaaacgtgtgttcttcgaag	2534	agataccaattgagtttgcagataatacacacactacagcttgattgagttgaagagtgct	420	aaatttcctttaaagattttgacagattatgacactaaacgaatttgaattgagtgatgta	2594	ctcccaaaacttggaattctgtctcaagattcagaagaataaaagaagaagccctcggaaga	480	cttcttcttcttctgatttctgctaaagagatccaaagacgaagagagactttgggaaaca

OY	2654	accctgtgagtttcgatctccaatccattgaaga	2690
Dd	540	ACATACTCCTCAAGTTTATGCGCTATGCACAAATTAGACA	576
RESULT	4		
LOCUS	AM979731	635 bp	mRNA linear EST 18-MAY-2001
DEFINITION	EST341354 tomato root deficiency esculentum cDNA clone CLEW8H19 5' , mRNA sequence.		
ACCESSION	AM979731		
VERSION	AM979731.1	GI:8171253	
KEYWORDS	EST.		
SOURCE	tomato.		
ORGANISM	Lycopersicon esculentum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;		
	Lycopersicon.		
	1 (bases 1 to 635)		
REFERENCE	van der Hoeven,R.S., Garvin,D.F., Mattern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T.S., Rinning,C.M., Craven,M.B., Bowman,C.L., Nieman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.		
AUTHORS	Generation of ESTs from tomato nutrient-deficient roots unpublished (1999)		
TITLE	Contact: CUGI		
JOURNAL	Clemson University Genomics Institute		
COMMENT	Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html		
FEATURES	5 prime sequence.		
source	Location/Qualifiers		
	1..635		
	/organism="Lycopersicon esculentum"		
	/cultivar="TA96"		
	/db_xref="taxon:4081"		
	/clone="CLEW8H19"		
	/clone_lib="tomato root deficiency, Cornell University"		
	/tissue.type="roots"		
	/dev_stage="5-6 weeks old"		
	/note="vector: pluviuscript SK-; Site_1: 5' EcoRI; Site_2: 3' XhoI; supplier: Tanksley; tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850). Roots were harvested from plants grown under the following deficiencies/stresses: 10 mM Al, Zn, P, K, Fe, N), and mRNA was isolated from individual treatments. Proportional aliquots of mRNA of each treatment were mixed and used for library construction."		
BASE COUNT	200 a 99 g 163 g 173 t		
ORIGIN			
Query Match	5.0%; Score 135.2; DB 9; Length 635;		
Best Local Similarity	54.7%; Pred. No. 6.3e-21;		
Matches 338; Conservative	0; Mismatches 268; Indels 12; Gaps 3;		
OY	452	ataatgttgacgtagtatgatacaagaagaacagtgttgaagaatcgtactagaacctact	511
Dd	30	ATAATGTGGGTTTTGGAGTAGACATRAGAANAATSTTTTCAGTATGTGATTGAGG--TA	86
OY	512	ctggaggaaaccaagaatcatcccgattgtcggatgtagagcatagtaagtaaacacctag	571
Dd	87	CAAATGATCTACACGTTTGCCCATTTGTAGAGCATGGGTGACAAAGGAAGAACAGACGTTG	146
OY	572	caaaaagaattacaaatgatgaatcaatctatgcgcttttgatgttcaatgcctgagcta	631
Dd	147	CTAAGAAAGGTCTACACATAGTGACAACATGTTTTCATTTGATGATGCTGTGAGAGATGCTCA	206
OY	632	cgaatctcaacaagacacaaaaaaggaaattgtctggagccttcgtatccacaatatca	691
Dd	207	TGCTTTCCAAACATATACCGGAGAAAGACTATTTCAGAGACATTTTGTAGTCAAGTTACC-	265





QY	1333	gagaagcttttcacagagctctgtcgatgatgattgcagcttcctgtctgaagcagaaggaattcga	1392
	470	-----ATTGTATGAGAGACTCTTTTGTAGCAGAGATCTCGGTATATGCTTTAGAAACAGGAGCTTTT	525
QY	1393	gatggaacaaaatatagatcattgaaggttctatgatctaatatataatgatgacctgtgcgtgaga	1452
Db	526	AATGC---CGAGACACAAAACATGCTGCTGTCATGATCGATTCGATTCGTATTTAATAAGA	582
QY	1453	gaagttcaagagagaga	1469
Db	583	AGAGCCGAGAAAGAGAA	599
RESULT	8		
LOCUS	BE923412	426 bp	RNA linear EST 02-OCT-2000
DEFINITION	EST427181 potato leaves and petioles Solanum tuberosum cDNA clone		
ACCESSION	BE923412		
VERSION	BE923412.1	GI:10449488	
KEYWORDS	EST.		
SOURCE	potato.		
ORGANISM	Solanum tuberosum		
REFERENCE	1		
AUTHORS	van der Hoeven,R.S., Bezzerides,J., Holt,I.E., Liang,F., Cho,J., uterback,T., Hansen,C.L., Doan,B., Bougri,O., Buehl,C.R., Ronning ,C.M., Fry,W.E., Tanksley,S.D. and Baker,B.		
TITLE	Generation of ESTs from potato leaves and petioles		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Cathy Ronning The Institute for Genomic Research For clone request: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdnaresgen.com.		
FEATURES	source		
	1..426		
	/organism="Solanum tuberosum"		
	/cultivar="Kennedec"		
	/db_xref="taxon:4113"		
	/clone="cSTB24L4"		
	/clone_1lb="potato leaves and petioles"		
	/tissue_type="leaflets and petioles"		
	/dev_stage="8 weeks old plants"		
	/lab_host="SOLR"		
	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Tissue was supplied by Dr. Fry (Cornell University) leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."		
BASE COUNT	130 a 76 c 102 g 118 t		
ORIGIN			
Query Match	4.4%; Score 120.4; DB 10; Length 426;		
Best Local Similarity	58.5%; Pred. No. 1.7e-17;		
Matches	261; Conservative 0; Mismatches 161; Indels 24; Gaps 2.		
QY	514	ggggaacccaagatccagatctcggatgaggagcatagttaaacacacttagca	573
Db	1	GGGGACACTAGAGAACTGTCTCAATCGTAGGAGATGGAGCAACGCGGAAACAACACTTTGGCT	60
QY	574	aaagaagttcaatgatgatcaatcattatgacgtttgatgtcattgcgctggctacc	633
Db	61	ACAATCTCTATAGATCTGTGCATTTATGTCTCATTTGATATTCGTCCAAAACCAACT	120
QY	634	atatctcaacagcaacaacaaaagaatttgcgcggcgctctgcattccacaatcaaa	693
Db	121	GTTCACAAAGATATTGTGTGGAATATGATACCCAAAGCGCTTCTTTTGACAACTAT	180
QY	694	atgatgcagggttaagatgatgttggtaagcagagctagacagatglttacagaaagt	753

Db	181	GAACTGATA-----ATCAGCTACGCGACCGACTGCAAAACCAT	219
OY	754	ttaaagagaaggtacttaatttcttgatgatgatcctggagtggaagtgaggat	813
Db	220	CtGAAAGCAGAGACTTGGTACTGATTCATGTATGACATATGACATACAGAAAGCTTGGAT	279
OY	814	ggcgtgagacgtatgcttccaacctgaagacaatgcagggagtcgaatactgttcacc	873
Db	280	GATATATAAACTATGTTTCCCA---GACGTATATATGACAGACAGATATCTCTGACTACT	336
OY	874	cgtaatgtgaagtagctgtgtatgctgcggtgtagaacatttcttcgcgatgacctc	933
Db	337	CGGATGTGGAAAGTGGCGAATATCTGTTCAGGTAAAGCTCTCATACATGCGCCTC	396
OY	934	atgagtcagatgagagcttgagctc	959
Db	397	ATGAATTTTTCACGAAAGTTGGAATTT	422
RESULT	9		
LOCUS	A0367206	701 bp	DNA linear GSS 07-MAR-2000
DEFINITION	tox00002A12r CUG1 Tomato BAC library Lycopersicon esculentum		
ACCESSION	A0367206		
VERSION	A0367206.1	GI:4221674	
KEYWORDS	GSS.		
SOURCE	tomato.		
ORGANISM	Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Asterales; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 701) Budimun,M.A., Mao,L., Wood,T.C. and Wing,R.A. A deep-coverage tomato BAC library and prospects toward development of an STC framework for genome sequencing Genome Res. 10 (1), 129-136 (2000) 201113122 Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: twing@clemson.edu Seq primer: GGAACACGTCATGACCATG Class: BAC ends High quality sequence stop: 387. Location/Qualifiers 1..701 /organism="Lycopersicon esculentum" /cultivar="Heinz 1706" /db_xref="taxon:4081" /clone="tox00002A12r" /clone_1id="CUG1 Tomato BAC library" /tissue-type="Nuclei preparation from leaf" /lab_host="E. coli DH10b" /note="Vector: pReloBAC 11. Site_1: HindIII, Site_2: HindIII; Tomato is a vegetable crop that ranks second only to potatoes in value and importance. Among plant geneticists and physiologists, tomato represents an ideal dicot model beside Arabidopsis and monocot rice to derive genomic information from. To facilitate the genome analysis of tomato, we have constructed a tomato BAC library that is suitable for positional cloning, physical mapping, and genome sequencing. The library contains 129 000 clones and a random sampling of 498 clones indicated an average insert size of 117.5 kb. With 15x haploid genome equivalents (1C equals 953 Mb) (Arumuganathan and Earle, 1991), the probability to recover any particular sequence is greater than 98%. High stability, large insert		



and ease in manipulation make BAC libraries the choice for genome sequencing. Pre characterization of a few hundred bases of insert ends will make BAC clones extremely useful for rapid contig assembly (Venter, Smith, and Hood, 1996). Here we present the construction, characterization of the tomato BAC library, and preliminary analysis of the 1536 tomato BAC end sequences."

BASE COUNT 214 a 101 c 182 g 204 t  
ORIGIN

Query Match 4.4%; Score 119.6; DB 12; Length 701;  
Best Local Similarity 53.6%; Pred. No. 2.8e-17;  
Matches 295; Conservative 0; Mismatches 249; Indels 6; Gaps 2;

Qy 759 gagaaagaggaactaattgtcttgatgatactgaggttgtaagtgatgagtgatg 818  
Db 4 GGGCAAGAGATATCATCTTGTGATGATATGTTGATGATGATGATGATGATGATG 63  
Qy 819 gagaagatgcttccactgaagacatgcaagagagtcgaactgttgaactaccgtaa 878  
Db 64 AAGGTTCTCTTCCAGATTCGGAAATGAGAGCA---GAATAGTAGTACACATCGACT 120  
Qy 879 tgatgaagtagctgttattgtgtgtgtagaattttcttgcgagatgagcttcagta 938  
Db 121 TGAGAAAGTGGCGCAAGATCAAGTGCATATCTGATCTTCTCTCCGTTCTCTCAC 180  
Qy 939 tcaagatgagagtgtagaattcttcaaaagtgcagcatttcaagtgagaccata 998  
Db 181 AAAAGAAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
Qy 999 tgaagtcgagagctgttgaagaaagacatgcaagatgtagatgtagcaggtaccatact 1058  
Db 241 TGAAGTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
Qy 1059 tgcgtgtgtcgaaggtcttcaaatctaaagagcaatagagattggaagactgttc 1118  
Db 301 TGTCTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
Qy 1119 taaagatgcaagatcattctgcacaaa---tgatcctgtagaagatgtagcaggtct 1175  
Db 361 GAAAGATCTTATTTGACACCTTATATGTCGAGTGAAGAAATATATCTTTCACTAT 420  
Qy 1176 tgggttgtagatgacatcctgtagaagacatgcaagacatgcttccatctgagat 1235  
Db 421 GCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
Qy 1236 tttccagaagacagtgatattccagtgagaagattgtagatcattgtagtgatg 1295  
Db 481 GTTTCAGAGAGATGCAATTAATTCGATGATGATGATGATGATGATGATGATG 540  
Qy 1296 gtctcgtgaag 1305  
Db 541 GATTTGTGAG 550

RESULT 10  
BI934083 515 bp mRNA linear EST 18-OCT-2001  
LOCUS  
DEFINITION EST353972 tomato flower, anthesis Lycopersicon esculentum cDNA  
clone cTOD18D10 5' end, mRNA sequence.  
ACCESSION BI934083  
VERSION BI934083.1 GI:16248555  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanales; Solanales; Solanum;  
Lycopersicon.  
1 (bases 1 to 515)  
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, T.,  
Uetcker, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M.,

TITLE Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.  
JOURNAL Generation of ESTs from tomato flower tissue, anthesis (2001)  
COMMENT Unpublished (2001)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
This clone is available through the Clemson University Genomics  
Institute  
Seq primer: 73.

## FEATURES

## source

Location/Qualifiers

1..515

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="cTOD18D10"

/clone\_11b="tomato flower, anthesis"

/tissue\_type="flower"

/dev\_stage="anthesis"

/note="vector: p Bluescript SK(-); Site\_1: EcoRI; Site\_2:

XhoI; supplier: Cornell University; sequencing: The

Institute for Genomic Research; Flower buds and flowers

were taken from greenhouse plants (4-8 wks old, TA496).

They were immediately frozen in liquid nitrogen and then

size-separated while remaining frozen."

BASE COUNT 157 a 77 c 121 g 160 t  
ORIGIN

Query Match 4.3%; Score 118; DB 10; Length 515;  
Best Local Similarity 58.7%; Pred. No. 6.3e-17;  
Matches 262; Conservative 0; Mismatches 175; Indels 9; Gaps 3;

Qy 859 atactgtgactaccogtaatgtagaagtagctgttattgtcgtgtgtagaagattttct 918  
Db 1 ATTATTTGAGCTAGTAGAGCAAGAGAGTGTCTAGTCAATGATGATGATGATGATG 60  
Qy 919 ttgcgagtagagcttcatgtagatgtagagtagagtagcttcaaaagtgcagcatt 978  
Db 61 CATAAATGAACTCTTAACTTGAATATGATGATGATGATGATGATGATGATGATG 120  
Qy 979 tcaagtgaa---gcatcacaatagtagctgtagagtagtggaagcaatgcagatgaa 1035  
Db 121 GGGGTGAGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
Qy 1036 tgtcaggggttaccactaactattgtcgtgttgtagaggtcttc---aatctaaagg 1092  
Db 181 TGCCAAGAGACTGCTTGTAGCTTGTAGGTAGCGGGGACATCTCTCTAAATTTCTAGA 240  
Qy 1093 acaatagaagattggaagaaactgttgcataaagatgtagcatttgcataaagattct 1152  
Db 241 ACACGAGAAAGTTGAGACAGATGTTCCAAAAGTGAATGAATGATGATGATGATGATG 300  
Qy 1153 gatgaagatgtagcagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtag 1212  
Db 301 GAT---ATATGCTAGAGAGTGTCTGCTATGATGATGATGATGATGATGATGATG 357  
Qy 1213 acatgtctctgtagcatttgcgaattttccagaagacagtgatattccagtgagaatttg 1272  
Db 358 CCATGTTTCTTACATGAGAGTGTCTTCCGAAAGACAGTGTGTTAACATGTTGATGATG 417  
Qy 1273 atgagatcatgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtagtgtag 1298  
Db 418 ATCAACTTATGAGATTTCTGAGGGTTT 443

RESULT 11  
BH142383 639 bp DNA linear GSS 16-AUG-2001  
LOCUS  
DEFINITION T06D021TH cT0G Lycopersicon esculentum genomic clone cT0624C17, DNA  
sequence.  
ACCESSION BH142383



Db	586	CACGCTGGGAACCTAGCATTTGTGGAAAAGATGATGAAGAAGATCTAAGAAACCAOACT	527
OY	744	acagaagaatttaagagaagaaggacttaattgtcttcttgatgatcatcgtgaatttgya	803
Db	526	TGCGTATCTATTTTGAAAAGAACGCCAATACTTGTTGTGTGGTTGATGTCTGCACAAGAGA	467
OY	804	agtgtggatgtagcgtagagaccgttgttcaccaactbaagaacaatlgaagggaafgcgaatact	863
Db	466	AGCATTGGGAGATTTGAAAAAGACATTCGCCGGATACAAAGAAAT---GGACGAGAGTCAT	410
OY	864	gttgacctaccgctaagatgaagtagctgtgtatgtctgtgtgaagaaattttctcttgcg	923
Db	409	TATTATCCAGCGCCCAAGAGGATATCGCTGTAAGAGACGCCGACAGATGTTTTGTTTCATTA	350
OY	924	gatgagcttcatalygalcaagaalysagagtttggatcctttccaagaatlycagaatlttcaa	983
Db	349	ACTTGTTGCCAATCTTAAGAAAGAAAGATTTGGAGTCTTTCTTAGAAACACTACTGANGT	290
OY	984	tgaagcattaccatatgttgagttcgtgagacgttlygaaagcaaatccgaagatgaatlytcaag	1043
Db	289	TCGACCATATGTTCGACGAATATGGAAGAAAGTCCTACTAAGGATATGATGTGAAGAG	230
OY	1044	gttaccactaacattgttcgttgcgttgcaggggttctccaatcataaagaagacataaga	1103
Db	229	TTTACTCTTGCAATGTGTGTATTAGGCGAATCTTTGCGCTATAAAGAGACTTGATGA	170
OY	1104	ttggaanaactgttgcataagaatlytcaagtlcatctgtlccaaaatlyatcctatgaagcagy	1163
Db	169	ATGGCAAAAAGGTGAAGAATCACCTTTGGAGAAGCACTTAAGAAAGATTAATCTGTGAAT	110
OY	1164	ttcaagtgctgtcgttgatgtgaatgacatcttgccaagcgatcctaaaaactgtctct	1223
Db	109	CTCCACATACTATCACTTAAGCTTAACAATGATTTGTCAATGTGACTCAAGCACTGTTTCT	50
OY	1224	gcatttcggaattttccagaagacagty	1252
Db	49	CTACTTTGGTATGTTTCCAGAAGATCGAG	21
RESULT	13		
LOCUS	BM408141	756 bp	mRNA linear EST 22-JAN-2002
DEFINITION	ESR582468 potato roots Solanum tuberosum cDNA clone CPRO33GZ0 5'		
ACCESSION	BM408141		
VERSION	BM408141.1		
KEYWORDS	EST.		
SOURCE	potato.		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterides I; Solanales; Solanaceae; Solanum.		
AUTHORS	van der Hoeven R., Sun H., Karanycheva S.A., Tsai J., Van Aken S., Utecherack T., Chiemingo A., Bougri O., Buell C.R., Konning C., Tanksley S. and Baker B.		
JOURNAL	Generation of ESTs from potato roots		
COMMENT	Unpublished (2001)		
	Contact: Research Genetics, Libraries Division		
	Tel.: 1-800-711-6195		
	Email: cdna@resgen.com		
	For clone info: Please contact Research Genetics, Libraries		
	Division tel 1-800-711-6195, email cdna@resgen.com		
	Seq primer: T3.		
FEATURES	Location/Qualifiers		
Source	1..756		
	/organism="Solanum tuberosum"		
	/cultivar="Kennebec"		
	/db_xref="taxon:4113"		
	/clone="CPRO33GZ0"		
	/clone_lib="potato roots"		
	/tissue_type="roots"		
	/dev_stage="in vitro grown stem cuttings"		

/lab.host="SQR"  
 /note="vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
 XhoI; supplier: Cornell University, Tanksley lab;  
 sequencing: The Institute for Genomic Research. Roots were  
 isolated from in vitro grown stem cuttings on CM medium.  
 Roots were isolated two weeks after placing the stem  
 cuttings from in vitro grown plants on medium."

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211	Indels 0	Gaps 0
BASE COUNT	229 a	150 c	166 g	211 t
ORIGIN				

Query Match 4.0% Score 108.4; DB 10; Length 756;  
 Best Local Similarity 52.7%; Pred. No. 1.1e-14;  
 Matches 235; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

Query Match	4.0%	Score 108.4	DB 10	Length 756
Best Local Similarity	52.7%	Pred. No. 1.1e-14		
Matches 235	Conservative 0	Mismatches 211		



Thu Sep 12 15:30:10 2002

us-09-864-680-4.rst

Page 11



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2002, 11:42:09 : Search time 881.41 Seconds  
(without alignments)  
6036.598 Million cell updates/sec

Title: US-09-864-680-2  
Perfect score: 3099  
Sequence: 1 caaatattcttgagtgaa.....tttagtttaaaaaaaaaa 3099

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

N.Geneseq\_032802.\*  
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3099	100.0	3099	22	AAD10204	Pepper Bs2 CDNA.
2	3099	100.0	3099	22	AAF63302	Pepper Bs2 CDNA se
3	2725.6	88.0	31491	22	AAD10203	Pepper Bs2 gene.
4	2725.6	88.0	31491	22	AAF63301	Pepper Bs2 resista
5	2718	87.7	2718	22	AAF63303	Pepper Bs2 open re
6	272.8	8.8	2739	21	AAZ50262	Coding region of p
7	272.8	8.8	2817	21	AAZ50652	Coding region of p
8	272.8	8.8	3683	22	AAZ50713	DNA encoding Rx 25
9	272.8	8.8	10529	22	AAZ50264	Genomic DNA of pot

10	272.8	8.8	10329	21	AAZ50653	Genomic DNA encodi
11	271.8	8.8	5820	20	AAZ37153	DNA sequence of BA
12	269.6	8.7	3066	20	AAZ37154	Partial nucleotide
13	268	8.6	3014	22	AAZ503715	DNA encoding Rx 72
14	266.4	8.6	2880	22	AAZ503717	DNA encoding Rx 19
15	266	8.6	2885	22	AAZ503719	DNA encoding Rx 32
16	264.8	8.5	3283	22	AAZ503716	DNA encoding Rx 39
17	256.8	8.3	2679	22	AAZ503718	DNA encoding Rx 7,
18	172.2	5.6	5475	19	AAZ17777	Tomato Prf CDNA.
19	170	5.5	10968	19	AAZ17789	Tomato Prf genomic
20	149.2	4.8	3997	19	AAZ26082	Tomato pest resist
21	149.2	4.8	9870	19	AAZ13935	Tomato Mi resistan
22	149.2	4.8	9870	19	AAZ16457	Wild tomato Mi res
23	149.2	4.8	51952	19	AAZ26084	Tomato pest resist
24	147.6	4.8	3982	19	AAZ26083	Tomato pest resist
25	132.2	4.3	23670	24	ABA97077	Tomato Hero gene c
26	119	3.8	3909	24	ABA97078	Tomato Hero gene A
27	103.4	3.3	534	21	AAZ51885	N. tabacum Class I
28	95.2	3.1	540	21	AAZ51891	N. tabacum Class I
29	94.4	3.0	3801	21	AAZ59332	Nucleotide sequenc
30	94.4	3.0	6558	18	AAZ79882	Tomato immunity 2
31	92.2	3.0	532	21	AAZ51889	N. tabacum Class I
32	88.8	2.9	517	21	AAZ51884	N. tabacum Class I
33	83.6	2.7	4465	17	AAZ42135	I2C-2 gene encodin
34	81.4	2.6	477	21	AAZ51880	N. tabacum Enh8 ge
35	76	2.5	472	21	AAZ51876	N. tabacum Enh4 ge
36	74	2.4	644	21	AAZ51886	N. tabacum Class I
37	72.2	2.3	2862	21	AAZ58295	Sorghum resistance
38	70.4	2.3	647	21	AAZ58299	Rice disease resist
39	66.6	2.1	469	21	AAZ51874	N. tabacum Enh2 ge
40	62.8	2.0	1028	21	AAZ59996	Rice disease resist
41	59.2	1.9	2954	21	AAZ58294	Sorghum resistance
42	59.2	1.9	6760	21	AAZ58293	Sorghum resistance
43	56	1.8	4948	17	AAZ42134	I2C-1 gene encodin
44	50.4	1.6	5910	19	AAZ6798	Rice bacterial lea
45	48.2	1.6	548	21	AAA40001	Rice disease resis

## ALIGNMENTS

RESULT 1	
ID	AAD10204 standard; cDNA; 3099 BP.
XX	AAD10204;
AC	AAD10204;
XX	
XX	24-SEP-2001 (first entry)
DT	
XX	
DE	Pepper Bs2 CDNA.
XX	
KW	Bs2 gene; pepper; resistance gene; plant pathogen; virulence gene;
KW	bacterial spot disease; Xanthomonas campestris pv. vesicatoria;
KW	AvrBs2; hypersensitive response; transgenic plant; tomato; tobacco;
KW	rice; corn; wheat; ss.
XX	
OS	Capiscum annuum.
XX	
EH	
FT	Key
FT	CDS
FT	
FT	Location/Qualifiers
FT	93..2810
FT	/*tag- a
FT	/product= "Bs2 protein"
FT	/note= "this region is claimed as SEQ ID NO:4
FT	In Claim 7"
XX	
XX	US6262343-B1.
PN	
XX	
PD	17-JUL-2001.
XX	
PF	23-JUL-1999;
XX	99US-0360186.
XX	
PR	23-JUL-1998;
XX	98US-0093957.

PA (REGC ) UNIV CALIFORNIA.  
 XX Staskawicz BJ, Dahlbeck D, Tai TH;  
 PI  
 XX WPI: 2001-450496/48.  
 DR P-PSDB: AAE05409.  
 XX  
 XX Nucleic acid molecules encoding Bs2 protein, useful for producing  
 PT transgenic plants having resistance to the plant pathogen *Xanthomonas*  
 PT *campestris* -  
 XX  
 XX Claim 7: Column 49-56; 37pp; English.  
 CC The present sequence is Bs2 cDNA from pepper. The Bs2 gene is shown  
 CC to confer resistance to plant pathogen  
 CC *Xanthomonas campestris* pv. *vesicatoria* which causes bacterial spot  
 CC disease. The Bs2 protein has Bs2 biological activity, i.e., when  
 CC co-expressed in a plant with a *X. campestris* AvrBs2 gene product,  
 CC it produces a localised hypersensitive response. The protein  
 CC includes a nucleotide binding motif and leucine rich repeats of the  
 CC type found in other plant resistance genes. The Bs2 nucleic acid  
 CC molecule is useful for producing transgenic plants such as pepper,  
 CC tomato, tobacco, broccoli, cauliflower, cabbage, grape, canola,  
 CC bean, soybean, rice, corn, wheat, barley, citrus, cotton, cassava and  
 CC walnut, that are resistant to plant pathogen *Xanthomonas campestris*.  
 CC The transgenic plants produced using Bs2 molecule develop a  
 CC hypersensitive response to the pathogen at the site of inoculation and  
 CC show an enhanced resistance to systemic infection. The Bs2 nucleic acid  
 CC molecule is also useful as polymerase chain reaction (PCR) primers for  
 CC amplifying portions of Bs2 nucleic acid molecule, as sequencing primers  
 CC to verify the authenticity of an amplified molecule, and as  
 CC hybridisation probes.  
 XX  
 XX Sequence 3099 BP: 970 A; 514 C; 693 G; 922 T; 0 other;  
 SQ

Query Match 100.0%; Score 3099; DB 22; Length 3099;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caaataattcttgagtgtaatttgaaagtgtatattcttcgcaattggaagtgtgctacag 60  
 Db 1 caaataattcttgagtgtaatttgaaagtgtatattcttcgcaattggaagtgtgctacag 60  
 QY 61 tcgcaaaagacaaaacagaaatacagatatataatgctcagcaagtggtgctctctcta 120  
 Db 61 tcgcaaaagacaaaacagaaatacagatatataatgctcagcaagtggtgctctctcta 120  
 QY 121 tgaagacaatagatctctcttgacatccaattcgcgagtgcaatctctatctctgtagtc 180  
 Db 121 tgaagacaatagatctctcttgacatccaattcgcgagtgcaatctctatctctgtagtc 180  
 QY 181 acagagaagaactttggcgtctctgtgaaaaagttaagttcccttggaatattttcaaga 240  
 Db 181 acagagaagaactttggcgtctctgtgaaaaagttaagttcccttggaatattttcaaga 240  
 QY 241 actttgagaanaacatgttttttggaatagacgagattttgaagtgaaggtaagaagaag 300  
 Db 241 actttgagaanaacatgttttttggaatagacgagattttgaagtgaaggtaagaagaag 300  
 QY 301 ttgcaagtgctgtcgaataacacatccaactgagagactaacaaggaaactgtactgggagaa 360  
 Db 301 ttgcaagtgctgtcgaataacacatccaactgagagactaacaaggaaactgtactgggagaa 360  
 QY 361 ataaagccagaanaaaagcgctcgaaagtttcgtcaaaagccttgcaacaagttagagag 420  
 Db 361 ataaagccagaanaaaagcgctcgaaagtttcgtcaaaagccttgcaacaagttagagagag 420  
 QY 421 aggaacttgatcatactctggaagaagtcgacaagaatccaagaataaagaaacaagtat 480  
 Db 421 aggaacttgatcatactctggaagaagtcgacaagaatccaagaataaagaaacaagtat 480  
 QY 481 caaagaatcatctgttcatgatttttcaagttcaacaagaatattttgaagtgaaga 540

Db 481 caaagaatcatctgttcatgatttttcaagttcaacaagaatattttgaagtgaaga 540  
 QY 541 acaatatggttgagcgtgatgatacaagaaacagtggttagaagatctgataagact 600  
 Db 541 acaatatggttgagcgtgatgatacaagaaacagtggttagaagatctgataagact 600  
 QY 601 actctgggaacccaagacatcccgatttgggatgggagagcctaagtaaacacact 660  
 Db 601 actctgggaacccaagacatcccgatttgggatgggagagcctaagtaaacacact 660  
 QY 661 tagcaaaagaagtttaacaatgataatctatctgacgttttgatgtttacgtcctggg 720  
 Db 661 tagcaaaagaagtttaacaatgataatctatctgacgttttgatgtttacgtcctggg 720  
 QY 721 ctacacatctcaacagcacaacaaaagaatttctgtggccttcgcattccacaa 780  
 Db 721 ctacacatctcaacagcacaacaaaagaatttctgtggccttcgcattccacaa 780  
 QY 781 tcaaatgtgatgacaggttaagatgttggaagcagaagctagaacacatgtacaga 840  
 Db 781 tcaaatgtgatgacaggttaagatgttggaagcagaagctagaacacatgtacaga 840  
 QY 841 aaagttaagaagaagaaggaacttaattgtcttgatgatactcgagtgtagaagtg 900  
 Db 841 aaagttaagaagaagaaggaacttaattgtcttgatgatactcgagtgtagaagtg 900  
 QY 901 ggaatggcgtgaacacatgcttccacacgaagacaaatcgagaggtcgaaactgtga 960  
 Db 901 ggaatggcgtgaacacatgcttccacacgaagacaaatcgagaggtcgaaactgtga 960  
 QY 961 ctacccgtaatgtatgaagtagctgtttagctgtgtgtatagaagaattttcttgcgatga 1020  
 Db 961 ctacccgtaatgtatgaagtagctgtttagctgtgtgtatagaagaattttcttgcgatga 1020  
 QY 1021 gcttcatggtatcaagaatgagtgagtggtcttcaaaagtgacagatttcaagtgaag 1080  
 Db 1021 gcttcatggtatcaagaatgagtgagtggtcttcaaaagtgacagatttcaagtgaag 1080  
 QY 1081 cattaccatagtgttcgaagactgttggaaggaacacgcagatgtagatcgaggttac 1140  
 Db 1081 cattaccatagtgttcgaagactgttggaaggaacacgcagatgtagatcgaggttac 1140  
 QY 1141 caactaactatgtctgtgtgttcgaaggtctcacaactcaaaagacaaatagaagattga 1200  
 Db 1141 caactaactatgtctgtgtgttcgaaggtctcacaactcaaaagacaaatagaagattga 1200  
 QY 1201 aaactgtgttaagaatgtgcaagttcatctgtcaacaatgatactctgaagatgttcac 1260  
 Db 1201 aaactgtgtgttaagaatgtgcaagttcatctgtcaacaatgatactctgaagatgttcac 1260  
 QY 1261 gttgtcttggtgtgagttacgacttgaacgagcctaataaacaatgtcttcgcat 1320  
 Db 1261 gttgtcttggtgtgagttacgacttgaacgagcctaataaacaatgtcttcgcat 1320  
 QY 1321 tcggaatttttccaagaagaagtgatattccagtgaagaatttgaagatccctgtgaag 1380  
 Db 1321 tcggaatttttccaagaagaagtgatattccagtgaagaatttgaagatccctgtgaag 1380  
 QY 1381 ctgaggggtccctgaagttggaanaatgatttgaagaagaaggttggaaggtgtttcgaag 1440  
 Db 1381 ctgaggggtccctgaagttggaanaatgatttgaagaagaaggttggaaggtgtttcgaag 1440  
 QY 1441 agctgtcgatagatgtctagtcctctgcagcaagaagaagtcgagatggaacaaatata 1500  
 Db 1441 agctgtcgatagatgtctagtcctctgcagcaagaagaagtcgagatggaacaaatata 1500  
 QY 1501 gatcatgtaaggttcaatgataatataatgactgtgcgtggaagaagttcaaaaggaga 1560  
 Db 1501 gatcatgtaaggttcaatgataatataatgactgtgcgtggaagaagttcaaaaggaga 1560  
 QY 1561 acattttatcatgaacgaatgttcttgacgtatcatatccagaagtctcatctct 1620



Db 1561 acattttatcatgaacagacatgttcttgacgtatcatatccagaatgtcatatctc 1620  
 QY 1621 gtatgtataaagcagcccttaagcggtgagctgtgtatgaatattatgtccct 1680  
 Db 1621 gtatgtataaagcagcccttaagcggtgagctgtgtatgaatattatgtccct 1680  
 QY 1681 atggtcttataaggtctctcttaccctgttaactcgttcagatgtgaagatcatgacaca 1740  
 Db 1681 atggtcttataaggtctctcttaccctgttaactcgttcagatgtgaagatcatgacaca 1740  
 QY 1741 acaactcttgaaagcaaccatctgttctctcttaccctgttgaagccttatatgt 1800  
 Db 1741 acaactcttgaaagcaaccatctgttctctcttaccctgttgaagccttatatgt 1800  
 QY 1801 ttctcaatcagaaggtgtgttcatcttcaaatctcaagcttgcagctgagacacagac 1860  
 Db 1801 ttctcaatcagaaggtgtgttcatcttcaaatctcaagcttgcagctgagacacagac 1860  
 QY 1861 agattgagttccctcgcagagataactaagcctcatctgttgaggtacctatctgt 1920  
 Db 1861 agattgagttccctcgcagagataactaagcctcatctgttgaggtacctatctgt 1920  
 QY 1921 tcaagctatgggaatttcagatgtacccctccagaatcttgcaagttatggaaatcagacat 1980  
 Db 1921 tcaagctatgggaatttcagatgtacccctccagaatcttgcaagttatggaaatcagacat 1980  
 QY 1981 tcaattgtcaaggttctgcagatataatattttgtcgtgaggaatttgggaactaa 2040  
 Db 1981 tcaattgtcaaggttctgcagatataatattttgtcgtgaggaatttgggaactaa 2040  
 QY 2041 ttgcaatgaagcactcttaaacctccagatcttatttgcagacttgcagactgagatct 2100  
 Db 2041 ttgcaatgaagcactcttaaacctccagatcttatttgcagacttgcagactgagatct 2100  
 QY 2101 ttgcaaaaggaagcacttgatcttcaaacacttacaactatcttactgtctccac 2160  
 Db 2101 ttgcaaaaggaagcacttgatcttcaaacacttacaactatcttactgtctccac 2160  
 QY 2161 gttgtgtcagaagaggttatattatgtgggaattcagaatgtcaaaaaattggaactagt 2220  
 Db 2161 gttgtgtcagaagaggttatattatgtgggaattcagaatgtcaaaaaattggaactagt 2220  
 QY 2221 gaaatagagtgactataaagttctcggagactgagctgtcccaaaaactgtgtcatc 2280  
 Db 2221 gaaatagagtgactataaagttctcggagactgagctgtcccaaaaactgtgtcatc 2280  
 QY 2281 tgcagcaacttgaataatagcttatactctgttgatataagccttttgcagtgatca 2340  
 Db 2281 tgcagcaacttgaataatagcttatactctgttgatataagccttttgcagtgatca 2340  
 QY 2341 ttccaagtgcaaaagcttttccagcaagcgtcagaagttgaaagtgtgaaagaactatc 2400  
 Db 2341 ttccaagtgcaaaagcttttccagcaagcgtcagaagttgaaagtgtgaaagaactatc 2400  
 QY 2401 taaagctgtatcacttggatcatatagctgtgagttgcttaaccttgcaggtgtcgaagtga 2460  
 Db 2401 taaagctgtatcacttggatcatatagctgtgagttgcttaaccttgcaggtgtcgaagtga 2460  
 QY 2461 tgaatgacgctgtgtgtgtgaaagaaatgcatcacaattgtatagtgatattacogattga 2520  
 Db 2461 tgaatgacgctgtgtgtgtgaaagaaatgcatcacaattgtatagtgatattacogattga 2520  
 QY 2521 agctttgtctaataatagtttctcgaagttctgaaagccacaacaatgtacatttc 2580  
 Db 2521 agctttgtctaataatagtttctcgaagttctgaaagccacaacaatgtacatttc 2580  
 QY 2581 ctgtccttgagcgcccatatattagaagttgcaaaaatttggaaagagatcccatgaagt 2640  
 Db 2581 ctgtccttgagcgcccatatattagaagttgcaaaaatttggaaagagatcccatgaagt 2640  
 QY 2641 ttgcaaatatacacactacagctgattgagttaaagagtttccctccaaaacttgggg 2700  
 Db 2641 ttgcaaatatacacactacagctgattgagttaaagagtttccctccaaaacttgggg 2700

QY 2701 aatctgtcagcagattccaagaacagaagacccctcgaaacacccctgtgatttc 2760  
 Db 2701 aatctgtcagcagattccaagaacagaagacccctcgaaacacccctgtgatttc 2760  
 QY 2761 gtatctcaatccatitgaagagagtgattcttgattcagaagaacattaggaagatct 2820  
 Db 2761 gtatctcaatccatitgaagagagtgattcttgattcagaagaacattaggaagatct 2820  
 QY 2821 caagggcagaagatgttaactcttgggatttcaatttcggcccttatcaaaaataccac 2880  
 Db 2821 caagggcagaagatgttaactcttgggatttcaatttcggcccttatcaaaaataccac 2880  
 QY 2881 taaattatcggttccaagcaatgtgtacttccaaagagagatgtatcttctgtgt 2940  
 Db 2881 taaattatcggttccaagcaatgtgtacttccaaagagagatgtatcttctgtgtgt 2940  
 QY 2941 aacatatttgaattgtactgattccctctctctctctctcttcttattgtacttacta 3000  
 Db 2941 aacatatttgaattgtactgattccctctctctctctctcttcttattgtacttacta 3000  
 QY 3001 attcaactcaagtaactagcagaccacatgtgtatgtgagttgagttgatttatt 3060  
 Db 3001 attcaactcaagtaactagcagaccacatgtgtatgtgagttgagttgatttatt 3060  
 QY 3061 tatacgaatgagacacacagtttattttaaanaaaaaa 3099  
 Db 3061 tatacgaatgagacacacagtttattttaaanaaaaaa 3099

RESULT 2  
 AAF63302  
 ID AAF63302 standard; cDNA; 3099 BP.  
 AC AAF63302;  
 DT 02-MAY-2001 (first entry)  
 DE Pepper Bs2 cDNA sequence.  
 DE Bs2; pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;  
 KW Xcv; bacterial spot disease; transgenic plant; crop; fruit; flower; ss.  
 OS Capsicum annuum.  
 PN WO200107635-A1.  
 PD 01-FEB-2001.  
 PF 23-DEC-1999; 99WO-US30891.  
 PR 23-JUL-1999; 99US-0360186.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Straskawicz BJ, Dahlbeck D, Tai TH;  
 PI WPI: 2001-168560/17.  
 DR P-PSDB; AAB72198.  
 XX Novel Bs2, polypeptide from Capsicum annuum for producing transgenic  
 PT plants having resistance to bacterial spot disease caused by  
 PT Xanthomonas campestris pv vesicatoria (Xcv) -  
 PS Claim 3; Page 57-61; 72pp; English.  
 CC This invention relates to the amino acid sequence of the Bs2 protein  
 CC isolated from Capsicum annuum (pepper). The protein and DNA sequences of  
 CC Bs2 can be used to confer resistance to the plant pathogen Xanthomonas  
 CC campestris pv vesicatoria (Xcv) which causes bacterial spot disease. Bs2  
 CC DNA and protein sequences are useful for producing transgenic plants such  
 CC as pepper, tomato, tobacco, broccoli, cauliflower, canola,  
 CC cowpea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton,

CC cassava and walnut, having resistance to *X. campestris*. The protein and  
CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
CC carnations and roses having resistance to *X. campestris*. The present  
CC sequence represents cDNA encoding Bs2.

XX Sequence 3099 BP; 970 A; 514 C; 693 G; 922 T; 0 other;

Query Match 100.0%; Score 3099; DB 22; Length 3099;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caaatattcttgagtggaatttggaattggaatttctgcaattgaattggttgatag 60  
DB 1 caaatattcttgagtggaatttggaattggaatttctgcaattgaattggttgatag 60  
QY 61 tcgcaaaagacaaaacagaaatacagatatatgctcatgcaagtggtgtctctta 120  
DB 61 tcgcaaaagacaaaacagaaatacagatatatgctcatgcaagtggtgtctctta 120  
QY 121 tagaacaataagatctctcttgacatcattcgccgagatctctatccctgtatc 180  
DB 121 tagaacaataagatctctcttgacatcattcgccgagatctctatccctgtatc 180  
QY 181 acagagaagaacttgcctctctctgtaaaaaagttagttccctggaagtattgtcaaga 240  
DB 181 acagagaagaacttgcctctctctgtaaaaaagttagttccctggaagtattgtcaaga 240  
QY 241 actttgagaanaaacaatgtttttggaagaatgacggaatttgaagtagaggtaagaag 300  
DB 241 actttgagaanaaacaatgtttttggaagaatgacggaatttgaagtagaggtaagaag 300  
QY 301 ttgcaagtcgtctgaataacacatcactgaagactaaggaacttacttggaagaa 360  
DB 301 ttgcaagtcgtctgaataacacatcactgaagactaaggaacttacttggaagaa 360  
QY 361 ataaagccagaaaaaaagagcgctcgaaaggtttcgtcaaaagcctggaacaagttagag 420  
DB 361 ataaagccagaaaaaaagagcgctcgaaaggtttcgtcaaaagcctggaacaagttagag 420  
QY 421 aggaacatgatactctggaagaagtcgcaacaagatccaagataaagaagaacaagrat 480  
DB 421 aggaacatgatactctggaagaagtcgcaacaagatccaagataaagaagaacaagrat 480  
QY 481 caaaggaatcatgtgttcaatgttttcaagttcaacaacagatattttgaagttaga 540  
DB 481 caaaggaatcatgtgttcaatgttttcaagttcaacaacagatattttgaagttaga 540  
QY 541 acaataatgttgagctgatacgaataaagaaacagttgttagaagatctgatagaagct 600  
DB 541 acaataatgttgagctgatacgaataaagaaacagttgttagaagatctgatagaagct 600  
QY 601 actctggggaacccaagtcatcccgatgttcggagatggagagcatagtaaaacaact 660  
DB 601 actctggggaacccaagtcatcccgatgttcggagatggagagcatagtaaaacaact 660  
QY 661 tagcaaaagaagttagaataatgaatcaattctatgacctttgaatttatcccttgg 720  
DB 661 tagcaaaagaagttagaataatgaatcaattctatgacctttgaatttatcccttgg 720  
QY 721 ctacacatactcaacagacacaaaagaagaatttctgctggcctcttgatccacaaga 780  
DB 721 ctacacatactcaacagacacaaaagaagaatttctgctggcctcttgatccacaaga 780  
QY 781 tcaaaaatgatacagaggttaagatgattggaagcagagctagcagacatgtttacaga 840  
DB 781 tcaaaaatgatacagaggttaagatgattggaagcagagctagcagacatgtttacaga 840  
QY 841 aaagttaagaagaagaaggtacttaattgtcttgatgatactcggaggttgtaaggt 900  
DB 841 aaagttaagaagaagaaggtacttaattgtcttgatgatactcggaggttgtaaggt 900

QY 901 gggatgagtgagacagatgcttccaaactgaagaacatgcaagagtcgaatactgtga 960  
DB 901 gggatgagtgagacagatgcttccaaactgaagaacatgcaagagtcgaatactgtga 960  
QY 961 ctaccctgaatgaagaagatgctgtatgctgtgtgtagaagaatttctcttgagaga 1020  
DB 961 ctaccctgaatgaagaagatgctgtatgctgtgtgtagaagaatttctcttgagaga 1020  
QY 1021 gcttcaatgataagaatggaagttgagagttcttcaaaagttagacatttcaagtgaa 1080  
DB 1021 gcttcaatgataagaatggaagttgagagttcttcaaaagttagacatttcaagtgaa 1080  
QY 1081 catcacacataatgattcgaagaactgttgaagaagcaaaatcgagaatgatacgaggttac 1140  
DB 1081 catcacacataatgattcgaagaactgttgaagaagcaaaatcgagaatgatacgaggttac 1140  
QY 1141 caactaactatgtcgtgtgtgcaaggtcttcaaaactaaagaagaatagaagattgga 1200  
DB 1141 caactaactatgtcgtgtgtgcaaggtcttcaaaactaaagaagaatagaagattgga 1200  
QY 1201 aaactgtgtcgaagaatgataagttcgaatcgttcaaaatgatacgaatgatacga 1260  
DB 1201 aaactgtgtcgaagaatgataagttcgaatcgttcaaaatgatacgaatgatacga 1260  
QY 1261 gttgtcttggtgtgagttacagatcacttgaacaagcgaactaaacaatgcttctgcat 1320  
DB 1261 gttgtcttggtgtgagttacagatcacttgaacaagcgaactaaacaatgcttctgcat 1320  
QY 1321 tcggaatcttccagaagaagaatgataatccaaatgagaatttgaatgataatgata 1380  
DB 1321 tcggaatcttccagaagaagaatgataatccaaatgagaatttgaatgataatgata 1380  
QY 1381 ctgaggggttcctcgaagttggaagaatgattggaagaaggttgaagaagtttccaag 1440  
DB 1381 ctgaggggttcctcgaagttggaagaatgattggaagaaggttgaagaagtttccaag 1440  
QY 1441 agcttgcgaatagatgtctagctcctcgtcgaagaagaagtcgagatggaacaataata 1500  
DB 1441 agcttgcgaatagatgtctagctcctcgtcgaagaagaagtcgagatggaacaataata 1500  
QY 1501 gatcatgataaggttcataatgataatgataatgataatgataatgataatgataatgata 1560  
DB 1501 gatcatgataaggttcataatgataatgataatgataatgataatgataatgataatgata 1560  
QY 1561 acattttatcatgaagaagaatgttcttgaagatcatcatccagaatgttcatatctct 1620  
DB 1561 acattttatcatgaagaagaatgttcttgaagatcatcatccagaatgttcatatctct 1620  
QY 1621 gtatgtataaatgacagccctttaaagcgtgagactgtgatagaataatattgtccct 1680  
DB 1621 gtatgtataaatgacagccctttaaagcgtgagactgtgatagaataatattgtccct 1680  
QY 1681 atgtgtctttaaaggtcttcttaacccctgtaaatgataatgataatgataatgataatgata 1740  
DB 1681 atgtgtctttaaaggtcttcttaacccctgtaaatgataatgataatgataatgataatgata 1740  
QY 1741 acaatctttgaaagaagaacccatctgttctccttcaatctccttgagccttataatag 1800  
DB 1741 acaatctttgaaagaagaacccatctgttctccttcaatctccttgagccttataatag 1800  
QY 1801 ttctcaaatcagaagttgttcatattcaaatctcaaatctgagagctgagacagac 1860  
DB 1801 ttctcaaatcagaagttgttcatattcaaatctcaaatctgagagctgagacagac 1860  
QY 1861 agatttgatgttccctcgaagagatacgaagcctatctggttgagatcctatctgt 1920  
DB 1861 agatttgatgttccctcgaagagatacgaagcctatctggttgagatcctatctgt 1920  
QY 1921 tcagctatggaatcttgcagatcctcagaagaatttgcagagttatggaatctgcaagat 1980  
DB 1921 tcagctatggaatcttgcagatcctcagaagaatttgcagagttatggaatctgcaagat 1980



CC to confer resistance to plant pathogen  
 CC *Xanthomonas campestris* pv. *vesicatoria* which causes bacterial spot  
 CC disease. The Bs2 protein has Bs2 biological activity, i.e., when  
 CC co-expressed in a plant with a *X. campestris* AVRBs2 gene product,  
 CC it produces a localized hypersensitive response. The protein  
 CC includes a nucleotide binding motif and leucine rich repeats of the  
 CC type found in other plant resistance genes. The Bs2 nucleic acid  
 CC molecule is useful for producing transgenic plants such as pepper,  
 CC tomato, tobacco, broccoli, cauliflower, cabbage, corn, grape, canola,  
 CC bean, soybean, rice, corn, wheat, barley, citrus, cotton, cassava and  
 CC walnut, that are resistant to plant pathogen *Xanthomonas campestris*.  
 CC The transgenic plants produced using Bs2 molecule develop a  
 CC hypersensitive response to the pathogen at the site of inoculation and  
 CC show an enhanced resistance to systemic infection. The Bs2 nucleic acid  
 CC molecule is also useful as polymerase chain reaction (PCR) primers for  
 CC amplifying portions of Bs2 nucleic acid molecule, as sequencing primers  
 CC to verify the authenticity of an amplified molecule, and as  
 CC hybridisation probes.

XX Sequence 31491 BP; 9652 A; 6344 C; 5992 G; 9503 T; 0 other;

Query Match 88.0%; Score 2725.6; DB 22; Length 31491;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2728; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 53 ggtcattgctcgcaagaaacagatacagatataatggtctcagcaagtgtgac 112  
 DB 1440 ggtcattgctcgcaagaaacagatacagatataatggtctcagcaagtgtgac 1499  
 OY 113 ttctctatgagacataagaaatctctctgacatcaattcgcgagtgcaatctatc 172  
 DB 1500 ttctctatgagacataagaaatctctctgacatcaattcgcgagtgcaatctatc 1559  
 OY 173 ctgtgacacagagaaagacttgcgtctctcgtgaaagtaattccctggaagtatt 232  
 DB 1560 ctgtgacacagagaaagacttgcgtctctcgtgaaagtaattccctggaagtatt 1619  
 OY 233 ttgtcagaacttggaaacaaacatgtttttgggaaatggacgatttggagttgagtt 292  
 DB 1620 ttgtcagaacttggaaacaaacatgtttttgggaaatggacgatttggagttgagtt 1679  
 OY 293 aagagagatttgcagtgctgtctgatacacaattcactgagacttaacagagactgtact 352  
 DB 1680 aagagagatttgcagtgctgtctgatacacaattcactgagacttaacagagactgtact 1739  
 OY 353 gggagagaataaagcccaaaaaaagcgctgcgaaggtttcgtcaaacgctcgcaaa 412  
 DB 1740 gggagagaataaagcccaaaaaaagcgctgcgaaggtttcgtcaaacgctcgcaaa 1799  
 OY 413 agtagcagagacatgcatatctctgaaagagtcgacaaagatccaagataaagaa 472  
 DB 1800 agtagcagagacatgcatatctctgaaagagtcgacaaagatccaagataaagaa 1859  
 OY 473 acaagatcaaaagaaatctgttcaatatttcaagttcaacaaacgatatttgaa 532  
 DB 1860 acaagatcaaaagaaatctgttcaatatttcaagttcaacaaacgatatttgaa 1919  
 OY 533 ggttaagaacaataatgtttgagcgtgataatcaaaagacagttgttgaagacttgc 592  
 DB 1920 ggttaagaacaataatgtttgagcgtgataatcaaaagacagttgttgaagacttgc 1979  
 OY 593 tagaagctactctgggaaacccaaagttcaccgattgctcgagatgggagatagtaa 652  
 DB 1980 tagaagctactctgggaaacccaaagttcaccgattgctcgagatgggagatagtaa 2039  
 OY 653 aacaaccttagcaaaagatttacaatgaatgaatcaatctcattgacgttttgatgttca 712  
 DB 2040 aacaaccttagcaaaagatttacaatgaatgaatcaatctcattgacgttttgatgttca 2099  
 OY 713 tgccttggttaccatattcacaagacacaaagaaatttgcgttgaccttctgaa 772  
 DB 2100 tgccttggttaccatattcacaagacacaaagaaatttgcgttgaccttctgaa 2159

OY 773 ttccacaatcaaaaatggtatgacaggtttaagatgatttgcgtgaagcagagcttaacagatc 832  
 DB 2160 ttccacaatcaaaaatggtatgacaggtttaagatgatttgcgtgaagcagagcttaacagatc 2219  
 OY 833 gttcagaanaagtttaagaagaagaggtacttaattgtcttggatgatatctggagttg 892  
 DB 2220 gttcagaanaagtttaagaagaagaggtacttaattgtcttggatgatatctggagttg 2279  
 OY 893 tgaagtgtggatgtggtgtgagacatgtcttccaaactgaaagacaatgcagggagtcgaat 952  
 DB 2280 tgaagtgtggatgtggtgtgagacatgtcttccaaactgaaagacaatgcagggagtcgaat 2339  
 OY 953 actgttactcccgtaaatgatgaagtagtctgttaatgcctgggtgtagaagattttctt 1012  
 DB 2340 actgttactcccgtaaatgatgaagtagtctgttaatgcctgggtgtagaagattttctt 2399  
 OY 1013 gcgagtagagcttcaatgatacaagatgagagttgagtcctttcaaaaatgcagcatcttc 1072  
 DB 2400 gcgagtagagcttcaatgatacaagatgagagttgagtcctttcaaaaatgcagcatcttc 2459  
 OY 1073 aagtgaaacattaccatataatggttcgagactgtttgaaagcaaatcgacagatgaatca 1132  
 DB 2460 aagtgaaacattaccatataatggttcgagactgtttgaaagcaaatcgacagatgaatca 2519  
 OY 1133 cgggttaccactaaactatgttcgtgtgtgcaagggcttctcaaatctaaagagacaataga 1192  
 DB 2520 cgggttaccactaaactatgttcgtgtgtgcaagggcttctcaaatctaaagagacaataga 2579  
 OY 1193 agatttgaanaactgttgcataaagatgcaatcaatcgttcaaaaatgatactcgtatgaag 1252  
 DB 2580 agatttgaanaactgttgcataaagatgcaatcaatcgttcaaaaatgatactcgtatgaag 2639  
 OY 1253 atgttcaagttgtctgt 1312  
 DB 2640 atgttcaagttgtctgt 2699  
 OY 1313 tctgcatctcgaaatttctccagaagaacagtgatattccagtgaaagatttgaatgagatc 1372  
 DB 2700 tctgcatctcgaaatttctccagaagaacagtgatattccagtgaaagatttgaatgagatc 2759  
 OY 1373 atggaatgctgaggggttccctgaaagttggaataatgatttggaaagaggtttgaagaagt 1432  
 DB 2760 atggaatgctgaggggttccctgaaagttggaataatgatttggaaagaggtttgaagaagt 2819  
 OY 1433 ttgtcaagagcttgcgataaagatgtctagtcctgtcgaagaagaagtcgagatggaac 1492  
 DB 2820 ttgtcaagagcttgcgataaagatgtctagtcctgtcgaagaagaagtcgagatggaac 2879  
 OY 1493 aaaaaatagatcagtgaaagttcagatcagatcagatcagatcagatcagatcagatcagatc 1552  
 DB 2880 aaaaaatagatcagtgaaagttcagatcagatcagatcagatcagatcagatcagatcagatc 2939  
 OY 1553 aagggagaaactttttatcagaacgacatgtgtcttgaagatcagatcagatcagatcagatc 1612  
 DB 2940 aagggagaaactttttatcagaacgacatgtgtcttgaagatcagatcagatcagatcagatc 2999  
 OY 1613 atattctgtatgataaataatgcagccctttaaagcgtgtgactgtgtgtgtgtgtgtgtgtgt 1672  
 DB 3000 atattctgtatgataaataatgcagccctttaaagcgtgtgactgtgtgtgtgtgtgtgtgtgt 3059  
 OY 1673 ttgtccatgtgtcttataagagcttcttcaaccctgttaaacogtcaagtttgagatca 1732  
 DB 3060 ttgtccatgtgtcttataagagcttcttcaaccctgttaaacogtcaagtttgagatca 3119  
 OY 1733 tgaacaacaacaactttttgaaagaaacaaacttgcgtttcttcttcaatcttgaagcctt 1792  
 DB 3120 tgaacaacaacaactttttgaaagaaacaaacttgcgtttcttcttcaatcttgaagcctt 3179  
 OY 1793 atattatgttctcaaatcaagaggtgtgttcaattcaaatctcaaatctcaaatctcaaatctca 1852  
 DB 3180 atattatgttctcaaatcaagaggtgtgttcaattcaaatctcaaatctcaaatctcaaatctca 3239

QY	1853	acacagacagatgtagtgtgttccctccgagaaatactaaagctcaatctgtgttgtagtacct	1912
Db	3240	acacagacagatgtagtgttccctccgagaaatactaaagctcaatctgtgttgtagtacct	3299
QY	1913	ataatgttccagctatgaggaatttcgaaatgtaacccccaagaaatttgcagattatgaaatct	1972
Db	3300	ataatgttccagctatgaggaatttcgaaatgtaacccccaagaaatttgcagattatgaaatct	3359
QY	1973	gcagacattcaattgttcaacgggttcgatccagataataattttgtctgaagaaatttg	2032
Db	3360	gcagacattcaattgttcaacgggttcgatccagataataattttgtctgaagaaatttg	3419
QY	2033	ggaacaaatgccaattgaaggcactcttaaacctgcacagattttatttgcacaattgcccag	2092
Db	3420	ggaacaaatgccaattgaaggcactcttaaacctgcacagattttatttgcacaattgcccag	3479
QY	2093	tggatctgtttgacaagaaggaggaagcacttggatttttcaaaactacaactatttctaact	2152
Db	3480	tggatctgtttgacaagaaggaggaagcacttggatttttcaaaactacaactatttctaact	3539
QY	2153	gtctccacggtgtgtgacagaaaggaggttattttggggattgaagaatgtccaaaattagg	2212
Db	3540	gtctccacggtgtgtgacagaaaggaggttattttggggattgaagaatgtccaaaattagg	3599
QY	2213	aatcagatggaataaagatgactataaaaagttttcggagctctggctctccaaaact	2272
Db	3600	aatcagatggaataaagatgactataaaaagttttcggagctctggctctccaaaact	3659
QY	2273	tgtctatctgcaggaacttggaaatatttgagttcttatctgtgtgtttatgacctttggcc	2332
Db	3660	tgtctatctgcaggaacttggaaatatttgagttcttatctgtgtgtttatgacctttggcc	3719
QY	2333	agtatcatcttccaagtgcacaaaagcttttccagcaacgctccaagaagtccaagtgcgaag	2392
Db	3720	agtatcatcttccaagtgcacaaaagcttttccagcaacgctccaagaagtccaagtgcgaag	3779
QY	2393	aactatcttaagctcgtgtccaaacttggaaactgaagtttgagttgtgtgtccaaacttgagtgct	2452
Db	3780	aactatcttaagctcgtgtccaaacttggaaactgaagtttgagttgtgtgtccaaacttgagtgct	3839
QY	2453	gaagctgtatgtatagaagctgtgtgtgtgtgaagaatgcatccaaattgttatgtggaatttaa	2512
Db	3840	gaagctgtatgtatagaagctgtgtgtgtgtgtgaagaatgcatccaaattgttatgtggaatttaa	3899
QY	2513	tcgatttgaagcttttgcataataataatagttttctccaagttctggaagccacaataatga	2572
Db	3900	tcgatttgaagcttttgcataataataatagttttctccaagttctggaagccacaataatga	3959
QY	2573	caatttctctctcttgaagcgcctcatgatctagaagtgcacaaaatttgaagaagatatacc	2632
Db	3960	caatttctctctcttgaagcgcctcatgatctagaagtgcacaaaatttgaagaagatatacc	4019
QY	2633	catltagtttgcagatatatacacacactacagctgatttgaagagtagtgcctccaa	2692
Db	4020	catltagtttgcagatatatacacacactacagctgatttgaagagtagtgcctccaa	4079
QY	2693	acttgggaaatctgtctgcagaaatttgaagaagaacaagaagacctctggaaacaacacctgt	2752
Db	4080	acttgggaaatctgtctgcagaaatttgaagaagaacaagaagacctctggaaacaacacctgt	4133
QY	2753	ggaatgtcgtatctcaaatccatgtgaaggaga	2784
Db	4140	ggaatgtcgtatctcaaatccatgtgaagtata	4171
RESULT 4			
AAAF63301 standard; DNA; 31491 BP.			
XX	AAAF63301;		
XX			
DT	02-MAY-2001 (first entry)		
XX			

DE	Pepper Bs2 resistance gene.
XX	
KM	Bs2: pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;
XW	Xcv; bacterial spot disease; transgenic plant; crop; fruit; flower; ds.
OS	Capsicum annuum.
PN	MO200107635-A1.
PD	
XX	01-FEB-2001.
PF	
PR	23-DEC-1999; 99WO-US30891.
XX	
PA	(REGC ) UNIV CALIFORNIA.
PI	Staskawicz BJ, Dahlbeck D, Tai TH;
XX	
DR	WPI: 2001-168560/17.
XX	P-PSDB; AAB72198.
PT	
PR	Novel Bs2 polypeptide from Capsicum annuum for producing transgenic plants having resistance to bacterial spot disease caused by Xanthomonas campestris pv vesicatoria (Xcv) -
XX	
PS	Claim 3; Page 40-57; 72pp; English.
XX	
CC	This invention relates to the amino acid sequence of the Bs2 protein isolated from Capsicum annuum (pepper). The protein and DNA sequences of CC Bs2 can be used to confer resistance to the plant pathogen Xanthomonas CC campestris pv vesicatoria (Xcv) which causes bacterial spot disease. Bs2 CC DNA and protein sequences are useful for producing transgenic plants such CC as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola, CC compea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton, CC cassava, and walnut, having resistance to X. campestris. The protein and CC DNA molecule are also useful for producing transgenic alfalfa, flax, CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits, CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots, CC carnations and roses having resistance to X. campestris. The present CC sequence represents the Bs2 gene of the invention.
XX	
SQ	Sequence 31491 BP; 9652 A; 6345 C; 5992 G; 9502 T; 0 other;
	Query Match 88.0%; Score 2725.6; DB 22; Length 31491;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 2728; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
OY	53 ggtcatagtgcgaagacacaaacgagaatacagatataatgatggctcatgcaagttgtgc 112 
Db	1440 ggtcatagtgcgaagacacaaacgagaatacagatataatgatggctcatgcaagttgtgc 1499
OY	113 ttctcttaagaacaatagatctcttcttgcaattccatgccgatgcaatctctatc 172 
Db	1500 ttctcttaagaacaatagatctcttcttgcaattccatgccgatgcaatctctatc 1559
OY	173 ctggtgaccagaagaagaacttcgctcgctcttgctgtaaaaagttagttccctggagaatl 232 
Db	1560 ctggtgaccagaagaagaacttcgctcgctcttgctgtaaaaagttagttccctggagaatl 1619
OY	233 tgtcaagaactttgagaaaaacaatgtttttgggaaatgacggattttaagtaaagt 292 
Db	1620 tgtcaagaactttgagaaaaacaatgtttttgggaaatgacggattttaagtaaagt 1679
OY	293 aagagaagttgcaagtgctgctgaatcacaaattccaactaggctaacaggaactgtact 352 
Db	1680 aagagaagttgcaagtgctgctgaatcacaaattccaactaggctaacaggaactgtact 1739
OY	353 ggaggaataataaagccagaaaaaaggcgctgcgaagtttcgtcaaacgctgcacaa 412 
Db	1740 ggaggaataataaagccagaaaaaaggcgctgcgaagtttcgtcaaacgctgcacaa 1799

QY 413 agtagcagagacatgatacatatctggaagaagtcgacaaagatccaaagataaagaaa 472  
|||||  
Db 1800 agtagcagagacatgatacatatctggaagaagtcgacaaagatccaaagataaagaaa 1859  
QY 473 acaagatcaaaagaaatattggttcaatgattttcaaaagtcacaacagatatttga 532  
|||||  
Db 1860 acaagatcaaaagaaatattggttcaatgattttcaaaagtcacaacagatatttga 1919  
QY 533 ggttaagaacaatagtctgagctgagatgatacagaagaacagttgtatagaagatcgac 592  
|||||  
Db 1920 ggttaagaacaatagtctgagctgagatgatacagaagaacagttgtatagaagatcgac 1979  
QY 593 tagaagctactcttgagggaaccccaagatcccgatgctggagatggagagatagtaa 652  
Db 1980 tagaagctactcttgagggaaccccaagatcccgatgctggagatggagagatagtaa 2039  
QY 653 aacaacctagcaaaagaagtttcaaatgataatgataatctatagccggttttgaatgta 712  
|||||  
Db 2040 aacaacctagcaaaagaagtttcaaatgataatgataatctatagccggttttgaatgta 2099  
QY 713 tgccttgagctacatctcacacagcaacaacaaagaatattgtctggccttcgca 772  
|||||  
Db 2100 tgccttgagctacatctcacacagcaacaacaaagaatattgtctggccttcgca 2159  
QY 773 ttccaacatcaaaatgatacagaggttaagaatgattgtgaagcagagctagcagacat 832  
Db 2160 ttccaacatcaaaatgatacagaggttaagaatgattgtgtgaagcagagctagcagacat 2219  
QY 833 gtacacagaagaagtttaagaagaaggttaactaatgtctgttgatgatactcggagttg 892  
Db 2220 gtacacagaagaagtttaagaagaaggttaactaatgtctgttgatgatactcggagttg 2279  
QY 893 tgaagtgaggatgagcgtagagacagatgcttccaactgaaagacaatgcaagagatcgaa 952  
Db 2280 tgaagtgaggatgagcgtagagacagatgcttccaactgaaagacaatgcaagagatcgaa 2339  
QY 953 actgttaactaccggttaataagaaggttattatgctgcggtgtagagaattttctt 1012  
Db 2340 actgtttactaccggttaataagaaggttattatgctgcggtgtagagaattttctt 2399  
QY 1013 gcggatgagctcatgatacagaatgagaatgtagagttcttccaagaagtcagacatttc 1072  
Db 2400 gcggatgagctcatgatacagaatgagaatgtagagttcttccaagaagtcagacatttc 2459  
QY 1073 aagtgaaagcattaccatagatgagtcgaagctgttggaaagcaaatcgagatgaatgtca 1132  
Db 2460 aagtgaaagcattaccatagatgagtcgaagctgttggaaagcaaatcgagatgaatgtca 2519  
QY 1133 cgggttaaccaactattgctgtgttgcagaggtcttccaatctcaaaagaaagataaga 1192  
Db 2520 cgggttaaccaactattgctgtgttgcagaggtcttccaatctcaaaagaaagataaga 2579  
QY 1193 agattggaanaactgtgtgaagaatgtaaatcagtcacaaatgatacctcgatgaagc 1252  
Db 2580 agattggaanaactgtgtgaagaatgtaaatcagtcacaaatgatacctcgatgaagc 2639  
QY 1253 atgttaactgtgctggttgaatgatacacttgacaagcagatctaaacatgtct 1312  
Db 2640 atgttaactgtgctggttgaatgatacacttgacaagcagatctaaacatgtct 2699  
QY 1313 tctgcatcttcggaattttccagaagaagatgataatccagtgagaagaatttgaatgata 1372  
Db 2700 tctgcatcttcggaattttccagaagaagatgataatccagtgagaagaatttgaatgata 2759  
QY 1373 atggaatgagctgagaggtcttcgaagtggaaaaatgatttggaaagagaggttgaagaatg 1432  
Db 2760 atggaatgagctgagaggtcttcgaagtggaaaaatgatttggaaagagaggttgaagaatg 2819  
QY 1433 ttgtcaagagctgttcgataagatgtcgtagctcgtcagcaagaaatcgagatgagac 1492  
Db 2820 ttgtcaagagctgttcgataagatgtcgtagctcgtcagcaagaaatcgagatgagac 2879  
QY 1493 aaaaattagatcatgtaaggttcatgataataatagacctgtgtagagagaagtca 1552  
|||||  
Db 2880 aaaaattagatcatgtaaggttcatgataataatagacctgtgtagagagaagtca 2939  
QY 1553 aagggaagaacattttatcatagacagacatgttcttgcagatcatcatccgaagatctc 1612  
Db 2940 aagggaagaacattttatcatagacagacatgttcttgcagatcatcatccgaagatctc 2999  
QY 1613 atactctgatagtataaataatgagccctttaagcggtgactgtgtgataatgaatga 1672  
Db 3000 atactctgatagtataaataatgagccctttaagcggtgactgtgtgataatgaatga 3059  
QY 1673 ttgtccctatggtcttataagagctcttcttaacccctgtaaatctgtaagatgata 1732  
Db 3060 ttgtccctatggtcttataagagctcttcttaacccctgtaaatctgtaagatgata 3119  
QY 1733 tgaacaacaacatcttgaanaacgaacccatctgttctctcttcaatctctgaacctt 1792  
Db 3120 tgaacaacaacatcttgaanaacgaacccatctgttctctcttcaatctctgaacctt 3179  
QY 1793 atataatgttctcaaatcagaaggttgttcaatcaaatcacaagttcttgagatgag 1852  
Db 3180 atataatgttctcaaatcagaaggttgttcaatcaaatcacaagttcttgagatgag 3239  
QY 1853 acaacagacagatgatagttccctcagagagataactaaagcccatctgttgagatgact 1912  
Db 3240 acaacagacagatgatagttccctcagagagataactaaagcccatctgttgagatgact 3299  
QY 1913 atcaatgttcagctatgggaatttcgaatgatacctccagaanaatttgcaggttatagaa 1972  
Db 3300 atcaatgttcagctatgggaatttcgaatgatacctccagaanaatttgcaggttatagaa 3359  
QY 1973 gcaagacatcatgttcaacggttccagatcagataataatatttgttgaggaaattg 2032  
Db 3360 gcaagacatcatgttcaacggttccagatcagataataatatttgttgaggaaattg 3419  
QY 2033 ggaactaatgcaatlaaagagcactaaactgcccagatcttatttgcagaatctcccaag 2092  
Db 3420 ggaactaatgcaatlaaagagcactaaactgcccagatcttatttgcagaatctcccaag 3479  
QY 2093 tggatcttgaacaaagaagaagcacttgatatttccaactacaacatattcttact 2152  
Db 3480 tggatcttgaacaaagaagaagcacttgatatttccaactacaacatattcttact 3539  
QY 2153 gtctccagctgttgcagaagaaggttataatgaggatgagaaatgcaaaaatcag 2212  
Db 3540 gtctccagctgttgcagaagaaggttataatgaggatgagaaatgcaaaaatcag 3599  
QY 2213 aatcagtgagaataaagagatgataaagttctcggagctcgggtctcccaacatct 2272  
Db 3600 aatcagtgagaataaagagatgataaagttctcggagctcgggtctcccaacatct 3659  
QY 2273 tgtcatctgagcaaaccttgaataatgagatctatctcgttgaatagatcctttgccc 2332  
Db 3660 tgtcatctgagcaaaccttgaataatgagatctatctcgttgaatagatcctttgccc 3719  
QY 2333 agtgatcaattcaagtgcaaaaagcttctccagcaacgctcacaagaagtgtgaagtggaa 2392  
Db 3720 agtgatcaattcaagtgcaaaaagcttctccagcaacgctcacaagaagtgtgaagtggaa 3779  
QY 2393 aactatcatagctgtgcatcaacttgagacatcaatgactgagatgacttaacctgaagtgct 2452  
Db 3780 aactatcatagctgtgcatcaacttgagacatcaatgactgagatgacttaacctgaagtgct 3839  
QY 2453 gaaactgaatgatacagctgttgcagtgagaagatgcaatcccaatggttattgagattaa 2512  
Db 3840 gaaactgaatgatacagctgttgcagtgagaagatgcaatcccaatggttattgagattaa 3899  
QY 2513 tgcattgaagcttctgtaataatagtttctcaagattcttgaaagcccaaatga 2572  
Db 3900 tgcattgaagcttctgtaataatagtttctcaagattcttgaaagcccaaatga 3959  
QY 2573 caatttcctgcttgagagcctcatgattagaagtgcgaataatttgaagaagatc 2632  
|||||



Db 3960 caatttcctctccttgagcgcctcatgattagaaatgcaaaaatttgaagaagatacc 4019  
 QY 2633 cattgaatttgagatatacacacactacagctgattgagtaagaagatgtctcccaa 2692  
 Db 4020 cattgaatttgagatatacacacactacagctgattgagtaagaagatgtctcccaa 4079  
 QY 2693 acttggggaatctgtctgcaggaattcagaagaagaagacctcggaaacacctgt 2752  
 Db 4080 acttggggaatctgtctgcaggaattcagaagaagaagacctcggaaacacctgt 4139  
 QY 2753 ggaattgtctatctcaatccattgaagagaga 2784  
 Db 4140 ggaattgtctatctcaatccattgaagagata 4171  
 RESULT 5  
 AAF63303  
 ID AAF63303 standard; cDNA; 2718 BP.  
 AC AAF63303;  
 DT 02-MAY-2001 (first entry)  
 DE Pepper Bs2 open reading frame sequence.  
 KM Bs2; pepper; pathogen resistant; Xanthomonas campestris pv vesicatoria;  
 KW Xcv; bacterial spot disease; transgenic plant; crop; fruit; flower; ss.  
 OS Capsicum annuum.  
 PN WO200107635-A1.  
 PD 01-FEB-2001.  
 PF 23-DEC-1999; 99WO-US30891.  
 PR 23-JUL-1999; 99US-0360186.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Staskawicz BJ, Dahlbeck D, Tai TH;  
 DR WPI: 2001-168560/17.  
 DR P-PSDB; AAB72198.  
 XX Novel Bs2, polypeptide from Capsicum annuum for producing transgenic  
 PT plants having resistance to bacterial spot disease caused by  
 PT Xanthomonas campestris pv vesicatoria (Xcv) -  
 PS Claim 3; Page 64-68; 72pp; English.  
 XX This invention relates to the amino acid sequence of the Bs2 protein  
 CC isolated from Capsicum annuum (pepper). The protein and DNA sequences of  
 CC Bs2 can be used to confer resistance to the plant pathogen Xanthomonas  
 CC campestris pv vesicatoria (Xcv) which causes bacterial spot disease. Bs2  
 CC DNA and protein sequences are useful for producing transgenic plants such  
 CC as pepper, tomato, tobacco, broccoli, cauliflower, cabbage, canola,  
 CC cowpea, grape, bean soybean, rice, corn, wheat, barley, citrus, cotton,  
 CC cassava and walnut, having resistance to X. campestris. The protein and  
 CC DNA molecule are also useful for producing transgenic alfalfa, flax,  
 CC sunflower, safflower, brassica, peanut, clover, lettuce, cucurbits,  
 CC potato, carrot, radish, pea, lentils, apples, pears, peaches, apricots,  
 CC carnations and roses having resistance to X. campestris. The present  
 CC sequence represents the open reading frame of Bs2.  
 XX Sequence 2718 BP; 851 A; 454 C; 623 G; 790 T; 0 other;

Db 1 atggcctcagcaagtgctgtctctcttatagaaacatagaaatctctctgacatcaat 60  
 QY 153 tcgcgcatgcaatctctatctctgtatcaacagagaagaacttgcgctctgtgaaaaa 212  
 Db 61 tcgcgcatgcaatctctatctctgtatcaacagagaagaacttgcgctctgtgaaaaa 120  
 QY 213 gttatgtccctggaagtatttgcgaagaacttggagaaaaaaatgttttggggaatg 272  
 Db 121 gttatgtccctggaagtatttgcgaagaacttggagaaaaaaatgttttggggaatg 180  
 QY 273 acggatttgaagtagaagtagaagaagtgcgaagtgcgtctgaatacacaaatccaatg 332  
 Db 181 acggatttgaagtagaagtagaagaagtgcgaagtgcgtctgaatacacaaatccaatg 240  
 QY 333 agactacaggaactgtactctggagaaaaataaaagccagaaaaaaaagcgctcgaaag 392  
 Db 241 agactacaggaactgtactctggagaaaaataaaagccagaaaaaaaagcgctcgaaag 300  
 QY 393 ttctgcctcaagcctgcgaacagtagaagagagatgatatctctgaaagagctgcaca 452  
 Db 301 ttctgcctcaagcctgcgaacagtagaagagagatgatatctctgaaagagctgcaca 360  
 QY 453 aagatccagaataaggaacaaagatatacaaaaggaatcattgttcaatgttttcaagt 512  
 Db 361 aagatccagaataaggaacaaagatatacaaaaggaatcattgttcaatgttttcaagt 420  
 QY 513 tcaacaaacgatatcttgaaggttaagaacaatatgtgtgaagtgatgataaagaaa 572  
 Db 421 tcaacaaacgatatcttgaaggttaagaacaatatgtgtgaagtgatgataaagaaa 480  
 QY 573 cagttttagaagaatcgtacagtagaagtagctctcggggaacccaagatcccgatgtc 632  
 Db 481 cagttttagaagaatcgtacagtagaagtagctctcggggaacccaagatcccgatgtc 540  
 QY 633 gggatgggaagcattagtaaaacaacacttgcgaagaagaatttcaaatgtatcaat 692  
 Db 541 gggatgggaagcattagtaaaacaacacttgcgaagaagaatttcaaatgtatcaat 600  
 QY 693 ctatgcgcttttgaatgtcaatgcctgggtccatcatctcaacagcacaacaaaagaa 752  
 Db 601 ctatgcgcttttgaatgtcaatgcctgggtccatcatctcaacagcacaacaaaagaa 660  
 QY 753 atttgcctggccttcgcgctccacatcaaaaattgaagtagaaggttaagatgtgt 812  
 Db 661 atttgcctggccttcgcgctccacatcaaaaattgaagtagaaggttaagatgtgt 720  
 QY 813 gaaagcagctacagacatggttacagaagaatttaagaagaagaagtagtaattgtc 872  
 Db 721 gaaagcagctacagacatggttacagaagaatttaagaagaagaagtagtaattgtc 780  
 QY 873 ttgatatatacttggaatttgaaagtgtggaatgggtgagacgaatgtcttccaactgaa 932  
 Db 781 ttgatatatacttggaatttgaaagtgtggaatgggtgagacgaatgtcttccaactgaa 840  
 QY 933 gaaatgcaagggtgcgaatctgttactacccgtaatatgaagtagctgtgtaagt 992  
 Db 841 gaaatgcaagggtgcgaatctgttactacccgtaatatgaagtagctgtgtaagt 900  
 QY 993 ggttgaagaattttcttgcgagatagcttcaatgatacaagaatgtggaagttt 1052  
 Db 901 ggttgaagaattttcttgcgagatagcttcaatgatacaagaatgtggaagttt 960  
 QY 1053 ttcaaaagtgcgaatcttcaagtgaagcatcaccatagatggtcgagactgttgaaga 1112  
 Db 961 ttcaaaagtgcgaatcttcaagtgaagcatcaccatagatggtcgagactgttgaaga 1020  
 QY 1113 caaatgcgaatgaatctcaaggggttacccaactatttgcgtgttcgaagggctctc 1172  
 Db 1021 caaatgcgaatgaatctcaaggggttacccaactatttgcgtgttcgaagggctctc 1080  
 QY 1173 aaatctaagaagcaatagaaatgtgaaacatgttctaagaatgttcaagatcctcgtc 1232

Query Match 87.7%; Score 2718; DB 22; Length 2718;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1081 aaatctaaagacaaatagaaagatttgaaactgttctaagaatcgaatcgaatcgttc 1140  
 QY 1233 acaaaagatccctgatgaagaatgacgtgctgctggttgatgaatgaatcattgaca 1292  
 Db 1141 acaaaagatccctgatgaagaatgacgtgctggttgatgaatgaatcattgaca 1200  
 QY 1293 aagcatctaaacaaatgctctcctgcatcttcggaattttccagaaagacgtgataatcca 1352  
 Db 1201 aagcatctaaacaaatgctctcctgcatcttcggaattttccagaaagacgtgataatcca 1260  
 QY 1353 gfgaaatatttgatgacatcgtgctggaaggttcctcgaagtgggaaatgatttg 1412  
 Db 1261 gfgaaatatttgatgacatcgtgctggaaggttcctcgaagtgggaaatgatttg 1320  
 QY 1413 gaagagaggttggaaggttgcgaaggttcgcatgaatgctgctgctgctgctgctg 1472  
 Db 1321 gaagagaggttggaaggttgcgaaggttcgcatgaatgctgctgctgctgctgctg 1380  
 QY 1473 aagagagatcgaatggaacaaatagatcatgtaaggtcgaatcgaatcgaatcgaat 1532  
 Db 1381 aagagagatcgaatggaacaaatagatcatgtaaggtcgaatcgaatcgaatcgaat 1440  
 QY 1533 cgtgctggaagagatcgaacaaaggaacatcttcacatgaacgacatgcttctgac 1592  
 Db 1441 cgtgctggaagagatcgaacaaaggaacatcttcacatgaacgacatgcttctgac 1500  
 QY 1593 gcatcatcgaagatgcatcatctcgtatgataaaatggaaccccttaagagctg 1652  
 Db 1501 gcatcatcgaagatgcatcatctcgtatgataaaatggaaccccttaagagctg 1560  
 QY 1653 actgctggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1712  
 Db 1561 actgctggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1620  
 QY 1713 aatgctggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1772  
 Db 1621 aatgctggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1680  
 QY 1773 tctttcatcctgagccttataatattgttctcaaatcagaggtgttcatttcaatga 1832  
 Db 1681 tctttcatcctgagccttataatattgttctcaaatcagaggtgttcatttcaatga 1740  
 QY 1833 cccaagctctggaatcgaacacagacagatgattgttccctcgaagatactgaagc 1892  
 Db 1741 cccaagctctggaatcgaacacagacagatgattgttccctcgaagatactgaagc 1800  
 QY 1893 ctcacatgctggaatcgaacacagacatgattgttccctcgaagatactgaagc 1952  
 Db 1801 ctcacatgctggaatcgaacacagacatgattgttccctcgaagatactgaagc 1860  
 QY 1953 atttgcaagttgaatgaatcgaacacatcgttcaacaggttccgaatcgaatga 2012  
 Db 1861 atttgcaagttgaatgaatcgaacacatcgttcaacaggttccgaatcgaatga 1920  
 QY 2013 atttgctggaatgaatggaacaaatgaatgaatgaatgaatgaatgaatgaatga 2072  
 Db 1921 atttgctggaatgaatggaacaaatgaatgaatgaatgaatgaatgaatgaatga 1980  
 QY 2073 atttgcaagttggaacaggtgattgttgaacaaaggaacaggttgaatgaatga 2132  
 Db 1981 atttgcaagttggaacaggtgattgttgaacaaaggaacaggttgaatgaatga 2040  
 QY 2133 ttacaacatcttctactgtctccacaggttgcgaagaggttattatgaggtgatt 2192  
 Db 2041 ttacaacatcttctactgtctccacaggttgcgaagaggttattatgaggtgatt 2100  
 QY 2193 cagaatgtcaaaaaattggaatcagtggaataaagatacgaatgaatgaatgaatga 2252  
 Db 2101 cagaatgtcaaaaaattggaatcagtggaataaagatacgaatgaatgaatgaatga 2160  
 QY 2253 tctggtctcccaacaaatcgtctatctgcaacaaatgaatgaatgaatgaatgaatga 2312  
 Db 2161 tctggtctcccaacaaatcgtctatctgcaacaaatgaatgaatgaatgaatgaatga 2220

QY 2313 gttgattatagcctttgccaagtgatcatcttcaagtgaacaaagctttccagaaagctc 2372  
 Db 2221 gttgattatagcctttgccaagtgatcatcttcaagtgaacaaagctttccagaaagctc 2280  
 QY 2373 aagaagttgaagttggaagaactatcctaagctgctgcaacacttggaacatcagctgag 2432  
 Db 2281 aagaagttgaagttggaagaactatcctaagctgctgcaacacttggaacatcagctgag 2340  
 QY 2433 ttgcttaaccttgaggtgctggaagctggaatgaagctgtgtgttggaatgagct 2492  
 Db 2341 ttgcttaaccttgaggtgctggaagctggaatgaagctgtgtgttggaatgagct 2400  
 QY 2493 ccaatgttgatggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 2552  
 Db 2401 ccaatgttgatggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 2460  
 QY 2553 ttctggaagaacaaatgaacaaatcttccgtctcgttggaagctcgaatgaatgaatga 2612  
 Db 2461 ttctggaagaacaaatgaacaaatcttccgtctcgttggaagctcgaatgaatgaatga 2520  
 QY 2613 aaaaattggaagaagatacccatgagttgcaagatacacacactcagctgattgag 2672  
 Db 2521 aaaaattggaagaagatacccatgagttgcaagatacacacactcagctgattgag 2580  
 QY 2673 ttaagagaggtgctcccaacttggaaggtggaatgctgctgcaagatgaagaagaaga 2732  
 Db 2581 ttaagagaggtgctcccaacttggaaggtggaatgctgctgcaagatgaagaagaaga 2640  
 QY 2733 gacctcggaacaaacccctggaatgctgcatcacaatccatgaagaagatgattc 2792  
 Db 2641 gacctcggaacaaacccctggaatgctgcatcacaatccatgaagaagatgattc 2700  
 QY 2793 gatcagaagaacattg 2810  
 Db 2701 gatcagaagaacattg 2718

RESULT 6  
 AAZ50262  
 ID AAZ50262 standard; DNA; 2739 BP.  
 AC AAZ50262;  
 XX  
 DT 18-MAY-2000 (first entry)  
 XX  
 DE Coding region of potato Gpa2 resistance gene.  
 KW Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p;  
 KW marker; IPM4C; 11R; Potato Cyst Nematode; PCN; Globodera; nematode;  
 KW nematode resistance; detection; diagnosis; ds.  
 XX  
 OS Solanum tuberosum.  
 XX  
 FH Key  
 FT CDS  
 FT 1..2739  
 FT /tag= a  
 FT /product= "Potato Gpa2 polypeptide"  
 FT /function= "Confers resistance to phytopathogenic  
 nematodes of the Globodera genus"  
 FT  
 XX  
 PN WO200006754-A2.  
 PD 10-FEB-2000.  
 XX  
 PF 30-JUL-1999; 99WO-NI00491.  
 XX  
 PR 31-JUL-1998; 98WO-NI00445.  
 XX  
 PA (CPRO-) CPRO-DLO CENT. PLANTENVEREDELINGS REPROD.  
 PA (UYNA-) LANDBOUWUNIVERSITEIT WAGENINGEN.  
 XX  
 PI Van Der Vossen EAG, Van Der Voort JNAMR, Lankhorst RMK, Bakker J;



PI Sclerema WJ;  
 XX WPI: 2000-183132/16.  
 DR P-PSDB; AAY44818.  
 XX  
 PT New isolated Gpa2 nematode resistance gene from potato, useful for  
 PT producing plants which are resistant to nematodes and polypeptides for  
 PT use in nematocidal compositions  
 XX  
 PS Claim 62; Fig 3a; 96pp; English.  
 XX  
 CC The present DNA sequence is the coding region of the potato resistance  
 CC gene Gpa2, that confers resistance to infection by phytopathogenic  
 CC nematode of the Globodera genus. It is mapped to short arm of chromosome  
 CC 12 (12P), between the markers IPM4C and 11R. This locus is associated  
 CC with resistance to Potato Cyst Nematodes (PCN) like G. pallida and  
 CC G. rostochiensis, that invade and damage the roots of Solanaceae. It has  
 CC nematocidal activity. A recombinant DNA sequence comprising the Gpa2  
 CC gene sequence can be transformed or transfected into plants, to provide  
 CC increased resistance to nematodes. The polypeptides can also be used in  
 CC nematocidal compositions and for detection and diagnosis of nematode  
 CC infections.  
 CC  
 XX  
 SQ Sequence 2739 BP; 814 A; 498 C; 600 G; 827 T; 0 other;

Query Match 8.8%; Score 272.8; DB 21; Length 2739;  
 Best Local Similarity 54.7%; Pred. No. 1.7e-61;  
 Matches 733; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

QY 232 ttgtcaagaacttggaaaacaatgttttggggaatgacggaatttgaagtaagg 291  
 DB 113 tggagaatcctcgatataatggtgcatgaggggttaacaatcttggaattgaa 172  
 QY 292 taagaagaattgcaagtgctgtaatacaaatcaactgagactaacaggaactgtga 351  
 DB 173 tcatagggtagcatacacacagaagatagtgtagctcggaatcaagaattgttttt 232  
 QY 352 tggagaagaataaagccagaaaagggcgctggaagtttcgtcaaaagctgtgac 411  
 DB 233 taagacgggaatgtgggaaaaggaagcaggtatgtggggaatttttgcgtctggagc 292  
 QY 412 aagtagagaagagatgcatatctgtgaaagagtcgcaagaagatccaagaataagaa 471  
 DB 293 aagacactagaatgattgattccacgctggaacagtgatgcaacatcgcaacgatga 352  
 QY 472 aacagatgataaagaatcattgtgtcatgattttcaagttcaacaagaatatttga 531  
 DB 353 aagatcttaaaacacacactagctcactgtcagtttaacctgaac--atgattgtgagc 409  
 QY 532 aggttaagaacaataatgttgagctgtagtgaatcaagaagcaagttgttaagaatcga 591  
 DB 410 agcccgagaatataatgtgtggccgtgaaaatgaaattggaatgtcgtgatacaactgt 469  
 QY 592 ctagaagctactctggygaacccaagtcacccgaattgtcggaatggygaagcataagta 651  
 DB 470 ctagaagc---aggaagggaactagaagttgtctcaatcgttagggagtcacgcggga 526  
 QY 652 aaaaacacctagcaaaaagatttaacaatgataatcaatctatgcccgtttgtatgttc 711  
 DB 527 aaaaaaactttggtcgcaaaactctatagttatccttcatatgttctcgatttataattc 586  
 QY 712 atgcttggttacatcatctcaacagcaacaagaagaagaaattttgtcgctcttcgc 771  
 DB 587 gtgcaaaagaacactgtctcaacaagaagatgtgtgagaatagtactccttaagcctcttc 646  
 QY 772 attccacaatcaaaatgtagtgcaggggtlaagatgattgtggaagcagagtaagaca 831  
 DB 647 ctgtgacaagtgatgaacccgtgattc-----agctagcggagc 685  
 QY 832 tgttaacgaaaagtttaagaagaaagagtgacttaattgtcttgatgatactgaggtt 891  
 DB 686 aactgcaaaagcatctgaaagcagagatactgtgatactgatactgatactgatactg 745

QY 892 gtgaagtgtggaatggtcg tgaacagatgtcttcccaactgaagaacatgcaaggagtcga 951  
 DB 746 cagaagcttggtgatgataataaactatgttccca--gactgcgataatggaacagaa 802  
 QY 952 tactgtgaactaccgtaatgtagagctgttatgtcgtgtgtagaagaattttctt 1011  
 DB 803 tactctgaactactcggatgtggaatgtagaatactgactgacgtaagtaagctcttc 862  
 QY 1012 tgggattgacttcatgatacaagaatgagatgttgagcttttcaaaagtgaagatttt 1071  
 DB 863 atcacatgacctcaatgtaattttgacgaagaatggaatttactacacaaaagatcttg 922  
 QY 1072 caagtgaag---cattacataatgagttcgagactgtggaagaacatcgagataatg 1128  
 DB 923 aaaaagaaggttctattctctcctcgtgatttgaataattggaagaacaaattgtattaat 982  
 QY 1129 gtcaaggttaccactaatatgtcgtgtgtgcaaggctctc---caacttaagaaga 1185  
 DB 983 gtgaggggttaacctgaacatttactgtatgtcgtgacttctcctcaaaatcagtaaa 1042  
 QY 1186 caatagaagattggaacactttgtgtaagaatgtcaagtcactgtgcaaaatgactctg 1245  
 DB 1043 catggaatgagtggaacaaatgttcggaagatgtacgttcggtgtgaacagacatctg 1102  
 QY 1246 atgaacgattgcaagtgatgtctgtggtggttgaatgacatctgtaacagcgaatcaaa 1305  
 DB 1103 aagcaaaatgcatgagatgtgtggttgaattacacactgtgcttctcctcaaaac 1162  
 QY 1306 catgtcttcgaatttcgaattttccagaagacatgataatccagtgagaatttga 1365  
 DB 1163 cgtgtttctgatttttcaattttcgcagagatgtaacgagattatgttaataaactgt 1222  
 QY 1366 tgaatcatgtagtgcgtgaggggttccgta-----agttgaaatgattttggaagag 1419  
 DB 1223 ttgagttatggccgtgaaggggtgttttgaatgaaagaggaagaaagcataggaagg 1282  
 QY 1420 aggtttgaagattgttgaagaagctgtgcataagatgtcctgctgcagcaagaga 1479  
 DB 1283 tggcagaacatgtataaagcaactgtgagatagaagcttaattcttccacaatgtga 1342  
 QY 1480 gtcaagatgtaacaanaattagatcatgttaaggttcatgatctaataatgacctgtgc 1539  
 DB 1343 gtttgaatggggaaacacagag---atgtggaatgcagatgtgacccgtgaactgtt 1399  
 QY 1540 tgaagaagatccaagggagaacattttta 1569  
 DB 1400 tgaagggaagctcgaaacatgaatttttga 1429

RESULT 7  
 AA250652  
 ID AA250652 standard; DNA; 2817 BP.  
 XX  
 AC AA250652;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Coding region of potato Gpa2 resistance gene.  
 KW Resistance; Gpa2; potato; phytopathogenic nematode; chromosome 12P;  
 KW marker; IPM4C; 11R; Potato Cyst Nematode; PCN; Globodera; nematocidal;  
 KW nematode resistance; detection; diagnosis; transgenic plant; ds.  
 XX  
 OS Solanum tuberosum.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2817  
 FT /frag= a  
 FT /product= "Potato Gpa2 polypeptide"  
 FT /function= "Confers resistance to phytopathogenic  
 FT nematodes of the Globodera genus"  
 XX

PN WO200006753-A1.  
 XX 10-FEB-2000.  
 PD 31-JUL-1998; 98WO-NL00445.  
 XX 31-JUL-1998; 98WO-NL00445.  
 PF 31-JUL-1998; 98WO-NL00445.  
 XX 31-JUL-1998; 98WO-NL00445.  
 PR (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.  
 XX (UWVA-) LANDBOUWUNIVERSITEIT WAGENINGEN.  
 PA Van Der Vossen EAG, Van Der Voort JNARM, Lankhorst RMK, Bakker J;  
 PI Stiekema MJ;  
 DR WPT: 2000-199310/17.  
 XX P-PSDB: AAY45004.  
 DR Recombinant Gpa2 polynucleotide from potato, Solanum tuberosum, useful  
 PT to confer resistance to phytopathic nematodes of the genus Globodera in  
 PT transgenic plants, e.g. resistance to potato cyst nematodes in potatoes  
 PT  
 XX  
 XX  
 PS Claim 1: Fig 3a; 96bp; English.  
 CC The present DNA sequence is the coding region of the potato resistance  
 CC gene Gpa2, that confers resistance to infection by phytopathogenic  
 CC nematode of the Globodera genus. It is mapped to short arm of chromosome  
 CC 12 (12p), between the markers IPM4C and 11IR. This locus is associated  
 CC with resistance to Potato Cyst Nematodes (PCN) like G. pallida and  
 CC G. rostochiensis, that invade and damage the roots of Solanaceae. It has  
 CC nematocidal activity. Recombinant DNA sequence comprising the Gpa2  
 CC gene can be used to produce transgenic plants with increased resistance to  
 CC nematodes. The polypeptides can also be used in nematocidal compositions  
 CC and for detection and diagnosis of nematode infections.  
 CC  
 XX  
 XX Sequence 2817 BP; 846 A; 503 C; 626 G; 842 T; 0 other;  
 SQ  
 Query Match 8.8%; Score 272.8; DB 21; Length 2817;  
 Best Local Similarity 54.7%; Pred. No. 1.8e-61;  
 Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

QY 712 atgcttggttaccatatactcaacagcacacaacaaaggaatttctggtggtcttcgc 771  
 DB 587 gtgcacaaagcaactgtttccacagagatgtgtgtgaatgtgaactccagagcttcctt 646  
 QY 772 atccacacaaatgtgaacagaggttaagatgtgtgtgaagcagagcttagcacaga 831  
 DB 647 ctttgacaagtgtgaacccgattatc-----agctagcgacc 685  
 QY 832 tgttacgaagaatttaagaagaagaggtacttaattgttctgtgatatacttgagct 891  
 DB 686 aactgcacaaagcatctgaagcagagatcttggtagcatgtgatgacatagagacta 745  
 QY 892 gtgaagtgtgagtggtgtgagacgagcttcccaactgaagaacatgcagagatctga 951  
 DB 746 cagaagcttvggtagatataaactatgttccca---gactgcataatgtgaagcaga 802  
 QY 952 tactgttactaccgtaatagtgaatgagctgtgtatgtctgtgtgagaattttctt 1011  
 DB 803 tactccgtactactcggaatgtggaagtgtgtgatatatgtctagctcagtgagcccttc 862  
 QY 1012 tgcgtagagcttcacatgaatgaatgaatgtgaggtgtctttcaaatgtcagcttt 1071  
 DB 863 atcacatgcgctcatgaatatttgacgaaagtgtgaattactacacaaagatcttgg 922  
 QY 1072 caagtgaag---cattacatagatctgcagagctgttgaagacgaatgcagatgaat 1128  
 DB 923 aaaaagaagttcttattccctcgaatttgaataatgttgaacaaatgtcattaaat 982  
 QY 1129 gtccaggttaccactaactatgtctgtgtgtgcagagcttct---caaatctaaagga 1185  
 DB 983 gtgagaggttaccctcagacttacttgaattgtctgtgacttctcccaaatcagtaaaa 1042  
 QY 1186 caatagaagattggaacactgtgtcctaagaatgtcaagtcattcgtccacaatgtactgt 1245  
 DB 1043 catgtagatgtgagcaaatgttcgcgagagatgtacgttcgtgtgtaagcagatcttg 1102  
 QY 1246 atgaacatgttccacgtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1305  
 DB 1103 aagaanaatgtcatgagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1162  
 QY 1306 catgtcttctgcattcgtgaattttccagaagaacagtgatattccagtggaatattga 1365  
 DB 1163 cgtgttcttctgtatttgcacatttccgcagagatgaacagatttgaataaacttg 1222  
 QY 1366 tgagatcatgagatggtcgtgaaggttccctga-----agtgcgaataatgttgaagag 1419  
 DB 1223 ttaggttagtggccgttagaggggttttgaatgaagaagaagggaagcatagaagagg 1282  
 QY 1420 aggttgaaggtgttgcagaagcttgcgtatagatgtctagtcctgcgtcgaagaagaa 1479  
 DB 1283 tgcgagaataatgtatataaagaactgttagatagaagctcaattctatccacaatgtga 1342  
 QY 1480 gtccagatgtgaacaaataatagatcatgtgaaggttcaatgtcatatatagactgtgcg 1539  
 DB 1343 gtttgaatgtgggaacacagag---atgtgaatgtgatgtgacccgtgaactctgtt 1399  
 QY 1540 tgagagaagttcaaaaggagagacattttta 1569  
 DB 1400 tgaggaagctcgaacacatgaattctgtga 1429  
 RESULT 8  
 ID AAS03713 standard; cDNA; 3683 BP.  
 XX AAS03713:  
 AC AAS03713:  
 XX 29-AUG-2001 (first entry)  
 DE DNA encoding Rx 25, a modified resistance protein.  
 XX  
 XX Rx: modified resistance; NBS; LRR; cell death; autoactivator;

KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant; ss.  
 XX Solanum tuberosum.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 37..2850  
 FT /\*tag= a  
 FT /product= "Modified resistance protein 25"  
 XX  
 FN WO200129239-A2.  
 PD 26-APR-2001.  
 PD 12-OCT-2000; 2000WO-GB03930.  
 PF 15-OCT-1999; 99GB-0024483.  
 PR (PLAN-) PLANT BIOSCIENCE LTD.  
 PA Bendahmane A, Baulcombe DC;  
 PI WPI; 2001-290924/30.  
 DR P-PSDB; AAU02143.  
 DR  
 XX  
 PS Disclosure; Page 46-60; 77pp; English.  
 XX  
 CC The sequence represents the coding sequence of Rx clone 25, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 CC  
 XX  
 SQ Sequence 3683 BP; 1149 A; 635 C; 782 G; 1117 T; 0 other;

Query Match 8.8%; Score 272.8; DB 22; Length 3683;  
 Best Local Similarity 54.7%; Pred. No. 2e-61;  
 Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

QY 232 ttgtcagaactttggagaacaatgttttgggggaatgacgagatttgaagtagagg 291  
 Db 149 tggggaataatcctggaataataatggcgatcagggggttlaacaatcttggaattgaa 208  
 QY 292 taagaagaattgcaagtgctgtaatacaattcaactcagactcaggaactgac 351  
 Db 209 tcgtagaggtgtacatacaacaagaagatagtgtgactcggatcaagaagtgtttt 268  
 QY 352 tgggagaataataaagccagaanaaaagcgctcgaaagtttcgtcaaaagcctgcac 411  
 Db 269 tagacagaatttggagaagaagcagggctatgtggagatttttctcctggagac 328  
 QY 412 aagtagcagagagatgatcatatctcgaaagagtcgcacaagaatccaagaataaggaa 471  
 Db 329 aagcactagatgcatgtatccacgctgaaacagtgatgccaacatcgacagcatga 388  
 QY 472 aacagatatacaagaatcatgtgttcatagttttcaagttcaacaagaatatttga 531  
 Db 389 aagatcccaaaacacaaactagctcgtgtcagtttaacctg---aacatgattgtgac 445

QY 532 aggttaagaacaatactgttgagcgtgatgatcaagaagaacagttgttagagatctga 591  
 Db 446 agcccgagaataataatgtgtggtcggtgaataatgaattgagatgagctcgatcaacttg 505  
 QY 592 ctagaagctactcttggggaaccccaagtcacccagatctcgggatggagagcatagta 651  
 Db 506 ctagaagg---aggaagggagactagaagttgtctcactatcgttaagagatggagcatcgga 562  
 QY 652 aacacacttgcaaaagaagtttcaatgatgatccaattatagccgtttgatgttc 711  
 Db 563 aacacacttggctacaacacccctatagtcgctgcatatgtctcgaatttgatattc 622  
 QY 712 atgctgggtctaccatctatctacacagcaacaacaaagaagaatttgcctgggctctgc 771  
 Db 623 gtgcacaaagcaactgtttccacaagatattgtgtagaatagtactccctcagctcttctt 682  
 QY 772 altccacaatccaatgtgacaggggtgaagatgattgtgtgaagcagagctagcagaca 831  
 Db 683 cttgacagaatgatgaactgtat-----gacagctagcggacc 721  
 QY 832 tgttacagaanaagtttaagaagaagagtgacttaattgtcttgatgatcttgagtt 891  
 Db 722 gactgcaaaagcatctgaagaagcagagatactgtgtgactatgtagatgacatagacta 781  
 QY 892 gtgaagttggagatgctgtgaagcagatccttcccaactgaagaacatgacaggaatcgaa 951  
 Db 782 cagaagcttggagatgataataaactatgtttcccgactgtatatac---ggaagcagaa 838  
 QY 952 taagtgtacttaaccgtaatgatgaagtagctgttatgtcgtgtgtgaagaatttctt 1011  
 Db 839 tactcctgactactcgaatgtggaagtgctgtaatatctgtgtlcaagtaagctctc 898  
 QY 1012 tgggagatgagctcctgatgataagaatgagatgagttgagtttccaagaagtgcagattt 1071  
 Db 899 atcacatgcccctcagatatttgcagaagaagttggaatttactacacaaagaatccttg 958  
 QY 1072 caagtgaag---cattacacatagtgttcagagactgttgaagaagaacatcgacagataat 1128  
 Db 959 aaaaagaagttcttattcttctcctgatttgaataatattgggaacaaatgtgataaatt 1018  
 QY 1129 gtacggttaccactaactatctcgtgtgtgcaggctctt---caaatcaaaagga 1185  
 Db 1019 gtggaggtactccttaacatctactgtgattgtgtcgtgactctcccaaaatgggtcaaa 1078  
 QY 1186 caatgaagatggagaacactgtgtcgaagaagtgaatgaatcgttcacaaatgtctcgt 1245  
 Db 1079 gattagaatgagtggaagaagaattggggaataatgttaagtgtgctgtgacacagatcctg 1138  
 QY 1246 atgaacgaatgttcaagtgctgtgtgtgtgagttacagatcacttgacaaagcgaatcctaa 1305  
 Db 1139 aagcacaatgcatgagagtggt 1198  
 QY 1306 catgtctctgcaatttcggaatttttccagaagaacagtgatattccagtgaagaatttga 1365  
 Db 1199 cgtgttcttatttcaatttcaatcagaaggaataacagaattcttcttaaatgtaactg 1258  
 QY 1366 tgaatcatcagatggtcgaagggtctcctga-----agttgaataatgatttggaggag 1419  
 Db 1259 ttgaatttgcctcgttagaaggagatttttgaatgaagaagaagggaacaaagcatagaagg 1318  
 QY 1420 aggttgaagaatgttctgaagaagcttgcgataagttgtctagttcctcgttcgaagaagaa 1479  
 Db 1319 tggcacaacacagtataaagaactatagataagaagcttaatttccacaaatttta 1378  
 QY 1480 gtcgagatggaacaaaatttgatcatgttaagtgatcagatcatataatgacctgtgcg 1539  
 Db 1379 gtttcgtggaacataagaag---tgttgaatgcatgcatgtgacccgtgaactcgtt 1435  
 QY 1540 tgagaagaattccaagggagacatattta 1569  
 Db 1436 tgaagggaagctcgaaacatgaaatttctgtga 1465

```

RESULT 9
AAZ50264
ID AAZ50264 standard; DNA: 10329 BP.
XX
XX AAZ50264;
XX
XX 18-MAY-2000 (first entry)
XX
XX Genomic DNA of potato Gpa2 resistance gene.
DE
XX Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p;
XX marker; IPM4c; 111R; potato Cyst Nematode; PCN; Globodera; nematode;
XX nematode resistance; detection; diagnosis; transgenic plant; ds.
XX
XX Solanum tuberosum.
XX
XX Key Location/Qualifiers
XX misc_signal 1..4874
XX /tag= a
XX /note= "Gpa2 regulatory region"
XX CDS 4875..7850
XX /tag= b
XX /product= "Potato Gpa2 resistance protein"
XX /note= "This region is specifically claimed"
XX exon 4875..7585
XX /tag= c
XX /number= 1
XX /tag= d
XX intron 7586..7822
XX /tag= e
XX /number= 1
XX /note= "Located within the coding region of Gpa2 gene"
XX exon 7823..7850
XX /tag= e
XX /number= 2
XX /note= "Includes the stop codon, TGA"
XX intron 7942..8053
XX /tag= f
XX /number= 2
XX /note= "Located in the 3' UTR of Gpa2 gene"
XX
XX MO200006754-A2.
XX
XX 10-FEB-2000.
XX
XX 30-JUL-1999; 99WO-NL00491.
XX
XX 31-JUL-1998; 98WO-NL00445.
XX
XX (CPRO-) CPRO-DLO CENT PLANTENVERDEDELINGS REPROD.
XX (UYMA-) LANDBOUMUNIVERSITEIT WAGENINGEN.
XX
XX Van Der Vossen EMG, Van Der Voort UNAMR, Lankhorst RMK, Bakker J;
XX Stiekema WJ;
XX
XX WPI; 2000-183132/16.
XX P-PSDB; AAY44818.
XX
XX New isolated Gpa2 nematode resistance gene from potato, useful for
XX producing plants which are resistant to nematodes and polypeptides for
XX use in nematode compositions
XX
XX Claim 62; Fig 3c; 96pp; English.
XX
XX The present sequence is the genomic DNA of the potato resistance
XX gene Gpa2, inserted in the pBINRG2 plasmid. This plasmid is used to
XX transform host plant cells to produce transgenic plants. Gpa2 confers
XX resistance to infection by phytopathogenic nematode of the Globodera
XX genus. It is mapped to the short arm of chromosome 12 (12p) between the
XX markers IPM4c and 111R. This locus is associated with resistance to
XX potato Cyst Nematodes (PCN) like G. pallida and G. rostochiensis, that
XX invade and damage the roots of Solanaceae. It has nematocidal activity.
XX A recombinant DNA sequence comprising the Gpa2 gene sequence can be
XX transformed or transfected into plants, to provide increased resistance

```

```

CC to nematodes. The polypeptides can also be used in nematocidal
CC compositions and for detection and diagnosis of nematode infections.
XX
XX Sequence 10329 BP; 3150 A; 1542 C; 1924 G; 3713 T; 0 other;
SQ
Query Match 8.8%; Score 272.8; DB 21; Length 10329;
Best Local Similarity 54.7%; Pred. No. 3.1e-61;
Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;
OY 232 ttgtcaagaactttgagaaacaatggttttgggaaatgaagcagatttgaagtgaag 291
DB 4987 ttggagaatcttcaatataatggtcgtatcatgaggggttaacaatcttgaagttgaa 5046
OY 292 taagagaagtttgaagtgctgctgtatcaacaattcaactgagactcaacggaactgtac 351
DB 5047 tcaatagagtagcatcacacacagagatgtgtgactcggatacaagaatgttttt 5106
OY 352 ttggagaataataaagccagaaanaaagcgctcgaaagtttcgtcaaaagcctgcaac 411
DB 5107 tagcaggaatttggggaaagaagcaggtctatgtggggattttttcgtcttggaa 5166
OY 412 aagtagcagggagcatgcatcatctgtgaaagatcogacaagaatccaaagaaagaa 471
DB 5167 aagcactagatgcatgtatccaccgtgaaacagtgtgagcaacatcggaacagatga 5226
OY 472 aacaagatcaaaaggaatcatgtttcatgattttcaagttcaacaacagatattga 531
DB 5227 aagatctaaacacacacacagctcacttctcgtttactctgaac---atgatttgagc 5283
OY 532 aggttaagaacaataltgttgcgcgtgtatgatacaaaaggaacagttgttagaagatcga 591
DB 5284 agcccggaatataatgttgcgcgtgaaatgattttgagatgactgtcgtacactgtg 5343
OY 592 ctagaagctactctcgtggaaacccaagtcactccgatttgcggatggaggagatagta 651
DB 5344 ctagaag---aggaagggaactagaagttgttcccaatcgaagggaaggagacgcgga 5400
OY 652 aaacaaccttagcaaaagagtttaccatgtatcatcatcattccgtttgattgttc 711
DB 5401 aaacaacttggctgcgaacaactctatagtatcttaccatcatatgctcgtattgtatcac 5460
OY 712 atgcttgggttaccatattctcaacagcacaacaaaggaatattgtctggcctctcgc 771
DB 5461 gtgcgaagaagcaactgttccacaagatgtgttgaaatgtaactccctagcctctctt 5520
OY 772 attccacaatcaaatgtatgacaggggttaagtattgttgaagcagagctcagcaaga 831
DB 5521 ctttgacaagtgtatgaaacctgattatc-----agctagcggagcc 5559
OY 832 tgttacagaagaagtttaagaagaagaggtacttaattgtcttgaatcgtatgattgaatt 891
DB 5560 aactgcgaagaagcatctgaagagcagagatacttggtagcatattgatatgataatgacta 5619
OY 892 gtgaagtgtggatgycgttgaagcagatgcttccaaactgaagaacaatcgaggaatcgaa 951
DB 5620 cagaagacttggatgataataaactatgttccca---gacttcgataatgaaagcaagaa 5676
OY 952 tactgttgactaccggaatgaatgaatgactgttatgtatgtgtgtgagagaattttctt 1011
DB 5677 tactccctgactaactcgaatgtgtgaagtggtgtgaataatgtaactgaagtaaacctccc 5736
OY 1012 tgcgtagtcatcatgatatgatatgagattgtgagttctttcaaaagtgcagcatlitt 1071
DB 5737 atcacatgagcgcctcatgatttttgacgaagaagtttggaatttactacaacaaagaatctgt 5796
OY 1072 caagtgaag---catccataatgagttcgagacgttggaaagcaaatcgacgaatgatt 1128
DB 5797 aaaaagaagttctatctatctccctgaatttgaataatttggaaacaatattgacttaaat 5856
OY 1129 gtcaacggttaccactaactactgtgtgtgttcgaaggtctc---caaatcnaaagaa 1185
DB 5857 ttggaaggttaccctcagcaattacttgaattgtcgtgacttctcccaaatcagcaaaa 5916

```



QY	712	atgctctgggcaccacatctcaacagcacaacaaaggaattttcttggccttcgc	771
Db	5461	gtgcacaagacacatgcttcacaaagatattgtgagaaatgtactctccttgccctctt	5520
QY	772	attccacaatcaaaaatgatagcagsgggttaagatgatgtgtgaaagcagagctagcaagaca	831
Db	5521	ctttgacaaagtatgaacctgtattatc-----agctagcggacc	5559
QY	832	tgttcagaaaaagtttaagagaagaagaggaacttaattgtcttgtagatattcgagtt	891
Db	5560	aactgcaaaagcactctgaagaagcagsggatacttgtgtagtcactatgacatactvggacta	5619
QY	892	gtgaagtgctggagatgpcgttgcagacatgcttcctccaactgcagaacaatgcaggagatgcogaa	951
Db	5620	cagaagcttgggatagatataaactatgtttccca---gactcgatataatgagaagcaag	5676
QY	952	tactgttgactacccgcgaatgatagtaaatgaactgtttctgtctgtatgagaaattttctt	1011
Db	5677	tactcttgcactactctgcgaatgtgaaatgctgtgatactgtactgcaggttaaacctctctc	5736
QY	1012	tgcgatatgactcatatgatcatcaaatgatagagttgagcttcttccaagaagtcgacatttt	1071
Db	5737	atcacatgcgcctcaatgaattttgacgaagaatttggaaatttactacacaaaagatctttg	5796
QY	1072	caagtgaag---cattaccataatgagttcgcagactgtttgaaaagcaaatcgcagatgaat	1128
Db	5797	aaaaagaaggtcttctatctcctgaatttcaaaatattgcgaacaacatgtgacttaaat	5856
QY	1129	gtcaaggtttccacactactactgttcgttggttcagagctctc---caatctcaaaaga	1185
Db	5857	gtgagaggtctaccctctcaactcaattacttgcgttgcgtgactctctccaatctagtaaa	5916
QY	1186	caatagaagaatttgcnaaactgttgcataaagatgcacgtcattcgcctgcacaatgcattcgt	1245
Db	5917	cattgatgagtgccaaactgatactgtgcggagatgaactgttcgtgtgtaagcacagactctg	5976
QY	1246	atgaacgatgtccatcggtctgtggtgttgatggttaacgatacttgcacaagcgatctctaaaa	1305
Db	5977	aagcaaaatgcatagcagatgttggcttggatgtactacactcattgccttccacttaaac	6036
QY	1306	catgtctctcgcattcttcggaattttcccaagaacagatgatactccagtgaaagaatttga	1365
Db	6037	cgtttcttcgtatttttgcgaattttgcgagagatgaacgattttatgtataataaaacttg	6096
QY	1366	tgaatcatgatagcgtcgcaggggttccctga-----agttgaaaatgatttgcgaagag	1419
Db	6097	ttgagatattggccgttagaaggggttttttggatgaagaaggggaaaaagcatgaagagag	6156
QY	1420	aggtcttgagaagtggttgcagaagctgttcgatagatgctcagtcctcgcgcagagaagaga	1479
Db	6157	tggcagaacaactgtataaagaacactgttgatagatgaagttcaatttctatccaaatagtgta	6216
QY	1480	gtcgaagatgcgaacaaaatagaatcatcatgtaagttcatgatcatatataatgacctgtgag	1539
Db	6217	gtttcttgatggggaacacacagag---atgtgaaatcatgatgagaccgttgaaactctgt	6273
QY	1540	tgaagagaagttcacaagggagacaattttta	1569
Db	6274	tgaaggaaagctcgaacaatgaattttgtga	6303
RESULT 11			
ID AA237153			
XX AA237153 standard; DNA; 5820 BP.			
XX			
AC AA237153:			
XX			
DT 01-FEB-2000 (first entry)			
XX			
DE DNA sequence of BAC77 including the potato Rx gene.			
XX			
KM Potato; Rx gene; resistance gene; potato virus X; PVX; transgenic plant;			
broad spectrum extreme resistance; Narcissus mosaic virus; NMV; NMV; VMV			

Query	Best Local Similarity	Matches 1298;	Conservative	Score 271.8;	DB 20;	Length 5820;
2361 ttgtcaagaactcttgagaanaacatgtlcttttggggaatgacgagatttgaagttagg 291	8.8%;	0;	0;	271.8;	DB 20;	Length 5820;
2361 ttgagaaatctctgacatatacgaatgagcgatcgtgaggggtttacacatttgaaattgaa 2420	48.9%;	0;	0;	4.5e-51;	Indels 105;	Gaps 17;

OY	292	taagaagaagtgtcaagtgcgtgcgtgaatacaacaattcaactgtgagctaaacaggaactgtac	351
Db	2421	tcgtatagaggtatgcatacaacacagaagatatgttctactcggaaaccaagaatgttctt	2480
OY	352	tgggagaagaattaaagaccagaataaaagcgcgctcgaaaggttctgtaaacgcgtcac	411
Db	2481	tagcaacgaatttvgaggaagaagacagggctatgtcggagaatttcttctcctcgaaac	2540
OY	412	aagtagcagagacatlygatalcatctvgaaagtcgcacaagaatccaaagataaagaa	471
Db	2541	aagcactagatgatgtattgtccacgcgtgaaacagtgagtcgcaacatcgcagcacgtga	2600
OY	472	aacaagtatcaaaaggaatcatgtgttcatgattttcaagttcaacaacagatatttga	531
Db	2601	aagatcttaaaaccaacaactagctgcgttgcatttcactt---aacatbattgttagc	2657
OY	532	aggttaagaacaatatgtgttgacgcgtgatgatcaagaagaaacagttgtttagaagatcga	591
Db	2658	agcccgagataataatgtgttcgcccgtgaaaaatgaattttagatgatcgtcgtgaacttg	2717
OY	592	ctagaagctactctctyggaaacccaagaagtcatacccgatttcggtgagtcggagagta	651
Db	2718	ctagag---aggaagggaaactagaagttgtctcaactgtagagtcggagacatcgga	2774
OY	652	aaacaaccttagcaaaaagaagtttacaatgatgaatcaattcatatcgogttttagtgc	711
Db	2775	aaacaacttvtgcatacaaaactctataatgatcgtgcatttgcgtcgtattgtatctc	2834
OY	712	atgccttggtcatcattcccaacacagaacaacaaaagaatattgtcgtggcctctgc	771
Db	2835	gtgcacaaagcaactglttccacaagatattgtgtgaaatgatctcttaggcctcttt	2894
OY	772	atccacaatloaaatlygatgacaggtgttaagaatgttvgtgaacagagctagcacaga	831
Db	2895	cttgcacaagtgatgaaacctgt-----gatcaagctagcgagcc	2933
OY	832	tgttacagaaaaagtttaagaagaagaagtgacttaattgtcttggatgatcatcvgaggt	891
Db	2934	gactgcacaaagcatctbgaagaagacagatgatctgttgaactatgatgacatatgacta	2993
OY	892	gtgaagatgtggagtggtgagacgctgtcttccaaactbaagaacatgcaggagtgcaa	951
Db	2994	cagaagcttgggagatagataataaacatbgttccca---gactgtatataitgaaacagaa	3050
OY	952	tactgttgactaccgcgttaaatgaatgaatgtagctgttatactgtgtttagaagaatttctt	1011
Db	3051	tactcctgactactcctcggaatgtgaaagtgctgtaatatgtctatgctcagttaagcctctc	3110
OY	1012	tgcgagatgagcttcaatlygatcaagaatgagaagttgtagtcttttccaagaatgcagcattt	1071
Db	3111	atccacatgcgctcatgaatttttgcagaagaattgtgatttactatacaaaaagaactcttg	3170
OY	1072	caagttagag---cattacataatgatctcgagacgttvgaaagcaaatcgcagatgat	1128
Db	3171	aaaaagaagaagttcttattctctcgaaatttggaaataatlyggaaacaacatitgatatnaat	3230
OY	1129	gtcacgggttacccactacattgtctgtgtgcaaggcttt---caacttaaaagga	1185
Db	3231	gtgagagattactcttagcaatataactcgtatattgctgtagcttctcccaaatagggtcaa	3290
OY	1186	caataagaagaatlygnaaaactgtgtctaaagatlytcaagtcaltcgtlccaatatgtctcg	1245
Db	3291	gattatagatgtggcaaaagattggggaaatagttaagtctggttagcacagatcctgt	3350
OY	1246	atgaacatgttcaatcgtgtccttggtgtatagatcatcaacttgcacaagcgatataaaa	1305
Db	3351	aagacaacaatlycatagaggtgttggctttagatcaatcatcaactgtcttcaacttaaac	3410
OY	1306	catgtcttcacatcttcggagaattttcccaagaagacagtgatataatcagtgaagaatttga	1365
Db	3411	cggttttctgtatttttgcacaatttcaacagagatgaaacagatttctgnaaatgtactg	3470

QY	1366	tgaatcatgtagatgctgcgaagggttctcga-----agttggaanaatgatgttggaaagg	1411
Db	3471	ttgagttatggtccgcttgagaaaggatcttttggataagaaagggaanaaagcatagaaagg	3530
QY	1420	aggttgagaagtggtttgcaaggagctgttcgatagatgctgcacgtccgcgcgaagaagaa	1479
Db	3531	tggcaacaacatgtatataacgaactatagatataagagcttaatttcatccacaatttta	3590
QY	1480	gtcagatgagcaaaaatatagatcatgltaaaggttcatgatcatatataatgacctgycg	1539
Db	3591	gttttcgtagaacaataagaaag---ttgtgaaatgatgatgttgaccgtgacctgtt	3647
QY	1540	tggagagaagttcacaaggagagaacatttta---tactgaagacattgttcttgacgtat	1596
Db	3648	tggaggaaagcttcgaaaataatgtaattttgtgaaatgtatcatagaaagagttgatacaaat	3707
QY	1597	catatccgaattgtcatatctcctgtatgatatataaagtcgaagcccttaagcgcgtgact	1655
Db	3708	catgtgcacaatccatgcagcgttccctttaagaagtcgaagtcgatacgaatccataag	3767
QY	1657	gtgagtaaatatattatgttcccatggttccttatagaggtcctctta-----	1704
Db	3768	tggaaagaattgcttggtgtcgttaacagtaggcctcatcttatcatcagttgtgtg	3827
QY	1705	-----cccttgtaaatgctgcagttgtagagatcatgacaacaaca--atcttttga	1755
Db	3828	tcgaaatgcgtacacatggaattgtcttccaagctaaagataagataactagatcttgtttga	3887
QY	1753	aagcaaccatctcggttcttcctttcatcttagccttatataatgtgtccaaatcag	1812
Db	3888	ataactgccaatttttccagctggagtaacttctcttaatccatttggataccatctt	3947
QY	1813	aggtgttcatltcaaatctactccaaggtcttggagcttgsa-----cacagacaga	1863
Db	3948	tgcgtttaactcctgttcttcaagaagatcaagatcagaagaagctgttcccatcaaa	4007
QY	1864	ttgatgttctccctcgagataactaagctcatcgtgtg-----agttacc	1911
Db	4008	taataagatctccctcatcgatatacgaagctcatgctatcttgaaaattttaaacttaacc	4067
QY	1912	tatactgttcagataagggaatttgatgtgtacctccagaanaatttgagttatgaaac	1971
Db	4068	ttccattccagttatattatcccttcatattaccatccggaattttgagaatgccacaat	4127
QY	1972	tgcagacattcatgttcaacaggttttcagatcagataataaattttgtcggagaatt	2031
Db	4128	tggagagcgtgtgtatagtgctgtgaattacttggggatcatgagctacagagaacagat	4187
QY	2032	gggaactaatgcaatt---aaggcatcttaaacctgccagatttatttgcagatgyc	2088
Db	4188	tgtttttgaaaaatttgcaltgcctcatcaatattgaccctcgatttgaagaagttct	4247
QY	2089	caagtgtatcgttgaaaagaaggagacttggatttttcaacatta--caaaatttct	2147
Db	4248	tttttagactatttcccaatttaagaagtttgcagatttgcggtccagagaagcttc	4307
QY	2148	tactgtgtccaggtttgtgcagaagaggttatatttgggattccagatgtccaanaaa	2207
Db	4308	gcataatgcagagactgtatgattttcgtactatataatcaagctcgaaagaattgaaattc	4367
QY	2208	ttagaatcagltgnaaataagatgataaagaatttccggactcgtggtcccaac	2267
Db	4428	aagatccctctgaagtttcagacgnaaatatgtcacaagaagatgtatttcggyggaact	4487
QY	2233	gccttttgcaggtatcatatttcaagtgcaaaagcttttccagacagctcgaagaagttga	2382
Db	4488	caactccaaacttactcttaccctccoccgagtgctttccacaaaactttaagaagtttaa	4547
QY	2383	agtt---ggaaaagaacttatcaagctgylcatacttggacatcatagctgaattgcta	2439



```

Db 4548 cttttagggagaattctctgtgctggaagatttgacattgttgaataaccaca 4607
      || || || || || || || || || || || || || || || || || || ||
Qy 2440 accttaagtgctgaagctgtagatgacgctgtgtgtgaagaatgcatcaattg 2499
      || || || || || || || || || || || || || || || || || || ||
Db 4608 aactcgaggtccctatactatactatcagaaatgccttcaaggaaggtggaagtgtg 4667
      || || || || || || || || || || || || || || || || || || ||
Qy 2500 ttatggatttaactgaagcttcttgtaataatagtttttccaagttctgga 2559
      || || || || || || || || || || || || || || || || || || ||
Db 4668 aggaagaggttccctcgaagttctgttcttctgagatgtatatactcgaatcga 4727
      || || || || || || || || || || || || || || || || || || ||
Qy 2560 aagcccaaatgacaatttccctcgtcttgagcgccctcaatgtagaagtgtcaaaat 2619
      || || || || || || || || || || || || || || || || || || ||
Db 4728 gagctagtgtgtacttctcgtactctggaacgagttatctttagagatttcgtaatt 4787
      || || || || || || || || || || || || || || || || || || ||
Qy 2620 tgaagaagataccattgtgtgttcgagatatacacacactacagctgattgtaagag 2679
      || || || || || || || || || || || || || || || || || || ||
Db 4788 tggattcaatccctcgaagattttgcagataataccacactagctcttattgataagatt 4847
      || || || || || || || || || || || || || || || || || || ||
Qy 2680 agtgcctcccaacttggggaattctgctgcagcaatcagaagaacagaagacctcg 2739
      || || || || || || || || || || || || || || || || || || ||
Db 4848 actgtcaacaatctgtgtggaattccgcaagcaaatccaagaacattcaagacaact 4907
      || || || || || || || || || || || || || || || || || || ||
Qy 2740 gaaacaacctgtgtagtctgcatcattcaatccattgaagaaggtgtgattgattcaag 2799
      || || || || || || || || || || || || || || || || || || ||
Db 4908 atggaagctctacgaggtccacactcgtcactcttcttgaagaacattcttctgtgt 4967
      || || || || || || || || || || || || || || || || || || ||
Qy 2800 aagaacattaggaat 2814
      || || || || || || || || || || || || || || || || || || ||
Db 4968 tacacaataatata 4982
      || || || || || || || || || || || || || || || || || || ||

RESULT 12
AAZ37154
ID AAZ37154 standard; cDNA; 3066 BP.
XX
AC AAZ37154;
XX
DT 01-FEB-2000 (first entry)
XX
DE Partial nucleotide sequence of Rx gene cDNA.
XX
KW Potato; Rx gene; resistance gene; potato virus X; PVX; transgenic plant;
KW broad spectrum extreme resistance; Narcissus mosaic virus; NMV; NVX; VMV;
KW Nandina virus X; Viola mosaic virus; Cymbidium mosaic virus; CYMV; PopMV;
KW Poplar mosaic virus; White clover mosaic virus; WCIMV; activate; ss.
XX
OS Solanum tuberosum.
XX
FH Key Location/Qualifiers
FT CDS 1..2864
FT /tag= a
FT /Product= Rx
FT /note= "Resistance gene product"
XX
PN WO954490-A2.
XX
PD 28-OCT-1999.
XX
PF 16-APR-1999; 99WO-GB01182.
XX
PR 16-APR-1998; 98GB-0008083.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Bendahmane A, Baulcombe DC, Kanyuka KV,
DR WPI; 1999-634006/54.
DR P-PSDB; AAY52152.
XX
PT New isolated plant virus resistance gene, used to produce transgenic
PT plants with resistance to virus infection -
XX

```

```

PS Claim 4; Page 87-90; 124pp; English.
XX
CC This is the DNA sequence of the potato Rx gene. The Rx gene is a
CC resistance gene which confers extreme resistance against potato virus X
CC (PVX). Sequence AAZ37153 is the Rx gene including introns. The Rx gene
CC can be used to create a recombinant vector which encodes the Rx
CC resistance polypeptide AAY52152, this vector can be used to transform
CC plant cells to produce a transgenic plant with resistance to PVX. The Rx
CC gene can be used to engineer resistance traits, preferably broad spectrum
CC extreme resistance, into plants. The Rx gene can also be activated by
CC non-PVX viruses, e.g. Narcissus mosaic virus (NMV), Nandina virus X
CC (NVX), Viola mosaic virus (VMV), Cymbidium mosaic virus (CYMV), Poplar
CC mosaic virus (PopMV) and White clover mosaic virus (WCIMV). Rx can be
CC used to offer specific protection against this group. The Rx gene
CC sequence can be used to create antibodies specific for Rx. The antibodies
CC can be used to down-regulate Rx activity and also for the detection,
CC identification or isolation of Rx or homologues.
XX
SQ Sequence 3066 BP; 913 A; 533 C; 675 G; 945 T; 0 other;

```

```

Query Match 8.7%; Score 269.6; DB 20; Length 3066;
Best Local Similarity 54.5%; Pred. NO. 1.3e-60;
Matches 736; Conservative 0; Mismatches 569; Indels 45; Gaps 8;

```

```

Qy 232 ttgtcaagaacttggagaacacaatgttttggggaatgacgagatttgaagtagag 291
      || || || || || || || || || || || || || || || || || || ||
Db 163 tggagaatcctgtcaataataatggtggtatcgtggtggttaacattcttgaaagtgaag 222
      || || || || || || || || || || || || || || || || || || ||
Qy 292 taagagaagttgcaagtgtgtctgaataacacaattcaactgagactaacsagaactgtac 351
      || || || || || || || || || || || || || || || || || || ||
Db 223 tcttagaagtagcatacacacaagaagatgtgtgactcggaatcagaagaatgtttt 282
      || || || || || || || || || || || || || || || || || || ||
Qy 352 tggagaagaataaagaagcagaagaagaagcgctggaaggttttcgccaagcctgcaac 411
      || || || || || || || || || || || || || || || || || || ||
Db 283 tagcacagaatttggagaagaagaagcaggtcgtatgtgtgagatttttctgctctggaac 342
      || || || || || || || || || || || || || || || || || || ||
Qy 412 aagtagcagagagatgatatcatctcgaagaagatcgaacaagaatccaagataaagaa 471
      || || || || || || || || || || || || || || || || || || ||
Db 343 aagcactagaatgatttgatccacgctgaacagtgatgacacatcgacagcagcaga 402
      || || || || || || || || || || || || || || || || || || ||
Qy 472 aacaagtatcaagaagatcatgtgttcatgtattttcaagttcaacaagaatatttga 531
      || || || || || || || || || || || || || || || || || || ||
Db 403 aagatcttaaacccacaactagctcgtctgtcagtttaccg--aacatgagtgtgagc 459
      || || || || || || || || || || || || || || || || || || ||
Qy 532 aggttaagaacaatatgtgtgagctgtagtcaacaagaagaaacggtgttagaagatctga 591
      || || || || || || || || || || || || || || || || || || ||
Db 460 agcccgagaataataatgtgtgtgcgtgaagaatgttagatgtgactgtgatcaacttg 519
      || || || || || || || || || || || || || || || || || || ||
Qy 592 ctagaagctactctgtgggaacccaagatcatccgattgttcgggagtggagacatagta 651
      || || || || || || || || || || || || || || || || || || ||
Db 520 ctagaag--aggaagggaaactagaagttgtctcaactcgttaggtatggagagatcgga 576
      || || || || || || || || || || || || || || || || || || ||
Qy 652 aaacaaccttagcaaaagaagtttacaatgtagtaataattctatgscgtttgattgt 711
      || || || || || || || || || || || || || || || || || || ||
Db 577 aaacaacttggctacaaactatcatatagtgatccgtgcatattgtccgatttgatattc 636
      || || || || || || || || || || || || || || || || || || ||
Qy 712 atgcttggtctacatatctcaacagcacaacaagaagaatttgcgtggcctctgc 771
      || || || || || || || || || || || || || || || || || || ||
Db 637 gtgcaaaagcaactgtttcacacaagaagtattgtgtgagaatgtactcctcctagcctctt 696
      || || || || || || || || || || || || || || || || || || ||
Qy 772 attcacaatacaaaatgtgtagcaggggttaagatgtattgttgaagcagagactgacgaca 831
      || || || || || || || || || || || || || || || || || || ||
Db 697 cttagacagtgatgaaactgtat-----gatcactagtcgagacc 735
      || || || || || || || || || || || || || || || || || || ||
Qy 832 tgttaagcaagaagttaagaagaaggttacttaattgtcttgtagatatacttgagtt 891
      || || || || || || || || || || || || || || || || || || ||
Db 736 gactgcaaaagcatctgtgaagaagcaggaataactgtgttagtcatgtgatactgtgacta 795
      || || || || || || || || || || || || || || || || || || ||
Qy 892 gtgaagtgtgagatgagcgttgagacgagcttccacaactgagaacaatgacagagagttcgaa 951
      || || || || || || || || || || || || || || || || || || ||
Db 796 cagaagcttgtagatataataactatgtttccagactgttataat---ggaagcagaa 852
      || || || || || || || || || || || || || || || || || || ||

```



QY	952	tactgttgaactaccgcyatgatgatgaagcttgtagtcgtgtgtatgaagaattttctt	1011
Db	853	tactccctgaactactcggaaatgltggaagtgctggaatgatctagttcagaagtaagctcttc	912
QY	1012	tgcggatgagcttccatcgtgatcagaagatggaagtttgaagctcttttccaagaagtgcagattt	1071
Db	913	atccaaagcgcctccatgaatttttgaacgaagaagtttgaatttactacacaaaagatcttg	972
QY	1072	caagtgaag---cattaccctatgaqtlctgagagctgttgaagaagaatcgcaagatgat	1128
Db	973	aaaaagaagaagttcttattcttcctcggaatttggaaataatattgsgaacaanaattgcattaat	10322
QY	1129	gtccagsggttaccactaactatctgtcgtgtgttgcagggctctt---caatctctaaagga	1185
Db	1033	gtggagatgattaccctctagcattaccgtgatgtctgtgactctctccaaaatggttcaaa	10922
QY	1186	caatagaagaatttgaaaacctgtgtccaaagaatgtaagtcacatctgttcacaaatgatctt	1245
Db	1093	gattagatgagtgycaaaagaatctggggaanaatgtaagttcgtctgttagcacagaatctgt	11522
QY	1246	atgacacatgtccgctgtgtcttgggttgaatagttacgatacactctgcaagcgaatcctaaa	1305
Db	1153	aagcacacatgcatagagagtggttgcgttgaatccatcactctgtcttccactcaaac	12122
QY	1306	catgtctcttcgcatttcggaattttccagaaagacagtgatattccagtlgaagaatttga	1365
Db	1213	cgtgtttttctgtattttgcatttccactttccacagagatgaacagatttctgtaaatgaactgt	12722
QY	1366	tgaatcatgtgatgctgcgaagggttccctga-----agttggaatatgtatttggaaagag	1419
Db	1273	ttgaattatgacctgtgaagggaatttttgaatgaagaagaagggaanaaagacataagaagag	13322
QY	1420	aggttggagaagatgtttgcaagagctgtgcgatatgatgtctagttcctgtcgcagcaagagaa	1479
Db	1333	tgggacaacacatgtatataaagcaactatagatagaagcctaattttccatccacaatttta	13922
QY	1480	gtcgaagatggacaacaaattatgatactgtaaggttcatgatcatatataatgacgtgtgcg	1539
Db	1393	gtttcgttggacaacatagaag---ttgtggaatgcatgattgtgacccgttgaactctgtt	1449
QY	1540	tgagagaagttcacaaggaggaacattttta	1569
Db	1450	tgagggaagctcgacaacatgaattttgtga	1479
RESULT_13			
AAAS03715	AAAS03715 standard; cDNA; 3014 BP.		
AC	AAAS03715;		
XX	AAAS03715;		
DT	29-AUG-2001 (first entry)		
XX	DNA encoding Rx 72, a modified resistance protein.		
DE	Rx; modified resistance; NBS; IRR; cell death; autoactivator;		
XX	nucleotide binding site; leucine rich repeat; pathogen resistance;		
KW	plant; ss.		
KM	Solanum tuberosum.		
OS	Synthetic.		
XX	Solanum tuberosum.		
OS	Synthetic.		
XX	Key		
PH	Location/Qualifiers		
FT	42..2855		
FT	/*tag= a		
FT	/product= "Modified resistance protein 72"		
XX	W0200129239-A2.		
XX	26-APR-2001.		
XX	12-OCT-2000; 2000MO-GB03930.		

```

Db      688      cttgcaagtgatgagaccgat-----gattcagctagcgagacc 726
QY      832      ttttacaagaagaatttaagaagaagagacttaattgtcttgatgatctgagtt 891
Db      727      gactgcaagaagacatccggaagagcagagatacttgtagcatctgtaagtgaactgacta 786
QY      892      gtgaagtgtggaatgagcgtgagagcagatgcttccaactgaagaacatgacagagtcgaa 951
Db      787      cagaagcttgagagtgatataaactatgttcccgagactgataat---ggaagagaa 843
QY      952      tactgttgactaccgtaataatgatgatagctgttaactgtggtgtagagaatttctc 1011
Db      844      tactcctgactactcgaatgtggaagtgtgctgaatatctagttcgaagtaagcctcc 903
QY      1012      tgcgagtgagcttcagatgagatgagatgagatgagcttcttcacaaagtcagacattt 1071
Db      904      atcactatgcgctcctcgaattttgacgaaagtgtgaatttactacacaaagaattcttg 963
QY      1072      caagtgaag---cattacatatgagctgcgagactgttgaaagcaaatgcagatgaat 1128
Db      964      aaaaagaagatcttacttctccctgaatttgaataatgtgaaacaacattgacttaact 1023
QY      1129      gtacgggtgtaccactcaactatgtcgtgtgttcgagagcttct---caaatcaaaaga 1185
Db      1024      gtggaagatctaccctcgaatctgactgtgactgtcgtcctcctcacaatgtgtcaaa 1083
QY      1186      caataaagatgtgaaactgtgtcctaagatgacagatgcacatcgtacatcctg 1245
Db      1084      gattgagatgagtggaagaagaatttggaagaatgtgaatgcgtcgttgacacagatcccg 1143
QY      1246      atgaacgatgttcaacgtgtgctgtggttgagtgacatacactgtgacaacgactcaaaa 1305
Db      1144      aagcaaatgacatgagagatgtgtgctgtgactgtacatcaactgtcctcctcactaaac 1203
QY      1306      catgtcttctgacttctcgaattttccagaagacagtgatattccagtgagaagaatttga 1365
Db      1204      cgtgtcttctgacttctcgaattttccagaagagtgacagagctgtgaacagatttctgaaatgaaacttg 1263
QY      1366      tgaatcatgacatgacgtgctgtgctcgtga-----agttgaaatgatttgaagagag 1419
Db      1264      ttgagttatgagcctgtgagagagatttttgatgaagaagaagaggaacatagagaagag 1323
QY      1420      aggttgagaagtgctgtgcaagagctgtcgaatagatgtctagtcctcgtcgaagaagaa 1479
Db      1324      tggcaacaacatgataaactatagatagagaacttaatttccatccacaacttta 1383
QY      1480      gtgcagatggaacaaatagatcatgtaaggttcatatcatatcatatgacctgtgag 1539
Db      1384      gtttctgtggaacaaatagaaga---ttgagaaatgcatgagtgcacccgtgaactctgt 1440
QY      1540      tgaagaagaattcaaaagggaacaacttta 1569
Db      1441      tgaagggaagctcgaaacatgaattttgtga 1470

RESULT 14
AAS03717
ID      AAS03717 standard; cDNA; 2880 BP.
AC      AAS03717;
DT      29-AUG-2001 (first entry)
DE      DNA encoding Rx 193, a modified resistance protein.
XX
XX      Rx; modified resistance; NBS, LRR, cell death; autoactivator;
KW      nucleotide binding site; leucine rich repeat; pathogen resistance;
KW      plant; ss.
XX
XX      Solanum tuberosum.
OS      Synthetic.
XX

```

```

FH      Key      Location/Qualifiers
FT      CDS      37..2850
FT      /tag= a
FT      /product= "Modified resistance protein 193"
PN      WO200129239-A2.
XX
XX      26-APR-2001.
PF      12-OCT-2000; 2000MO-GB03930.
XX
XX      15-OCT-1999; 99GB-0024483.
XX      (PLAN-) PLANT BIOSCIENCE LTD.
XX      Bendahmane A, Baulcombe DC;
XX      WPI; 2001-290924/30.
DR      P-PSDB; AA002147.
XX
XX      Modifying activation characteristics of plant resistance proteins to
PT      produce autoactivator polypeptide capable of activation in absence of
PT      elicitor, by introducing modifications in amino acid sequence of
PT      protein -
XX
XX      Disclosure; Page 46-57; 77pp; English.
XX
XX      The sequence represents the coding sequence of Rx clone 193, a modified
CC      resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a
CC      nucleotide binding site (NBS), leucine rich repeat (LRR), and which
CC      mediates cellular response leading to pathogen resistance and/or cell
CC      death or dysfunction in response to an elicitor. The Rx was modified by
CC      introducing modification to the amino acid sequence to produce an
CC      autoactivator polypeptide, capable of activation in absence of an
CC      elicitor. Decoupling of resistance response from its natural elicitor is
CC      useful for developing novel pathogen resistant plants. The modified
CC      resistance proteins are useful for conferring resistance to non-natural
CC      agents or stimuli and also for investigating resistance response pathways
CC      and protein interactions e.g. with activators and repressors.
XX
XX      Sequence 2880 BP; 864 A; 512 C; 641 G; 863 T; 0 other;
SQ
Query Match      8.6%; Score 266.4; DB 22; Length 2880;
Best Local Similarity 54.4%; Pred. No. 8,7e-60;
Matches 734; Conservative 0; Mismatches 571; Indels 45; Gaps 8;
QY      232      ttgtcaagaactttggaataaacaatgttttggggaatgaagagatttgaagtgaag 291
Db      149      tgaagaataatcctgcaataataatggtgcatcatgaggttaacaacttggaaagtga 208
QY      292      taagaagaattgcaagtgtcgtgtaatacaactcaactgagactaagagactgtac 351
Db      209      tctgtagagtgatcatcaacaacagaagatagtgttaccctcggaatcaagaatgtttt 268
QY      352      tgggagaataataaagccagaataaagagcgcgtgcgaaggttctgccaagcctcgaac 411
Db      269      tagcacagattttgagagaagaagaagcaggtcatgtggtgagatttttctgcctcgaac 328
QY      412      aagtagcaagaagacatggtcatatcttgaagaagatgcgacaagaatccaagaataagaa 471
Db      329      aagcactagaatgcatgttcatccacgttgaaacagtgtgacatgcaaatcgacacatga 388
QY      472      aacaagatcaagaagaatcatgttcatgatttttcaagttccaacaacaaatatttga 531
Db      389      aagatctaaaccacaacaactagctcgtgtcagtttaccgt---aacatgttgtgagc 445
QY      532      aggttaagacataatgtgtgagctgtgatcatcaagaagaagaagatgtttagagaatctga 591
Db      446      agcccgagagataatagtgtgcgttgaaatgtaaatgtgatgtatgctgcgtgccaacttg 505
QY      592      ctagaagactactctgaggaaacccaagtcacatcccgatttgcggatggaggacatagta 651

```

Db 506 ctgagag---aggaaggaactagaaagtgltcctaactcgaaggatggagcgatcggga 562  
 QY 652 aagaacattgagaaagaaagttacatgatgatcaatcattacgttcttgatgtc 711  
 Db 563 aagaacattgagaaagaaagttacatgatgatcaatcattacgttcttgatgtc 622  
 QY 712 atgctgggtacatcattcacaacagacacaacaaagaaatttgctggccttcgc 771  
 Db 623 gtgcacaagaacattgttccacaagagattgtgtgagaatgttaactccttagccttc 682  
 QY 772 attccacaatcaaaatgagatgacagaggttaagatgattgttgaaagcagagctgcaaca 831  
 Db 683 cttgacaagtgatgaacccgtat-----gacagctagcggacc 721  
 QY 832 tgttacgaaagtttaagaagaagagagtaacttaattgtcttgatgagatcctggagt 891  
 Db 722 gactgcacaagacatctgaaagcgagagatactgtgtaagcatatgacatacagacta 781  
 QY 892 gtgaagtggtgagatgagcgtagacagcttcccaactgaaagacatgcaagggagcga 951  
 Db 782 cagaagcttggtgagatataaaactatgttccagactgttataat---ggaagcagaa 838  
 QY 952 tactgttgaactaccgtaatagataagatgactgttattgctggtgtgagaaatttctc 1011  
 Db 839 tactcctgactactcgaatgtggaagtggtgataatgtcagatgtcaggttaagcctcctc 898  
 QY 1012 tgcgagtagcttactgataagaatgagatgagatgagcttcttcaaaagtcagacattt 1071  
 Db 899 atccacatgagcctcatgatttctgacgaagatggaatttctcacaacaaagattcttg 958  
 QY 1072 caagtgaag---cattaccatagatcgcagactgtgtggaagcaaaatcgcaagatgat 1128  
 Db 959 aaaaagaaagttctattctcctcctgatttgaataatttgggaacaaatcgtaataat 1018  
 QY 1129 gtcaaggttaccactaactattgtcgtgtgacagggctct---caatctaaagaa 1185  
 Db 1019 gtgagagattacccctcgaacttactgtgattgtgagcttctcctcacaatgtggtcaa 1078  
 QY 1186 caatagaagattgtaaaactgttctaagaagttaagatcattcgttcaaatgtactcgt 1245  
 Db 1079 gattagatgagtggaagaaatcgggaaatgttaagtcgtgctgtgacagatcctgt 1138  
 QY 1246 atgaacagatgttcacgtgtgtgtgtgagttacgatacacttgaacagcgatctaa 1305  
 Db 1139 aagaacatgcatgagatgt 1198  
 QY 1306 catgtctctcgaattcggaaatttccagaagaacagatgatacttccatgtaagaatttga 1365  
 Db 1199 cgtgttctgtatttgcacacttccacagagatgaaacagatgttctgttaaatgaa 1258  
 QY 1366 tgagatcagatgagcgtgagaggttccctga-----agttggaatattgttgaagag 1419  
 Db 1259 ttgagatcagcgtgagagagatttcttgaagaagaagaggaagaaagcattagaagag 1318  
 QY 1420 aggttgaagatgttctgcaagagcgttgcagatagatgtctagctcgtcgcagagagaa 1479  
 Db 1319 tggcaacaacatgataaagactatagatagaagacttaattcattccacatttca 1378  
 QY 1480 gtccgagatggaacaaatattgatacatgttaagttcatgatatataatgacgtgtg 1539  
 Db 1379 gtttctgtggaacaaatagaag---ttgtggaatgcatgtgtgtgacccgtgacatcgt 1435  
 QY 1540 tgaagagatcagaagggagacatttca 1569  
 Db 1436 tgaaggaagctcgaaacatgatttgtga 1465

## RESULT 15

AAS03719  
 ID AAS03719 standard; CDNA; 2885 BP.  
 XX AAS03719;  
 XX

DT 29-AUG-2001 (first entry)  
 XX DNA encoding Rx 32, a modified resistance protein.  
 DE  
 XX  
 XX  
 KW R; modified resistance; NBS; LRR; cell death; autoactivator;  
 KW nucleotide binding site; leucine rich repeat; pathogen resistance;  
 KW plant; ss.  
 XX  
 OS Solanum tuberosum.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT 37-2850  
 FT CDS /\*tag= a  
 /product= "Modified resistance protein 32"  
 W0200129239-A2.  
 PD 26-APR-2001.  
 XX  
 XX  
 PF 12-OCT-2000; 2000WO-GB03930.  
 XX  
 PR 15-OCT-1999; 99GB-0024483.  
 PA (PLAN-) PLANT BIOSCIENCE LTD.  
 XX  
 XX Bendalmane A, Baulcombe DC;  
 PI  
 XX  
 DR WPI: 2001-290924/30.  
 DR P-PSDB; AAU02149.  
 XX  
 PT Modifying activation characteristics of plant resistance proteins to  
 PT produce autoactivator polypeptide capable of activation in absence of  
 PT elicitor, by introducing modifications in amino acid sequence of  
 PT protein -  
 XX  
 PS Disclosure: Page 46-57; 77pp; English.  
 XX  
 CC The sequence represents the coding sequence of Rx clone 32, a modified  
 CC resistance autoactivator. Rx encodes an NBS-LRR polypeptide having a  
 CC nucleotide binding site (NBS), leucine rich repeat (LRR), and which  
 CC mediates cellular response leading to pathogen resistance and/or cell  
 CC death or dysfunction in response to an elicitor. The Rx was modified by  
 CC introducing modification to the amino acid sequence to produce an  
 CC autoactivator polypeptide, capable of activation in absence of an  
 CC elicitor. Decoupling of resistance response from its natural elicitor is  
 CC useful for developing novel pathogen resistant plants. The modified  
 CC resistance proteins are useful for conferring resistance to non-natural  
 CC agents or stimuli and also for investigating resistance response pathways  
 CC and protein interactions e.g. with activators and repressors.  
 CC  
 XX  
 SQ Sequence 2885 BP; 861 A; 514 C; 649 G; 861 T; 0 other;

Query Match 8.6%; Score 266; DB 22; Length 2885;  
 Best Local Similarity 54.7%; Pred No. 1; Le-59;  
 Matches 724; Conservative 0; Mismatches 555; Indels 45; Gaps 8;

QY 258 gttttgggaaatgacgagatttgaagtagaagaaagttgcaagtgctgta 317  
 Db 175 gatcatgaggggttaacattcttggaattgaaatcgtagagtagatacaagaagaa 234  
 QY 318 tacacaattcaactgagactaacaaggaactgttactgtggagaataaagccagaanaaa 377  
 Db 235 gatattgttgaactcgaatcaagaatgttctttagcacaagaatttgaagtagaagac 294  
 QY 378 aaggcgctcgaaggttctgcaagcctgcaacaaagtagcaagtagatcatatc 437  
 Db 295 agggcattgtggagagattgttctcctggaaacaagcactgaagaatgattgctcacc 354  
 QY 438 tgaagagatcgacaagaatccacaagtaaaagaaacaaatgatacaagaagatcattgt 497  
 Db 355 gtgaacagtgtagtgcacaatcgcgacagcatgaaagatctaaacacgaactagctgc 414

```

QY 498 catgattttcaagttcaacaacgataattgaagtgtaagaacataatgttgaagt 557
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 415 ctgtcgttttaacctgaa---catgattgtgacgagcccggaataataatgttgcgt 471
QY 558 gatgatcaagaagaaacagttgttagaagatctgataagaactactctggtgaaccca 617
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 gaaatgaatttgatgtgtgataactctgataagagaa---gggaactaga 528
QY 618 gtcatcccgatgtgcgagatggagagcagaagtaaaacacttagcaaaagaagttac 677
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 529 gtgttccaatcgttagagatggagagcagcgggaaacaaacttgcatacaaaactcat 588
QY 678 aatgataaatcaatctatgacctttagatgtcatgtcgtggtacatctcaacag 737
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 agtgcgcgtgcatctatgtctcgtatgtatctgtgcaaaagcaactgtttcacaagag 648
QY 738 caacaacaaagaaatttgcgtgcgtctcgtcattccacatcaaaatgatgcagag 797
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 tatgtgtgaaatgtactctctagcctcttcttcttgacaagtgtgaacctgat--- 705
QY 798 gttaaagtattgtggaagcagagctagcagacatgttaccgaaagttaagaagaaag 857
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 706 -----gatcagctagcggagccgactgcaaaagcaltcgaagcgag 747
QY 858 aggtactaatgtcttgaatgatatactggaagtgtgaagtgtgagtgcggtgaagcga 917
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 748 agatacttgtagcatgtgatacatatgacatacagaagcttggatgatataaacta 807
QY 918 tgccttccaactgaagaacatgcagagagtcgaactgttgaactaccgtaatgatgaa 977
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 808 tgttccca---gaccttaatggaagaaatactcctgaactactcgaaatgtgaa 864
QY 978 gtagctgttatgtcgtgtgagaagaatttcttctgagatgagcttcatgatcaagat 1037
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 865 gtgctcgaataatgtctgattcagtgtaagcctcccatcacatgcgcctcgaattgac 924
QY 1038 gagaagtggagctcttcaaaatgacgaatcttcaagtgaag---catlaccatagag 1094
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 925 gaaagtggaaattactacacaaaagaatcttggaaaagaaggttcttctcctgaa 984
QY 1095 ttgagagactgttggaaagcaatcgcagatgatagtcaggttaccactaactattgtc 1154
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 985 ttggaataatgttggaaacaaatltgcatlaaaatgttgaagattacctctagcaattact 1044
QY 1155 gtgtgtcagggctctc---caaatctaaagacacataagaattggaaaactgttgc 1211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1045 gtgattgctggaacttctcccaaatggtcacaagattagatgagtgcgaagaattggg 1104
QY 1212 aaaagtatcaagtcattcgtcacaaatgatcgtatgaacatgttcaacgtgtgctggg 1271
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1105 gaaaatgtlaagtcggtcgttagcacagatccctgaagcacaaatgcattgagagtgtgct 1164
QY 1272 ttgagttacgattcacttgacaagcgatctctaaacatgtctctgcatttcgaaatttt 1331
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1165 ttgagttaccacacttgcctctccacctaaacggttcttctgtatatttgcaatttc 1224
QY 1332 ccagaagaacagtatatactccagtgaaagttagatgatacatgagtggtcgtgaggggtc 1391
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1225 aagagagatgaaacagattctctgtaaatgnaactgttgaattatgacctgtgagggattt 1284
QY 1392 ctga-----agtggaaaatgtatttgaagagagaggttgagaagtgttgcagaagcct 1445
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1285 tctgaatgaaagagaggaagacatagaggttgcacaacaacatgtataaagcgaactt 1344
QY 1446 gtcgataagatgtctagtcctcgttcagcagagagaagtcgagatgnaacaaattgatca 1505
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1345 atagataagaagcttaatttctccacaaattttagtttctgcgaaacaaatagaaag---t 1401
QY 1506 tgtaaagttcatgatctaaatataatgacctgtgtgagagagagttcaagggagaaact 1565
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1402 tgtggaatgcagatgtgacccgtgacctgttcttgaggaagagctcgaaacatgaatttt 1461

```

QY 1566 tta 1569  
 Db 1462 gta 1465

Search completed: September 11, 2002, 22:37:03  
 Job time: 39294 sec



•  
•  
•  
•



	/codon_start=1 /protein_id="CAC32382.1" /db_xref="GI:13121543" /translation="MAHSAVASLMTTISLTSPMOSLSCDHRRELCALREKVS SL EYVKNFEKNVNEFEMTDEEVEREVSAAEYTLQRLTGVILEKNSQKKARRER OSLOOVADMDHIMKESSTKIDOKKOVNSKESLIVDSSSPNOLIKAMNMYGDOOR K QLEEDLRSYSSEGPVIVGMSIGKTLAKREVYNDISLREPHVAMATISOQHNK KEILGLHSTIKMDKVMIGIEALMDLOKSLKRRYLIVLDIMSEVMDGVARC PEPEDNAGSRILLTRNDVACVAVENSLRMSMDDESNLSKSAFSEALPYE FEVSGQLADECHGLPLTIVVAGLKSRTIEDKTVAKVSKFVINDPERCSRVL GLSYHLISDLKTLHLGIFPEDSDI PVNKLMSWAEGFLKLENDLEGEKLOE LYDRCLVYSKRSRGTIKRSKVHDLVLDLCEVREKRENTFINMDIVLDVSECSY LCMKOPEKRYTGDEINCPYGLYRALTLPVNRDLRDNHNNLLKTHSVSESLP LTVYLSSEVHFRLKLVLRLRHOIDGPPRELSTLMRYSLSEGNFVPEPELRL WMNQFVORRSDIIFAEIEMQLRLKLPFVYPCDPSGVOKGRHDFSNLO TYSISPRCKTEVIMGIONVKKLGISNKDDYKFSRSGCLPNNLVYIQLEITSLIS VDYSLPVYISSAKAPATLKLKLERLYLSMSYLDITIAELPNLEVLKLMADACC GE MHPYVGFNRKLILIKYSPFKFWKATNDNPFVERLMRSCKNLKEIPFADIHTL OLIEIRECPKLESARIOKEOEDLGNNPVDVIRISNPLKESDSEEH"
BASE COUNT	970 a 514 c 693 g 922 t
ORIGIN	
Query Match	100.0%; Score 3099; DB 6; Length 3099; Best local Similarity 100.0%; Pred. No. 0; Matches 3099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 caaatattctcttgatgaatttgaagtgatattatctgcaattgaattgtgtcatag 60
DB	1 CAAATATTTCTTGAGATTTGAAGTTGATATCTCGAATTTGAATGGTTGGCTATAG 60
QY	61 tcgcaagaacaaacaggaatatacagatatacagatgaagtggtgtctctctta 120
DB	61 TCGCAAGAGCAAAACGAGAAATACAGTATATATGCTCATGCAAGTGTGGCTTCTCTTA 120
QY	121 tggagaacaatagaaatctctcttgaacatcaattcgcgagatgaatctctatg 180
DB	121 TGAGAACAAATAGAAATCTCTTGCATTCATTCGCGAGTGAATCTCTATCTGTGATC 180
QY	181 acagagaagaacttgcgctctcgtgaaagaattagctccctggaagatattgtcaga 240
DB	181 ACAGAGAGAACTTTGGCCTCTTGGAAGATTAGTCCCTGGGAATATTGTCTCAGA 240
QY	241 actttagaagaacaaatgttttctgggaaatagcagatttgaagtagagtaagaag 300
DB	241 ACTTTGAGAAACAAATGTTTTGGGAAATGACGATTTTGAAGTAGAGTAAGAGAAG 300
QY	301 ttgcaagtgctcgtcgtgaataacaaatcaactgaactaagaagaactgtactgggagaa 360
DB	301 TTGCAAGTGCTGTAATACACAATTCACCTGAGACTAACAGAACTGTACTGGGAGAAA 360
QY	361 ataaagccagaaaaaagcgctcgaaggtttcgtcaagcctcgaacagtagcag 420
DB	361 ATAAAAGCCAGAAAAAAGCGCGCTCGAAGGTTTGTCTCAAAAGCCCTGCAACAAGTAGCAG 420
QY	421 aggaacatgatacatctcggaagagtcgacaagaatccaaagataaaggaacaaagat 480
DB	421 AGGACATGATCATATCTGGAAGAGTCCGACAAAGATCCAAAGATTAAGGAAAAACAATAT 480
QY	481 caaagaatacatgtgttcattatcttcaagttcaacaaacgatatcttgaaggttaaga 540
DB	481 CAAAGAAATCATTTGTTTCATGATTTTCAAGTTCAACAAACGATATTGTAAGGTTAAGA 540
QY	541 acaatatggttgtagcgtgatgatcaaaagaaacagtgtagaagatctgactagaagct 600
DB	541 ACAATATGTTGTTGACAGCTGATGATCAAAAGAAACAGTGTGTAAGAGATCTGACTAGAGCT 600
QY	601 actctgggaacccaaagatcccgatgttcggagtgtaggagatgtaaaacaaact 660
DB	601 ACTCTGGGAAACCCAAAGATCCCGATGTGTCGGGATGGAGGCAATAGGTAAACAACCT 660
QY	661 tagcaaaagaagttacatgaatgaatcaatctatgcgctttagatgtcatgtccgtggg 720
DB	661 TAGCAAAAAGAGTTTACATGATGAAATCAATTCATGCGCTTTTATGTTCAATGCCCTGG 720
QY	721 ctacacatactcaacagacacacaaagaaatattgtcgggctctctgattccacaa 780
DB	721 CTACCATTTCTCAACAGACACACAAAAGAAATTTTGTGGGCTCTTGTGATTTCCACAA 780
QY	781 tcaaaatlgatgaaggtttaagaatgttgtagaagcaggagctcagacagatgttaca 840
DB	781 TCAAAATGATGACAGGTTAAGATGATTTGGTGAAGCAGAGCTAGCAGACATGTTCAGA 840
QY	841 aaagtttaagaagaagtagtaactaattgtctcttgaatgatactcggaatgttgaag 900
DB	841 AAAGTTTAAAGAGAAAGAGTACTTAATTTGCTTGAGATATCTGGAAGTGTGAAGTGT 900
QY	901 gggatggcgtgaagcagatgtcttcaactaaagcaatgcaagggaatcgaaatactgt 960
DB	901 GGGATGGCCTTGAGACATGCTTCCAACTGAAGCAATGCGAGGAGTGCAGATACGTTTGA 960
QY	961 ctacccgtaatgaatgaatgactgttgaatcgtgtgtagaagaattctctctgcgata 1020
DB	961 CTACCCGTAATGATGAGTACTGTTATAGCTGTGATGAGAAATTTTCTTGGCGATGA 1020
QY	1021 gcttcaatgatacagaatgaagatgtgaggtcttccaagtgacagatcttcaagtag 1080
DB	1021 GCTTCATGATCAAGATGAGATGAGTGTGAGTCTTTTCAAAAGTCAGACATTTCAAGTGAAG 1080
QY	1081 catlacacatagaatctcgaacatgttgaagaacaaatcgacagatgaatgtcaaggttac 1140
DB	1081 CATTAACATATGATGTTGAGACTGTGGAAGCAAAATCGCAGATGATGTACACGGCTTAC 1140
QY	1141 caactaactatgtcgttgaatgtcgaaggtctcacaatctaaagaacaaatagaaga 1200
DB	1141 CACTAATCTATGTCGGTGTGACAGGCTTCTCAATTCATAAAGCAATAGAAATGGA 1200
QY	1201 aaactgttgcataagaatgaatgaatcgttcaaaatgtccatgaagcagatgtttac 1260
DB	1201 AAACGTGTGCTAAAGATGCAAGTCAATTCGTCACAAATGATCTGATGAAACGATGTTAC 1260
QY	1261 gttgtcgttggttgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1320
DB	1261 GTGTGCTTGGGTTGAGTTAGATCATCTTGACAAACGATTAATAACATGTCTGTGAT 1320
QY	1321 tcggaatttccagaacagatgaatataccagtgaaatcttgaatgaatgaatga 1380
DB	1321 TCGGAATTTTCCAGAAAGACAGTATATTCACAGAAATTTGATGATGATGATGATGATG 1380
QY	1381 ctgaggggttctcgtgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1440
DB	1381 CTGAGGGGTTCTGAAAGTTGAAATGATTTGGAAGAGAGGTTGAGAAAGTGTTCGCAAG 1440
QY	1441 agcttgcataagatgtctatctcgtcagcaagaagaatcgagatgaaatgaatga 1500
DB	1441 AGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
QY	1501 gataatgaaagttcagatgaatataatgaatgaatgaatgaatgaatgaatgaatga 1560
DB	1501 GATATGAAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
QY	1561 acaatttatcatgaacacatgttctcgtcagatcataatccagaatgtctatctct 1620
DB	1561 ACATTTTATATGAAACGACATTTGTCTTGACGATCATATCCAGATGATGATGATGATG 1620
QY	1621 gtaatgataaagtcagaccccttaagcgcgtgagtgatgaatgaatgaatgaatga 1680
DB	1621 GTATGATTAATAATGACAGCCCTTAAAGCGCGAGTGTGATGAAATTAATTAATGATG 1680
QY	1681 atgttcttataaggtctcttaccctctgaaatctgctgagtgatgaatgaatgaatga 1740
DB	1681 ATGTCTTTATAGGCTCTTCTTACCCCTGTAATTCGTGATGAGATGATGATGATGATG 1740
QY	1741 acaatcttgaagaacacacatctgttctctcttcaatctgagccttatatg 1800
DB	1741 ACAATCTTTTGAACGAAACCATCTGTCTTTCTTTTCAATCTTGGACCTTTATATATG 1800



QY 1802 ttctcaaatcagaaggtgttcatctcaattcaaatcgaagcttggagctgagacacagac 1860  
 Db 1801 TTCTCAAAATAGAGAGTGTTCATTTCAAAATTACTCAAGAGCTGTGGAGCTGAGACAGAC 1860  
 QY 1861 agattgatgttccctcgcagagataactaagccatcctggttggagttactatcattgt 1920  
 Db 1861 AGATTGATGTTCCCTCGAGAGATTAAGCCCATCTGTTGAGGTACTACTATCATTTGT 1920  
 QY 1921 tcagctatgggaatttcgatgtaccctccagaatttcgaggttaaggatctcagacat 1980  
 Db 1921 TCAGCTATGGGAATTTGAGAGTACCTCCAGAAATTTGACAGTTATGGAATCTGAGACAT 1980  
 QY 1981 tcaattgctcagaggttccgctcagataataatttttctgtaggaatttggaaactaa 2040  
 Db 1981 TCATTGTTCAACGGTTTCGATCGATTAATTAATTTTGTGAGAGAAATTTGGGAATTA 2040  
 QY 2041 tgcataatgaagcatcttaactcctccagatcttatttgcagagattgcccagtgatctg 2100  
 Db 2041 TGCAATTAAAGCANTTTAAACTGCCGATTTTATTTGCCAGATTTGCCCAAGTGGATCTG 2100  
 QY 2101 ttgacaaaggaagagcattgagatttttcaactacaaactatttcttactgtctccac 2160  
 Db 2101 TTGACAAAGGAGGACACTTGGATTTTCAAACTTACAACTATTCTTACTTGTCTCCAC 2160  
 QY 2161 gtgtgtgcaagaagaggtattataggggattcgaatgtccaataaattggaatcagtg 2220  
 Db 2161 GTTGTGTGCAGAGAGAGGTATTATGGGGATTGAGATGTCAGAAATTTGAGATCAGTG 2220  
 QY 2221 gaataagagtgagctataaagaatttccggagcttggtctcccaaatctgtctcact 2280  
 Db 2221 GAATAAGATGACTATAAAGTTTTCGGGACCTTGGGCTTCCCAACAATCTTGTCTATC 2280  
 QY 2281 tgcagcaacttgaataatagagcttatactatcgttgtgataatagccttttgcagtgatca 2340  
 Db 2281 TGCAGCAACTTGAATAATGAGCTTATATCTGTGATATAGCCTTTTGCAGTGTATCA 2340  
 QY 2341 ttctcaagtgcaaaagcttttcccaagcctcagaagcttgaagttggaagtaactatc 2400  
 Db 2341 TTCTCAAGTGCAGAAAGCTTTTCCAGCAAGCTTCAGAGAGTGAAGTTGGAAGAACTTATC 2400  
 QY 2401 taagctgtgatacttggagacatcatagctgagttgcttaaccttgaagtgctgaagctga 2460  
 Db 2401 TAAGCTGTGATCATCTGGAGATCATAGCTAGTTCCTTAACCTTGAAGTCTGAAGCTGA 2460  
 QY 2461 tggagtaagcgtgtgtgtgtgaagaatgagcatccaatgttcatgaggattaatcagatga 2520  
 Db 2461 TGGATGACGCTGTGTGTGTGGAGAAATGGCATTCCAATTTGATGGGATTAATCGATTGA 2520  
 QY 2521 agcttttgcctaatataatagtttctcaagttctggaaagccacaatgacatatttc 2580  
 Db 2521 AGCTTTTGCCTAATTAATATATAGTTTCTCAAGTTCGGAAGCCACAAATGACAAATTTTC 2580  
 QY 2581 ctgtcccttgaagcctcctcatgattagaaagtgtcaaaaaattgaaagagatcccatgagt 2640  
 Db 2581 CTGTCCCTTGAAGCCCTCATGATTAGAAAGTTGCAAAATTTGAAAGAGATATCCATTGAGT 2640  
 QY 2641 ttgcagatatatacaacaactacagctgattgagttgaagagagttcctcccaaatctggg 2700  
 Db 2641 TTGCAGATATAACACACTACAGCTGATGATGATTAGAGAGAGTTCCTCCCAAACTTTGGG 2700  
 QY 2701 aactcttgcagaaattcaagaagaagaagaagcctcgaaacaaccctgtgagatttc 2760  
 Db 2701 AACTCTGTCACGAATTTCAAAAGAACAGAAAGACCTCGGAAACAACTGTGTGATTTTC 2760  
 QY 2761 gtaactcaaatccattgaagagagatgattcgtatccaagaagaacattgaagaagatct 2820  
 Db 2761 GTATCTCAAAATTCATTGAAGAGAGATGATCTGATTCAGAAAGCAATTAGGAAAGATCT 2820  
 QY 2821 caagtcgaagaagatgaaactcttggagattcaattccgacctctatcacaaatataccac 2880  
 Db 2821 CAAGTCGACGAAGATGAAACTCTTGGATTTCAATTCGGCCCTCTATACAAATAATACAC 2880

QY 2881 taattatcggttccaagcaatgtgtacttccaaggaagatgatatcttgtgtgt 2940  
 Db 2881 TAAATTATCGGTTTCAAGCAATGTGTGACTTCCAAGAGAGATGATATCTTTGTGTGT 2940  
 QY 2941 aacataattttagttagtactgattcccttcccttcccttcttattatgtaacttacta 3000  
 Db 2941 AACATATTTTGAATGAGTACGATTCCTCTCCCTCTCTTTTATGTAACCTTACTA 3000  
 QY 3001 attcaacttcaagtaactagcagaccacatggttattgttgatcgagttgattatctt 3060  
 Db 3001 ATTCAACTTCAAGTACGACGACACATGTTATGTCGACAGTTGATGATTATTT 3060  
 QY 3061 tataagtagacacacagatttagtttaaaaaaataa 3099  
 Db 3061 TATACGATGAGACACACAGTTTATGTTTAAAAAATAA 3099  
 RESULT 2  
 AF202179  
 LOCUS 3099 bp mRNA linear PLN 29-NOV-1999  
 DEFINITION Capsicum chacoense disease resistance protein BS2 (BS2) mRNA,  
 complete cds.  
 ACCESSION AF202179  
 VERSION AF202179.1 GI:6456754  
 KEYWORDS  
 SOURCE Capsicum chacoense.  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.  
 1 (bases 1 to 3099)  
 Tai,T.H., Dahlbeck,D., Clark,E.T., Gajiwala,P., Paslon,R.,  
 Whalen,M.C., Stall,R.E. and Staakawicz,B.J.  
 Expression of the Bs2 pepper gene confers resistance to bacterial  
 spot disease in tomato  
 Proc. Natl. Acad. Sci. U.S.A. 96 (24), 14153-14158 (1999)  
 20040692  
 JOURNAL MEDLINE  
 REFERENCE  
 AUTHORS Tai,T.H., Dahlbeck,D., Clark,E.T., Gajiwala,P., Paslon,R.,  
 Whalen,M.C., Stall,R.E. and Staakawicz,B.J.  
 Direct Submission  
 Submitted (05-NOV-1999) Biology, San Francisco State University,  
 1600 Holloway Avenue, San Francisco, CA 94132, USA  
 FEATURES  
 source  
 1..3099  
 /organism="Capsicum chacoense"  
 /db\_xref="taxon:107817"  
 1..3099  
 /gene="BS2"  
 93..2810  
 /gene="BS2"  
 /function="confers resistance to bacterial pathogen  
 Xanthomonas campestris pv. vesicatoria"  
 /note="NBS-LRR disease resistance protein; functions in  
 tomato"  
 /codon\_start=1  
 /product="disease resistance protein BS2"  
 /protein\_id="AF09256.1"  
 /db\_xref="GI:645675"  
 /translaction="MAHASYAASLARTTESLTPNSPMQSLSCDREELCALREKVESL  
 EYVKNRKNVNGEMTDPEVEEREAASAEYVTLRIETVIGENKSKOKKRRPR  
 OSIIOYAEEMDHITWKESTKIODKGOVRSKSLVHDFSSINDILAKNNVNGDDOR  
 QLELIDLTSTIKMDRVRKIGFAELADMLOKSLKKRRYILVDDITVHAARATTSQHNK  
 KETILLULSHSTIKMDRVRKIGFAELADMLOKSLKKRRYILVDDITVHAARATTSQHNK  
 PTFEDNAGSRILITTRNDDEVAACVAFENFSLRMSFMDODESMLEFSAASSBALYE  
 FETVGRQIDAECHGLEPLTIVVAGLAKSKRTIEDKRTVAADVSEFTNPDEKCSFL  
 GLSYDHLTSDKCTLHPGLFEPDSIDIPYKNIARMSMAEGFLIENDLKEGVKCOE  
 IYDRCLIVTSKRSRDEGFKIRSCVHLLIYDLCYREVOREIIFIMNDIIVLDSVPCSY  
 LCMYKQPKRYTGDDEINCPYLIALTLTPVROLRDNDNNLAKRTSHVSEFHLPE  
 LTVLKSSEVVEHRLKLVLEDRHROIDGFEPIILSLIMLRTLSLSTGNGFNPVEIKL  
 WNIQTFIVQFRSDIITFAEEHLMQDLRLKILPRYLDPCCPGSGSVDKGHLDFSLQ  
 TISLSPRCCTKEVINGIONVKKLGISGNKDYKSPRDSGLPNMLVYLQDLITLSLIS  
 VVSLIPVLISSAKAFPATLKKLERTYLSMSYLDITIELPMLVYLKIMDDACGEE

MHPVGMENRLLKLLIKYSFLKEMKATNDNPNVLERIMISCKNIKEPIEFADHHL  
 QLIBRECPKLEGSARIOKEOEDJNNVDRIRISNPKESDSEBH  
 BASE COUNT 970 a 514 c 693 g 922 t  
 ORIGIN

Query Match 100.0%; Score 3099; DB 8; Length 3099;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3099; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caaatctctctgagtgaaatttgaaagtgtatatactgcaattgaatgtgtgtag 60  
 Db 1 CAAATATTTCTTGAGTGAATTTGAAGTTATATCTGCAATGAATGTTGGACAG 60  
 QY 61 tcgcaaaagacaaaacagaaatacagatatatgtctcagtgcaagtgtgtctctta 120  
 Db 61 TCGCAAAAGACAAAACAGAAATACATATATATGCGCAAGCAAGTGTGCTCTCTA 120  
 QY 121 tgagacacataagatctctctgacatcgaattcgcgatgcaatctctctgtgac 180  
 Db 121 TCGAACAATAGAAATCTCTCTTGACATTCATTCGCCATGCAATCTTATCCTGTATC 180  
 QY 181 acagaaagaaactctgctctctctgtaaaaagttagtccctggaagattgtcaaga 240  
 Db 181 ACAGAGAAAGAACTTGGCCCTCTCTGTAAGAAAGTTAGTCCCTGGAAGTATTTGTCAAGA 240  
 QY 241 actttgagaaacaaatgttttttgagaaatgagcagatttgaagtagagtagaag 300  
 Db 241 ACTTTGAGAAAACAAATGTTTTTGGGAAATGACGAGATTTGAAATAGAGTAAAGAGAG 300  
 QY 301 ttgcaagtctgctgtaatacaaatcaactgagactcaagaaactgtactgtggaaga 360  
 Db 301 TTGCAAGTCTGCTGAATACAAATTCACAGACACTAACAGAAAGTACTGTGCGAGAAA 360  
 QY 361 ataaagacagaaacaaagcgcgctgaaaggttctcfaaagcctgtgaaacaaagtag 420  
 Db 361 ATAAAAGCCAGAAAAGGCGCGTGAAGGTTCTGTAAGCCGTGAACAAAGTAGAG 420  
 QY 421 agagacatgatactctggaagaagtcgaacaaagatccaagataaagaacaaagat 480  
 Db 421 AGGACATGATATATCTGGAAGAGTGCACAAAGATCCAGATTAAGAAACAAAGATAT 480  
 QY 481 caaagaaatcattgttcaatgattttcaagtccaacaaagataatttgaagtaga 540  
 Db 481 CAAAGAAATCATTTGGTTCATGATTTTCAAGTCAACAAAGATATTTGAAGGTTAAGA 540  
 QY 541 acaatagtgtgagcgtatagatacaaaagaaagattgttgaagatctgtcgaagct 600  
 Db 541 ACAATATGTTGGAGCGTATGATCAAAAGAAACAGTTGTTGAAAGATCTGACTGAAAGCT 600  
 QY 601 actctgagaaacccaagtcatcccgatgtcgcgagatgagagcaatgataaaacaact 660  
 Db 601 ACTCTGGGGAACCCAAAGTCATCCGATTTGTGGGATGGAGGCAATAGTAAACAACCT 660  
 QY 661 tagcaaaagaagttacaatgataatctctacgttttgaatgttcaatgtcgtg 720  
 Db 661 TAGCAAAAAGAAAGTTACATGATGATCATCTATGCCGTTTTCATGATGCTGCGG 720  
 QY 721 ctaccatctcaacagacacaaacaaagaaattgtctgagcctctgtatctccaa 780  
 Db 721 CTACCAATATCTCAACAGCACAAACAAAGAAATTTTCTGAGGCTTGTGCAATTCACAA 780  
 QY 781 tcaaaatgatacagaggttcaagatgtgtgaacagagactagcaagacatgttcaaga 840  
 Db 781 TCAAAATGATACAGGGTTAAGATGATGTTGGAAGCAGAGCTAGCAACATGTTACAGA 840  
 QY 841 aaagttaagaagaagaagtaacttaattgtcttgatgatactgtgagttgtgaagt 900  
 Db 841 AAAGTTTAAAGAAAGAGGTACTTAATGTTCTTGATGATATCTGAGTGTGTAAGTGT 900  
 QY 901 gggatggcgtgagacagatgttccaactgaagacaaatgcagagagtagtaactgttga 960  
 Db 901 GGGATGGCGTGAGACGATGCTTTCCAACTGAAGACAATGCAGAGGAGTGGAAATGCTTGA 960

QY 961 ctaccgtaatgataagtagcttctgtatgtcgtgtgtgagaatcttctctgcagaga 1020  
 Db 961 CTACCGTAATGATGAAGTAGTGTGTTATGCTGTGTGATAGAAATTTTCTTGGCGATGA 1020  
 QY 1021 gcttcatacgaatacagaatgagatgtgagatcttctcaaaagtgcagacatttcaagtgaag 1080  
 Db 1021 GCCTCATGATCAAGATGAGATGTGAGTCTTTCAAAAGTGACAGATTTTCAAGTGAAG 1080  
 QY 1081 caatacacaatgagctcagactgttggaaagcaaatcgcagatgaatgtcaggggtac 1140  
 Db 1081 CATTACCATATGAGTTCGAGACTGTTGAAAGCAAAATCCAGATGAAATGTCAAGGGTTAC 1140  
 QY 1141 caataactatgtcgtgtgtgtgagggcttctcaaatctaaagagacaaatagaagattga 1200  
 Db 1141 CACTAACATATGTGTGTGTGTGACAGGCTTCTCAAAATCTTAAAGACAAATAGAAATGGA 1200  
 QY 1201 aaactgtctcaaaagtgtcaagtcactgcacaaatgatacctgataagaagtgtaac 1260  
 Db 1201 AAACGTGTCTAAGATGTCAGATCATTCGTCACAAATGATCCTGATGAACGATGTTAC 1260  
 QY 1261 gctgtcgt 1320  
 Db 1261 GTGTGCTTGGGTGAGTTAGATCACTTGAACAAGCCATCTAAACAAATGTCTTGTGCAAT 1320  
 QY 1321 tcggaatttctcagaagaacagatgatactccagtgagaatgtatgatacattgagatg 1380  
 Db 1321 TCGGAATTTTCCAGAAAGACAGATATTCACATGAAGAAATTTGATGAGATCATGATGAG 1380  
 QY 1381 ctgaaggggtctcgtgaagtgtgaaatgatttgaagaagaggtgtggaagtgtttgcaag 1440  
 Db 1381 CTGAGGGGTTCTGAAAGTTGGAAGAAATGATTTGGAAGAGAGGTTGGAAGTGTGTTGCAAG 1440  
 QY 1441 agctgtcgaatagatgtcgtcctcgtcgaagaagaagtcgagatggaacaaatata 1500  
 Db 1441 AGCTGTGATATGATGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1500  
 QY 1501 gatactgataagatcattatataatgacctgtcgtgagagaagttcaagaggaga 1560  
 Db 1501 GATCATGTAAAGTTGATGATCTAATATATGACCTGTGCGGAGAGAAAGTTCAAGGAGAA 1560  
 QY 1561 acatttctacatgaacagacatgttctctgagatcatcatatccagaatcttcaatctct 1620  
 Db 1561 ACATTTTATCATGACGACATGTTCTTGTGACCTATCATATCCAGATGTCTCATATCTCT 1620  
 QY 1621 gtaatgataaagcagcccttaagcgcgtgacgtgtgagatgaatataatgttccct 1680  
 Db 1621 GTATGTATTAATGCAAGCCCTTAAAGCGCGTGTGATGTAATTAATTAATGTCCT 1680  
 QY 1681 atggtcttataaggtctcttaccctgtataatcgtcagttgagatcatgacaaca 1740  
 Db 1681 ATGCTCTTATAGGGCTCTTATACCCCTGTAATGCTGATGAGATGATCATGACAAACA 1740  
 QY 1741 acaacttttgaagaagacccatctcgttctcttcaatccttgaagccttataatag 1800  
 Db 1741 ACAATCTTTTGAAGCAAGCCATCTGTTTCTCTTCAATCTGAGCCCTTATTAATTAAG 1800  
 QY 1801 ttctcaaatcagaagtgatcatcttcaaatctcaaatctcaaatcttgaagcctgaagacagac 1860  
 Db 1801 TTCTCAAAATCAGAGGTTGTTCAATTTACTTCAAAAGCTTGGAGCTGAGACACAGAC 1860  
 QY 1861 agattgtgttccctcgaagatacgaagcctcaatcgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1920  
 Db 1861 AGATTGTGTGTTCCCTCGAGAGATCTAAGCCCTCATCTGTTGAGAGTACTCATCTTGT 1920  
 QY 1921 tcaagctatggaaatttcagatgatacctccagaagaatttgcaggttataagatctgcagacat 1980  
 Db 1921 TCAGCTATGGAATTTGATGATGATCTCCAGAAATTTGCAAGGTATGGAATCTGACACACT 1980  
 QY 1981 tcaatgtcagaagttcgaatcagataataatcttctgctgagagaatttggaaactaa 2040  
 Db 1981 TCATTTGTTCAACGGTTTGCATCAGATATTAATTTTGTGAGGAAATTTGGAACTGA 2040

QY 2041 tgcataaaggcatcttaaacctccagatttatttgcagatgcccagatgactg 2100  
 |||||  
 Db 2041 TGCAATTAAGGCACTTAAACTGCCCAGATTATTTCGCCAGATTGCCAAGTGGATGTG 2100  
 QY 2101 ttgcaaaaggagagcacttggatttttcaaaacttacaactatttctactgtctccac 2160  
 |||||  
 Db 2101 TTGACAAAGGAAGGACACTTGGATTTCCTCAAACTATATCTTACTGTCTCCAC 2160  
 QY 2161 gttgttcagcagaaggagttatttattgggattcagaatgtcaaaaaaataggaaatcagt 2220  
 |||||  
 Db 2161 GTTGTTCACACAGAGAGGTTATTAATGGGGATTCAGAAAGTCGAAAAAATTAAGAAATCACTG 2220  
 QY 2221 gaataaggatgactataaaagatttcgggacttgggacttcccaacaactttctatc 2280  
 |||||  
 Db 2221 GAAATTAAGATGACTATTAATAAGTTTGGGACTTGGGCTTCCCAACATCTTGCTATTC 2280  
 QY 2281 tgcagcaacttgaataattgacttataatctgttgaattatagacttttgcagtgatca 2340  
 |||||  
 Db 2281 TGCAGCAACTTGAATAATTGAGCTTTATCTGTGATTAAGCTTTTGGCAGTGATCA 2340  
 QY 2341 ttcaagtgcagaaagctttccagcaacgctcaagaagtgtgaagttggaagaactatc 2400  
 |||||  
 Db 2341 TTTCAGGTGCAAAAGCTTTTCCAGCAACGCTCAAGAAAGTTGAAGTTGAAAGAACTTATC 2400  
 QY 2401 taagctggtacttggacatactagctgagtgctgaacttgaagtgctgaagctga 2460  
 |||||  
 Db 2401 TAAGCTGCTACTTATGGACATCTAGCTGAGTTGCTTAACCTTGAGGTGCTGAAGCTGA 2460  
 QY 2461 tggatgagcgttctgtgtggaagaatggacatccaatgttataaggttataatcgatga 2520  
 |||||  
 Db 2461 TGGATGAGCGCTTGTGTGTAAGAAATGGCATCCAAATGTTATGGGATTTAATGATGTA 2520  
 QY 2521 agcttggcttaataataatagatttcttcaagttctggaagcgcaacaataatcttctc 2580  
 |||||  
 Db 2521 AGCTTGGCTAATTAATAATAGTTTCTCAAGTTCTGAAAGCCCAATATACAAATTTTC 2580  
 QY 2581 ctgaccttgaagcgccatgataagatttgcagaaacttgaagaagataccacttgaat 2640  
 |||||  
 Db 2581 CTGCTCTTGAAGCGCTCATGATGATGAAGTTGCAAAATTTGAAAGATACCAATGAGT 2640  
 QY 2641 ttgcagatatacacacactacactgtatgattgaagagagtgctccccaacttgggg 2700  
 |||||  
 Db 2641 TTGCAGATATACACACTACAGCTGATTTGAGTTAAGAGATGTCTCCCAAACTTGGGG 2700  
 QY 2701 aatctgctgcaggaattcagaagaagaagaagacctcgcgaagaacacttggatgtc 2760  
 |||||  
 Db 2701 AATCTGCTGCAGAAATTCAGAAAGAACAGAACTCCTCGAAACAACTTGATGTTTC 2760  
 QY 2761 gtaactcaaatcacttgaagagagtgatctgtatcagaagaacattagaaagatct 2820  
 |||||  
 Db 2761 GATCTCAAAATCCATTTGAAGAGAGTGTATCTGATTCAGAAACATTAGAAAGAGATCT 2820  
 QY 2821 caagcgcaagaagattgaactcttgggatttcaattcgcgcctctatcaaaaataaccac 2880  
 |||||  
 Db 2821 CAAGCGCAAGAAGGATTTGAACCTTGGGATTTCAATTTGCGCCCTATACACAAATATACAC 2880  
 QY 2881 taatttgcggttcaagcaaatgtgtgacttcaagagagatgtatattcttltgtgt 2940  
 |||||  
 Db 2881 TAAATTTTCGGTTTCAAGCAATGTGTGACTTCCAAAGAGATGTATCTTTTGTTGTGT 2940  
 QY 2941 aacataattttgagttgactgattccctctccctctctcttcttataacttacta 3000  
 |||||  
 Db 2941 AACATATTTTGAAGTTGACTGATTCCTCTCTCTCTCTTTTATAGTAATCTTACTA 3000  
 QY 3001 attcaacttcaagtagcagagacacatggtgtgattgtgacgaagtttgaattatct 3060  
 |||||  
 Db 3001 ATTCAACTTCAAGTACTAGCAGACACATGTTGATTCAGAGTTGATGATTAATTT 3060  
 QY 3061 tatacagtagaagcaacagtttagttttaaataaaaaaaa 3099  
 |||||  
 Db 3061 TATACGATGAGACACCAAGTTTATGTTTAAAAAATAAAA 3099

RESULT 3  
 AX076880  
 LOCUS AX076880 31491 bp DNA linear PAT 22-FEB-2001  
 DEFINITION Sequence 1 from Patent WO0107635.  
 ACCESSION AX076880  
 VERSION AX076880.1 GI:13121541  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Capsicum annuum.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.  
 1 (bases 1 to 31491)  
 Staskiewicz, B.J., Dahlbeck, D. and Tai, T.H.  
 B52 resistance gene  
 Patent: WO 0107635-A 1 01-FEB-2001;  
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
 REFERENCE  
 JOURNAL  
 TITLE  
 FEATURES  
 location/Qualifiers  
 1. 31491  
 /organism="Capsicum annuum"  
 /db\_xref="taxon:4072"  
 BASE COUNT 9652 a 6344 c 5992 g 9503 t  
 ORIGIN  
 Query Match 88.0%; Score 2725.6; DB 6; Length 31491;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2728; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 53 ggtcataagtcagaaagacaaacgagaatcacatataatgacttgcagtgctgc 112  
 |||||  
 Db 1440 GGTCAATAGTCCCAAAAGGACAAACGAGAAATACAGTATATATATGCTCATGCAAGTGGC 1499  
 QY 113 ttctcttatgagaacaatagaatctctcttgaatcaatccgcgcatgcaatctctatc 172  
 |||||  
 Db 1500 TTCTCTTATGAGAACAAATAGATCTCTTACATTCATTCGCGATGCAATCTCTATC 1559  
 QY 173 ctgtgatcacagagaagaacttgcgctctcgttgaagaagttagttccctgaagatct 232  
 |||||  
 Db 1560 CTGCTATCACAGAGAAAGACTTTGGGCTCTTCGTGCAAAAAGTATGTTCCCTGGAAGTAT 1619  
 QY 233 tgtcaagaactttgagaanaacaatglttttctggggaatgacggaatttgaagtagagt 292  
 |||||  
 Db 1620 TGTCAAGAACTTTGGAATAAACAATGTTTGGGGAATGACGGAATTTGAAGTGAAGT 1679  
 QY 293 aagagaagtgcagtgctgtctgtgaatacaaatcaacttgaactgaagaactgtact 352  
 |||||  
 Db 1680 AAGAGAACTTCAAGTGTCTGTAATACACAATTCMACTGAGACTAACAGAACTGTACT 1739  
 QY 353 gggagaataataaagccagaaanaaagcgctgcgaaggttctgtaaaagcctgcaca 412  
 |||||  
 Db 1740 GGGAGAAATTAATAAACCAGAAATAAAGGCGGTGCAAGGTTTCTCAAGCCTTCAACA 1799  
 QY 413 agtagcagagacatgatactatctggaagaagtcgacaagaatcacaagataaaagaa 472  
 |||||  
 Db 1800 AGTAGCAGAGACATGATGATATCTGGAAGAGTCGACAAAGATCCAAAGTAAAGGAA 1859  
 QY 473 acaagatcaagaagaatcatgtgttcatgatttttcaagttcaaaaaacgatatattgaa 532  
 |||||  
 Db 1860 ACAAGTATCAAAAGGAATATTTGGTTCATGATTTTCAAGTTCAACAAACGATATTTTAA 1919  
 QY 533 ggttaagaacatatggttgcagtgatgatacaagaagaacagttgttagaagatctgac 592  
 |||||  
 Db 1920 GGTTAAGAACAAATATGTTTGGACGTGATGATCAAAAGAAACAGTTGTTAGAAAGCTGAC 1979  
 QY 593 tagaagctactctggygaaccacaaagtcacccgatttgcggatggygaagcatagtaa 652  
 |||||  
 Db 1980 TAGAAGCTACTCTGTGGGAACCAAGATCATCCGATGTGCGGATGGGAGCATAGGTAA 2039  
 QY 653 aacaacttgaagaaagagtttacaatgatgaatcaattctatgacgttttgaatttca 712  
 |||||  
 Db 2040 AACCAACTTAGCAAAAAGAGTTTACAAATGATGATCAATCTTATGCGCTTTGATGTCA 2099

QY	713	tgctgggctaccacatctctcaaacagacacaaaaggaatcttgctgggctcttca	772
Dp	2100	TGCTGGGCTACCAATCTCTAAGACACACAAAAAGAAATTTGCTGGGCTTCTCA	2159
QY	773	ttccacaacaataatggtatgcagaggltlaagatgattgtgaagcagagctagacagat	832
Dp	2160	TTCCACAATCAAAATGATGTACAGGGGTAAAGATGATGGTGAAGCAGAGCTAGCAGACAT	2219
QY	833	gttcagaaaaagttlaaaggaaagggtacttaatttgcttgatgatattctggaagt	892
Dp	2220	GTTACACAAAAGTTTAAAGAAAGAGGTCTTAATTTGCTTGATGATCTGGAGTTG	2279
QY	893	tgaagtgaggatgagcgctgagacgatgcttccaaactgaagacaaatgcagaggatcgat	952
Dp	2280	TGAAGTGTGGGATGGCGGTGAGACGATGCTTTCCAACTGAAGCAATGCGAGGAGTGCAGAT	2339
QY	953	acgtgtgactaccocgtaagatgaagtgaaactgttatactgtgtgtggtgataagaaatttcttc	1012
Dp	2340	ACTGTTGACTACCCGTAATATGATGAAGTAGTGTGTATGCTGGTGTAGAGAAATTTTCTTT	2399
QY	1013	gcgagatgagcttactgaatcaagaatgaagggttggaatctttccaaagtgcagacttcc	1072
Dp	2400	GCGGATGAGCTTCATGATATGAATGAGACTTGGACTCTTTTCCAAAGTGCAGCATTTTC	2459
QY	1073	aagtgaaagcaatcaacatgagtctgcagactgtgtggaagacaaatcgagatgtaatgca	1132
Dp	2460	AAGTGAAGCATTTACCAATATGAGTTTCGAGACTGTTGGAAGCAATCCGAGATGATGCA	2519
QY	1133	cgggtaccactaactactgttcgtgtgttcgagggtcttccaaactaaaggacaatga	1192
Dp	2520	CGGGTTTACCACTAACTATTTGCTGGTTCAGGGCTTCCAAATGTAAAGACCAATGGA	2579
QY	1193	agattggaaaaacgtgtgcataaagtctcaagatcttcgaatcttcgcaaaatgtaacctgaagc	1252
Dp	2580	AGATTGAAAAACTTGTCTTAAGATGTCAAGTATTCGTGCACAAATGATCCTGATGAGACG	2639
QY	1253	atgttccagtgtgctgtgggttgagttaagatcaatcaacttgacaagcgatcttaaaacatgctc	1312
Dp	2640	ATGTTCACGTTGCTGGTGGTGTGAGTTACGATCACTTGCACACCGATCTAAAMACATGTCT	2699
QY	1313	tctcatcttcggaattcttccagaagaagatgatatcttcagtgaaagaaatttgatagaatc	1372
Dp	2700	TCTGCATTTTGGGAATTTTTCACAAAGACAGTGTATTCACAGTGAAGAATTTGATGAGATC	2759
QY	1373	atggaatggtctgaagggttccctgaagtttgaaaaatgatttgaaagagaaggttgagaagt	1432
Dp	2760	ATGATATGCTGAGGGGTTTCTCTGAAATTTGGAATAATTTGGAGAGAGGTTTGACAAATGT	2819
QY	1433	tttccagaagcttgatagatagatgattagtccttcctgcacagaagaagaatgcagatgagac	1492
Dp	2820	TTTGCAAAGAGCTTGTGCATGTAGTGTCTAGTCTCGTCAAGCAAGAAAGTCCGATGGAC	2879
QY	1493	aaaaatagatcatgtlaaagttcatatgatactaaatatatgacctgtgcgtgagagaagtca	1552
Dp	2880	AAAAATTAGATCAATGATGAAGGTTTCATGATCAATATATGTACCTGCTGAGAGGAAGTTCA	2939
QY	1553	aaggagaacatttttatactgaagaacattgttcttgaagatataatataccaagaatgtc	1612
Dp	2940	AAGGGAACAATTTTATTCATGTAGACACATGTCTTGTGACGATATATATCCAGAAATGTTC	2999
QY	1613	atacctctgatgataaataatgcagcccttaagcgcgtgactgtgtgaatgaattaatla	1672
Dp	3000	ATATCTCTGATGTATATAAATGAGCCCTTTAAGCCGTGACTGGTGTGTAATTAATTAATTA	3059
QY	1673	ttgtccctatggtcttataagggctcttcttaacctgtlaaactgctcaagttgagagatca	1732
Dp	3060	TTGTCCCTAATGAGCTTATATATGGGCTCTTCTTCAOCCCTGTAATATCGTCAAGTTGAGAGATCA	3119
QY	1733	tgaacaaacaaatcttltgaagaagacccatctgttctctcttcaacttgaacccctt	1792
Dp	3120	TGACAAACAAATCTTTTGAAAGAACCAATCTGTGTTTCTCTTTTCACTTTGACCCCTTT	3179
QY	1793	atactatgcttccaaatcgaaggtgtgtcaattccaattactcaaaagctctgagagctgag	1852

[illegible]

VERSION AX076883.1 GI:13121544  
 KEYWORDS Capsicum annum.  
 SOURCE Capsicum annum.  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I; Solanales; Solanaceae; Capsicum.  
 REFERENCE 1 (bases 1 to 2718)  
 AUTHORS Staskawicz, B. J., Dahlbeck, D. and Tai, T. H.  
 TITLE Bz2 resistance gene  
 JOURNAL Patent: WO 01/06357-A 4 01-FEB-2001;  
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
 FEATURES  
 source  
 location/Qualifiers  
 1..2718  
 /organism="Capsicum annum"  
 /db\_xref="taxon:4072"  
 CDS  
 1..2718  
 /note="unnamed protein product"  
 /codon\_start=1  
 /protein\_id="CAC32383.1"  
 /translation="MAHASVSLMRTTESLTPSPMOSLSCDREELCARREYSSL  
 EYFKNEKNNEBEMTDFEVEVEVASAETTYQLRLTGLVLENNKSKKARRER  
 QSLQVADMDHMKESTKIQDKGVSKESLVHDFESSINDILKANNMVGRODK  
 QLEDLIRSYSGEPKVIPIVGMGIGITTLAKEVYNDESILCRPDVAMATISQHNK  
 KEILGLHSITKMDRVMKIGEAELMDLQKSLKRYLIVLDIDMSCEWDEVRC  
 PTEIDNAGSRILLTTRNDENVACYGAVENESLRMSMODESMLSEKSAFSEALPYE  
 FEYVKQIADCEHGLPLIYVAGLILKSKRTIEMLKTYAKVDFSVNDDPERCSRL  
 GLSYDHLISDLCGLHFGIPEDSDIPYKILMSMAEGFLKLENDLESEVEKLOE  
 LYDRCLIVSRSRSDGTRKIRCKVHDITDLCREVORENIFIMNDIVLADSEPCST  
 LCKTKMPFRKVTGDEINCYGILYRALLTPEVNQLDHDNNILKRLHVSFSEHLEP  
 LYLKSEVVAFLKLKLELHRQIDEPREILSLIMLRYLSLSYSGNFDVPEPCRL  
 MNLOTFIVORESDIIFAEIEMLMQLRHLKIDRYLPDPSGVNFRILDESNLO  
 TISLSPRCSTKEVIMGIOWKRLKISGNKDKYSPFDSGLPNLVYLOOETISLS  
 VDSLPLVITISAKAPATLKLKLERTYLSMSYLDIAELPNLEVEYKIMDDACGGE  
 WHYVMSFNRKLILIKKSPLEKFKATNDNPNVYERLMIRNCKWLKEPIEFADITLL  
 QLELRCPPLGLESARIQEDEDLGNPNVDVIRISNPLESDSSEH"  
 BASE COUNT 851 a 454 c 623 g 790 t  
 ORIGIN  
 Query Match 87.7%; Score 2718; DB 6; Length 2718;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 513 tcacaaacgatatattgaaggttaagaacaataatgttgagcgtgatcatgaagaa 572  
 DB 421 TCACAAACGATATTTTGAAGGTTAAGAACATATGTGTTGAGCGTATATCAAGGAAA 480  
 QY 573 caattgttaagaatctgaactagaactactctcgtggaaacccaagtcatccgatgtgc 632  
 DB 481 CAGTTGTTGAAGATCTGACTGAGAGCTACTCTCGGGGAACCCAAAGTCATCCCGATTGTC 540  
 QY 633 gggatgggagcgcatggttaaaccaaccttgaacaaaagaagtttacatgaatcaatt 692  
 DB 541 GGGATGGGAGCGCATGGTAAACCAACCTTAGCAAAAAGATTYACATATGATGATCAATT 600  
 QY 693 ctatgccgtttgatgattcatgctcgtgggttacatcatcccaacagacacaaaaggaa 752  
 DB 601 CATGCCGTTTGTGATGTTTATGCTCGGTGACCATATCTCCAACAGCACACAAAAAGGAA 660  
 QY 753 atttgcctgggcttccttgatccacaaatgaatgaatgaatgaatgaatgaatgaat 812  
 DB 661 ATTTGCTGGGCTTCTGTCATCCCAATCAAAATGATGACAGGGTTAAGATGATTGGT 720  
 QY 813 gaaagcagcgtcagcagcgttgaagaagaatttaagaagaagaaggttaagattgtc 872  
 DB 721 GAAGCAGACCTAGCAGACATGTTACGAAAAGTTTAAAGAAAAGGTTAATTTGTC 780  
 QY 873 ttggaatgatatcgtgaatgttgagtgagtgagtgagtgagtgagtgagtgagtgag 932  
 DB 781 TTGGAATGATATCTGGAGTTGTGAAGTGTGAGTGGCGGTGAGAGATGCTTCCAACTGAA 840  
 QY 933 gacaaatgcagggagtcgaatctgtgactaccgtaataatgaatgaatgaatgaat 992  
 DB 841 GACAAATGCAGGGAGTCGAATGTTGACTGTGACTACCGGTAAGAAAGAAAGTACTGTTATGCT 900  
 QY 993 ggtgagaagaatttctcttcgtgagtgagtgagtgagtgagtgagtgagtgagtgag 1052  
 DB 901 GGTGTAGACAAATTTTCTTCTTGGCGGATGACCTTACGATCAAGATGAGGTTGCACTTT 960  
 QY 1053 ttcaaaatgcagcatttcaaatgaagcattaccatgaatgaatgaatgaatgaatgaat 1112  
 DB 961 TTCAAAAGTCAGCATTTTCAAGTGAAGCATTACCATATGAGTTGAGATGAGATGTTGGAAG 1020  
 QY 1113 caaatgcagatgaatgtcagcgtgttaccaactaatatgtcgtgtgagcgttcctc 1172  
 DB 1021 CAAATGCAGATGAATGTGCACCGGTACCATATGTTGCTGTTGTCAGAGGCTTTC 1080  
 QY 1173 aaactaaaggaacaaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 1232  
 DB 1081 AATCTAAAGACCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGCTTC 1140  
 QY 1233 acaaatgacctgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 1292  
 DB 1141 ACAATGATTCGATGAAGATGTCACGTGCTTGGGTTGAGTTAGATGATGATGATGATGAT 1200  
 QY 1293 agcgaatcaaaaacatgtctctcgtcattcggaaattttcagaagaacagtgatattcca 1352  
 DB 1201 AGCGATCTAAAAAACATGTCTCTGCAATTCGAAATTTTCCAGGAAGACAGTCAATTTCCA 1260  
 QY 1353 gtgaagaattgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 1412  
 DB 1261 GTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
 QY 1413 gaaggaaggtttgaagaatgtttgacaagcctgtcgaatagatgtcctgtcctgc 1472  
 DB 1321 GAAGGAGAGGTTGACAAGTGTTCGAAGGCTTGCATGATGATGATGATGATGATGATGATGAT 1380  
 QY 1473 aaggaagtcgagatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 1532  
 DB 1381 AAGGAAGTCGAGATGAAGCAAAAATTTAGATCATGATGATGATGATGATGATGATGATGAT 1440  
 QY 1533 ctgtgcgtgaggaaggttcaagaggagaaacattttacatgaagaacatgtgtttac 1592  
 DB 1441 CTGTGCTGAGAGAGATTCAAAGGGAGAACATTTTATCATGAAAGCAATGTTGTTTAC 1500  
 QY 1593 gtatcatatccagaatgtcatatctcgtatgtataaagcagccctttaagcgctg 1652

Db 1501 GATATCATCCAGAAATGTCATCTCTGATGTAATAATGAGCGCTTTAAAGCGGTG 1560  
 Qy 1653 aacggtgatbaaataattatgtccctatgtgtcttataaggctcttctaaccctgta 1712  
 Db 1561 ACAGGATGTAATTAATTAATTTGCTTATGAGGCTTCTCTTAACCCCTGTA 1620  
 Qy 1713 aatcgtcagttgagagatacgaacaacaatcctttgaaacgaaccatctgttttc 1772  
 Db 1621 AATCGTCAGTTGAGATCATGACAAACAACCTTTTAAACGAACCCATCTGCTTTC 1680  
 Qy 1773 tcttcaatctgagccttataatgttctcaaatcagaggttttcaattcaaat 1832  
 Db 1681 TCTTTTCATCTTACGCTTTATTTATGTTCTCAATTCAGAGGTCTTCTATTTCAATTA 1740  
 Qy 1833 ctcaaaagtttgagcttgagacacagacagatgtgttccctcgagagatactaaagc 1892  
 Db 1741 CTCAGAGCTTTGGAGCTGAGACACAGACAGATGATGTTCCCTCGAGAGATACTAAGC 1800  
 Qy 1893 ctcatctgtgtgaggtacctatcatctgttcagctatgggaatttgatlaacctcagaa 1952  
 Db 1801 CTCATCTGGTTGAGTACTATCTATCTGCTAGTGAATTTGATGTACTCTCAGAA 1860  
 Qy 1953 atttcaggtatgagaaatctgacagacatcatgttcaacggttccgacagataata 2012  
 Db 1861 ATTTCAGGTTATGGAATCGCAGACATTCATTTCAACGGTTTCGATCAGATATAATA 1920  
 Qy 2013 attttgtcgaagaaatttggaactaatgcaatgaagcatcttaactgccagatt 2072  
 Db 1921 ATTTCGCTGAGAAATTTGGGAATTAATGCAATTAAGCATCTTAACCTGCGCAATTT 1980  
 Qy 2073 tatttcagagattggccaaagtgaatctgttgaagaagaagagacttgattttcaaac 2132  
 Db 1981 TATTTCGCAAGATTGCCAAGTGAATCTGTGACAAAGAGAGCCATTGGAATTTTCAAC 2040  
 Qy 2133 ttacaactatcttactatgttccacgltgttgacgaaggaaggttataatggagatt 2192  
 Db 2041 TTACAAACATTTCTTACTGTTCTCCACGTTGTCACAGAGAGGATTTATTTGAGGATTT 2100  
 Qy 2193 cagaagtcgaaataatagaaatcagtggaataaagatgacataaaggttttcggagc 2252  
 Db 2101 CAGAAATGTCAAAATTAAGGAATCAGTGGAAATTAAGGAATGATTAATAAGTTTCCGGAC 2160  
 Qy 2253 tctgggtctccacaactctgtctactctgacgaactgaaatatttgatctatcatc 2312  
 Db 2161 TCGGGCTCCCAACATCTGTCTATCTGACCAACTTGAATTAATTTGAGTCTTATATCT 2220  
 Qy 2313 gttgattatagccttttgacagtgatcaatctcaagtgcgaagcctttccagcaagctc 2372  
 Db 2221 GTTGATTTATAGCCTTTTGGCAGATCATTTCAAGTGCAAAACCTTTCCAGCAACGCTC 2280  
 Qy 2373 aagaagtgtgaagtgtgaagaacttactgaagtgtgtcacttgagacatcaagtctgag 2432  
 Db 2281 AAGAAGTGTGAAGTGGAAAGAACTTTATCTAAGCTGTGATCTTGGACATCATAGCTGAG 2340  
 Qy 2433 ttcgctaactctgaggtgtcgtgaagctgatatgacgctgtgtgtgtgtgaagaatggcat 2492  
 Db 2341 TTGGCTTAACCTTGAGGTGCTGAAGCGATGATGAGCGCTTGTGTGTAAGAAATGGCAT 2400  
 Qy 2493 ccaattgtatggagatttaataatgaaagcctttgctaataataatgcttttccaag 2552  
 Db 2401 CCAATTCCTATGGGATTTAATCATGAAACCTTTTGTCTAATTAATAATGTTTCTCAAG 2460  
 Qy 2553 ttcggaagaaccaaataatgcaatttccgtctctgagagcgtctcagttgataagttgc 2612  
 Db 2461 TTCTGGAAACCCCAAAATGCAATTTTCCGTCTTGAAGCGCTCATGATTAAGAAATTTGC 2520  
 Qy 2613 aaaaatttgaagaagataccatctgagtttcagatatcacacacttaagctgattgag 2672  
 Db 2521 AAAAATTTGAAGAGATACCATTTGAGTTTGCAGATATACACACTTACAGCTGATTTGAG 2580  
 Qy 2673 ttaagagatgtccctccaaacttgagggaatctgctgcagcaaatctcagaagaagaaga 2732

Db 2581 TTAAAGAGGTGCTCCCAAACTTGGGGAATCTGCTGCAGCAATTTGAGAAAGAACAGAA 2640  
 Qy 2733 gacctcggaacaacacctgtgagatgttcgtatctccaatccatctgaaagagatgtctc 2792  
 Db 2641 GACCTCGGAAACAAACCTGTGATGTCTGATTCATCAATCCATGGAAGAGATGATCT 2700  
 Qy 2793 gattcagaagaacattag 2810  
 Db 2701 GATTTCAGAAACATTAG 2718

## RESULT 5

AX012619  
 LOCUS AX012619 3201 bp DNA linear PAT 07-SEP-2000  
 DEFINITION Sequence 14 from Patent WO954490.  
 ACCESSION AX012619  
 VERSION AX012619.1 GI:9998603  
 KEYWORDS

## SOURCE

ORGANISM Solanum juzepczukii.  
 Solanum juzepczukii  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; eusterids I; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 3201)  
 AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
 TITLE Plant-derived resistance gene  
 JOURNAL Patent: WO 954490-A 14 28-OCT-1999.  
 BAILCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA KONSTANTIN VALEKIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)

## FEATURES

Location/Qualifiers

1..3201

/organism="Solanum juzepczukii"

/db\_xref="taxon:136614"

BASE COUNT 953 a 556 c 682 g 1010 t

## ORIGIN

Query Match 8.9%; Score 275.6; DB 6; Length 3201;  
 Best Local Similarity 55.1%; Pred. No. 3.1e-52;  
 Matches 730; Conservative 0; Mismatches 549; Indels 45; Gaps 8;

Qy 258 gtttttggaagaatgaagatcttggaagtagaagtagaagagatgtgcgtcgaa 317  
 Db 176 GATCATYAGGAGTTAAACATCTTGGAAGTTGAATCTTGAAGTACATTCACACAGAA 235  
 Qy 318 tacacaactcactgagctacaggaactgtactggaagaataataaagccagaataaa 377  
 Db 226 GATACGTTGACTCGGATTCAGAAAGTGTCTTTTACGACAGAAATTTGAGAGAAAGAAC 295  
 Qy 378 aagcgctcgaaaggttctgcgaagcctgcaacaagtagcagaagacatgacatcatc 437  
 Db 296 AGGGCTAAGTGGAGATTTTCTGCTTTGGAAACAGCACTAAGTAATGCATTGATTCACAC 355  
 Qy 438 tggaaaggttcgacaagaatccagaatgaagaagaagaatcagaagaatcattgct 497  
 Db 356 GTGAAGACGTGGAGGCAACATCGGACAGCATGAAAGATCTTAAACCAACAACTACGTCA 415  
 Qy 498 catgattttcaagttcaacaacagatatttgaagttgaagaacaatatgtgtgagcgt 557  
 Db 416 CTTTGCACTTTAACCTGACAC---ATGCTTTTGAGCAGCGCTGAGAAATTAATGCTGGCGCT 472  
 Qy 558 gatgtcaagaagaacagttgttagaagatcgtactagaagctactctgtggaaacccaa 617  
 Db 473 GAAATGAAATTTGAGATGATGCTGAGATCACTTTGAGAGAGGANA--GGGAACCTGAA 529  
 Qy 618 gtcaatccgattgttcggaatggaagagacatgaataaacaacttagaagaagaagttac 677  
 Db 530 GTTGCTCAATCGTAGGAGTGGAGGTGCGGAAACAACTTTGGCTACAAACTCTAT 589  
 Qy 678 aatgataatcaatctatgcggtttgagtgtcatgctcgtggtctacacatactcacaag 737  
 Db 590 AGTATCTCTTACATTAATGCTCGATTTGATTAATTCGTGCAAAAGCACTGTTTCAAGAG 649



QY 738 cacaacaaagaagaatttgcctgagccttcgtacatccacaatacaatgatgacag 797  
 Db 650 TATGTGTGAGAAATGATACCTCTAGGCTCTCTTCTTGACAAAGATGAACTGAT --- 706  
 QY 798 gttgaagatgatgtgtgaagcagagcagacatggttaacagaaagtttaagagaag 857  
 Db 707 -----GATCAACTACCGGACGACACTGCAAAAGCATCTGAAAGGCGAG 748  
 QY 858 aggtactaatgtctgagcagatcgtgaggtgtgagagtgtaggggtgagaga 917  
 Db 749 AGATACCTGGTAGTCATGATGACATATGACTACAAAAGCTTGGGATGATATAAATA 808  
 QY 918 tgccttccaactgaagaacatgagagagtgagacatggttgaactaccgttaagatga 977  
 Db 809 TGTTCCTCA---GACTGTTATAGGGAAGACAGAACTACCTGACTACTCGGAATGTGAA 865  
 QY 978 gtaactgttatgctgtgtgtgagagaatttctcttgagatgagctcaatgataag 1037  
 Db 866 GTGCTGATATGCTAGTACGATAGGCTCTCATCAACAGCGCTCATGATATTTTGAC 925  
 QY 1038 gagaggtgagctcttcaaaagtcagacatttcaagtgaag---catcaacatag 1094  
 Db 926 GAAAGTTGGAATTTACTACACAAAAGATCTTTGAAAAGAGAGGTTCTTATTCCTGAA 985  
 QY 1095 ttccagactgttgaagaacacatgcagatgacatgacaggttaccactaactatgtc 1154  
 Db 986 TTTGAAATATATTGGGAACAAATGATTAATATGTGGGATTAACCTCTGACAAATTACT 1045  
 QY 1155 gtgtgtcagaggtctc---caaatctaaagacaatagaagattggaagaactgtgct 1211  
 Db 1046 GTGATGTGCTGACTCTCTCCAAAATCAGTAAACATGATGATGAGTGCACAAAATGTTGCG 1105  
 QY 1212 aaagatgtcaagatcattcgtacaaatgatcctgatgaacagatttccagctgtgctgg 1271  
 Db 1106 GAGATGTGAATGCTGGTGTGTAAGCAGATCTTAAGCAAAATCAGTACAGATGTTGGCT 1165  
 QY 1272 ttgagttacagctcacttgaacaagcagatcactaaacaatgtcttcgcatttcggaatttt 1331  
 Db 1166 TTGAGTTACCATCACTTCCCTTCTCACCCTAAACCGTCTTTCTGTATTTGCAATTTTC 1225  
 QY 1332 ccagaagaacagtgataltccagtgagaagatttgatgacatgagatgctcagaggttc 1391  
 Db 1226 GCACAAATATGAAACGATTTCTGTAACTTAACCTGTTGAGTTATGCGCTGTAGAGGGCTTT 1285  
 QY 1392 ctga-----agttggaataatgatgttgaagaagaggttgaagagctt 1445  
 Db 1286 TTGATGAAGAGAGGAAAGAGATGAGAGAGGTGCGAAGACATGATTAACGAGCTT 1345  
 QY 1446 gtccatagatgtctagtcctcgtcagcaagaagtcgagatggaacaaatgatcatca 1505  
 Db 1346 GTATATGAAGCTTAATTTCTATCCACATTTTGATTTTGATGG---GAAAATGAAAAGT 1402  
 QY 1506 ttttaagttcaatgactaataatgacctgtcgtgagagaagttcaaaaggaagaacatt 1565  
 Db 1403 TGTGGAATGCAATGATGTGACCCCTGAACTCTGTTTGAAGGAACTCGAACAATGAATTTT 1462  
 QY 1566 ttta 1569  
 Db 1463 GTAA 1466

RESULT 6  
 STU249449  
 LOCUS Solanum tuberosum GPA2 gene for NBS-LRR protein, exons 1-3.  
 DEFINITION Solanum tuberosum GPA2 gene for NBS-LRR protein, exons 1-3.  
 ACCESSION AJ249449  
 VERSION AJ249449.1 GI:5911744  
 KEYWORDS GPA2 gene; NBS-LRR protein; nucleotide binding and leucine-rich repeat.  
 SOURCE potato.  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE  
 1 (bases 1 to 3254)  
 AUTHORS Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 TITLE Agrobacterium transient expression system as a tool for the isolation of disease resistance genes: application to the Rx2 locus in potato  
 JOURNAL Plant J. 21 (1), 73-81 (2000)  
 MEDLINE 20117531  
 REFERENCE 2 (bases 1 to 3254)  
 AUTHORS Bendahmane, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-SEP-1999) Bendahmane A., Sainsbury Laboratory, John Innes Center, Colney Lane, Norwich NR4 7UH, UNITED KINGDOM  
 FEATURES  
 source  
 1..3254  
 /organism="Solanum tuberosum"  
 /variety="CARA"  
 /sub-species="andigena"  
 /db\_xref="taxon:4113"  
 /chromosome="12"  
 /tissue\_type="Root"  
 /tissue\_11b="Root"  
 /country="Peru"  
 /note="NEW"  
 join(<47..2757,2995..3113,3226..>3254)  
 /gene="GPA2"  
 /product="NBS-LRR protein"  
 47..3254  
 /gene="GPA2"  
 47..2757  
 /gene="GPA2"  
 /number=1  
 join(47..2757,2995..3022)  
 /gene="GPA2"  
 /function="Globodera pallida disease resistance gene"  
 /codon\_start=1  
 /product="NBS-LRR protein"  
 /protein\_id="CA855838.1"  
 /db\_xref="GI:5911745"  
 /db\_xref="SPTREMBL:Q9S704"  
 /translation="MAYAAVTSIMRTIHQSNEIQLGCDLPYERLKLRLATLEKSCNI  
 MGDEGLTLEVEIIEVAVTEDVDESRLVFLARNGKSRAMGIFVLEQALBC  
 IDSTVKOMMATSDMDKLPQTSLSVLPEDVDQPEININWRENEREMDOLARGL  
 RELVEVSIIVGGIGKTTIAAKIISDPIINSRPDIRAKATYSOBYCVARNVILGLISL  
 SDEPDYDLOLOLKHIGKRLIVYIDIMTEANDDIKLCPPDCDNGSRILITRRNE  
 VAETASSGKPPHHRLNPFDSNMLHKKLFEKGSIPFENIGKQALKGGPLA  
 ITLLAGLLSKISKTLDEMONVAENVRVSTDLKACMRVIALSYHHLPSHLKPCFLY  
 FAIPEDEIRIYVNLVELMAVEGFLNEEGKSIDEVETCINELVDSLISIHVSPD  
 GEIQRCEMHIDVRELCLREARNMNFVNIIRKSDONSCAOSQCSFSRSRISIHNEE  
 ELVWCRNSEASHSITTLICIPKCVTLSPFKLVRYVDLGLTTCPIRPSGVLSLIRYLS  
 LRNPRIQOYRGSKEAVPSSTIDIPLESISSICYOTKIVHPNPNYPTILSPILTM  
 POLRLDKGMWNTLSHPTERRLVLSLQCLNEINPRTGSPFLRLPNKLKEVGY  
 KEDRRNRKDLIDFERYLYQLERLAFSTYSSSACFLKNTAPGSLPPDPLRQMETLHL  
 ETHSRATAPPDVFLPPDCFPOMLKSITFGDFELMKDLSIVGLKPLKLVQL  
 SHNFKGEEMVEVEGPHLKFLELDSIYIRYVASSDHPFYLERLFLSDCFYDSIP  
 RDPADITTLALIDIFRCQGSVGNASKQIQDQIQNYSISIEVHRYLYRNAGFLVW"  
 2758..2994  
 /gene="GPA2"  
 /number=1  
 2995..3113  
 /gene="GPA2"  
 /number=2  
 3114..3225  
 /gene="GPA2"  
 /number=2  
 3226..>3254  
 /gene="GPA2"  
 /number=3  
 957 a 577 c 689 g 1031 t

BASE COUNT  
 ORIGIN  
 Query Match 8.8%; Score 272.8; DB 8; Length 3254;





```

Db      446 AGCCGAGAAATATATGTTGGCCGTGAAAATGATTTGGAGATGANGCTGGATCAACTTG 505
Oy      592 ctgaagactactctgggaaacccaaagtcaccccgatctgcggatggagagcaga 651
Db      506 CTGAGAG---AGGAAGGAACTAGAACTGTCTCAATCGTAGGGATGGAGGATCGGGA 562
Oy      652 aaacacacttagcaaaaagaagtttaacaatgataatcaatctcattcgctttgat 711
Db      563 AACCACTTGGCTACAAAACCTATAGTATCCGTCGATATTATGTCGATTGATATTC 622
Oy      712 atgctggggtaccatatactcaacagacacaaaagaagaatttgcgtgacctgc 771
Db      623 GTCCAAAGCAACTGTTTCAACAAGATATTGTGTGAAATGATCTCCCTGGCCCTTTT 682
Oy      772 attcccaatcaaatgagatgacagggttaagatgattggtgagacagagctagaca 831
Db      683 CTTTGACAACTGATGAACCTGAT-----GATCAGCTAGCGGAC 721
Oy      832 tgttaagaanaagtttaagaagaagaagttacttaattgtcttgatatactgagtt 891
Db      722 GACTGCAAAAGCATCTGAAAGGAGGAGATCTGTAGTACATGATGACATATGACATA 781
Oy      892 gtgaagttgagagtcgctgagacgagatgcttccaactgagaacaatgcaggagtc 951
Db      782 CAGAAGCTGGGATGATATTAACCTATGTTCCAGACTGTATTAAT---GGAAGCAGA 838
Oy      952 tactgttactaccgtaattgataagtagctgttaagtgtgtgtagaagaattttctt 1011
Db      839 TACTCTGACTACTCGAATGAGAGTGGAGTGAATATGCTGATGAGTAACTCTCTC 898
Oy      1012 tgcgagttgagcttcaatgataagatgagatgagatgagcttccaagaatgcagact 1071
Db      899 ATGCAATGGGCTCCTGATGATTTTGAGCAAAAGTTGGAATTTACTACAAAAGATCTTG 958
Oy      1072 caagtgaag---cataccatagatcgagactgttgaagaacaatgcagatgaat 1128
Db      959 AAAAAAGGTTCTTATTTCTCCCTGGAATTTGCAAAATTTGGAACAACAAATGATTAAT 1018
Oy      1129 gtacaggtttacacactactgtctgtgtgcaaggctct---caacttaagaaga 1185
Db      1019 GTGGAGGATTTACTCTTACGCAATTTACTGTGATCTGTGACTTCTCTCCAAAATGGCTCAA 1078
Oy      1186 caatagaagaattgaaacactgtctgtaagaatgataagtcacatcgcacaatgactc 1245
Db      1079 GATTATGATGAGTGAAGAAGATTTGGGGAATAAGTTAGTTCGCTTAGCAGACATCTG 1138
Oy      1246 atgaacgagttcaagtgctgtggttgaagttacgatacactgacaagcgacttaaa 1305
Db      1139 AAGCAAAATGCAATGAGAGTGTGGCTTTGAGTTACCATCTTCCCTTCTCACCTTAAC 1198
Oy      1306 catgtctctgcatcttcggaattttccagaagaacagttgatatccagttgaagaatt 1365
Db      1199 CGGTTTCTGTATTTTGGCAATTTTTCACAGAGGATTAACAGATTTTCTTAATGAACCTG 1258
Oy      1366 tgaatcatgagatgctgagaggttctctga-----agtgaanaatgatttgaagg 1419
Db      1259 TTGAGTTATGGCCTGTAGAGGAGATTTTGAATGAGAAGAGGAAAAAGCATGAGAAG 1318
Oy      1420 aggttgaagaagtggttgcagaagcctgtcgatagatgctagtcctcgctgaagaaga 1479
Db      1319 TGGCAACAACATGTATTAAGCACTTATAGTAGAAGCTTAATTTTATTCATCCAAATTTTA 1378
Oy      1480 gtgagaagtgaacaaaatagatcatgttaagttcatgatcaatatatgacctgtgc 1539
Db      1379 GTTTTGTGGAACAATAGAAAG---TTGTGGAATGCATGATGACCCCGTAACCTCTGT 1435
Oy      1540 tgaagaagttcaaaaggagacatttta 1569
Db      1436 TGAGGAGAGCTCGAACAATGAATTTTGTGA 1465

```

RESULT 8  
AF195939

```

LOCUS      AF195939      10331 bp      DNA      linear      PLN 31-Oct-1999
DEFINITION Solanum tuberosum disease resistance protein Gpa2 gene, complete
ACCESSION  AF195939
VERSION     AF195939.1
KEYWORDS   potato.
SOURCE      Solanum tuberosum
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE  1 (bases 1 to 10331)
AUTHORS   Van der Vossen, E.A.G.
TITLE      Direct Submission
JOURNAL    Submitted (19-OCT-1999) Genomics, CPRO, Droeendaalsesteeg 1,
            Wageningen 6708 PB, The Netherlands
FEATURES   source
            source
            1..10331
            /organism="Solanum tuberosum"
            /db_xref="taxon:4113"
            /chromosome="12"
            /clone="BAC 111"
            /sub_clone="PB1NRG2"
            /note="Introgressed from Solanum tuberosum ssp. andigena"
            /join("4876..7586,7824..>7851)
            /product="disease resistance protein Gpa2"
            /join(4876..7586,7824..7851)
            /note="L2-NBS-LRR protein; confers disease resistance to
            potato cyst nematode Globodera pallida Pa2-D383"
            /codon_start=1
            /product="disease resistance protein Gpa2"
            /protein_id="AF04603.1"
            /db_xref="GI:6164969"
            /translation="MAYAVTSIMPTIHOSMETGCDLPYFKLSIRALIEKSCNI
            MGHBSLTLLEVEITLAVATTEDMVDSESNVFLANVGRKSRAMGCTFFVLEALBEC
            IDSTVQMMATSDSMKDLKPQTSVLSLEPHEVDEQENITWGENEVEEMLDLARG
            RELLEVSVIVMGIGIGTTLAKLYSDPYINSRDIAKATVSOEYEVRLVGLISLT
            SPEVDOLDOHLKGRRLVYVIDIWTTEAMDIDIKLCPDGDGSRLLTTRNVE
            VAEVASSGKPPHMRMLNMFDSNMLLHKITFEEGSYSPFENIGQIALKGGPLA
            IYILAGLLSKISTLDEMONVANENSVYSTDLKACMYLALSYHHLSHLKPCLY
            FAFADERITYNKLVEALNVAEGLFNEEGRKSEAEVETCNLNVRSLSINVSFD
            GTFQRCGMHDVTELECLREARNNNFNVNLRKSDNSCAQSMQCSKRSNRSIINHE
            ELVWNCSEANSHLITLCIFKCYVLESLFKLYVLDGLTTCPLFGSGVSLHLRYLS
            LRFNPLQOYRSGKEAVPSIIDIPLSISLCYLOFKLYHPNCPYPLIPSEILTM
            POLRKICGMNNTYRSHEPTENRNVYKSLQCNLEINRYCGSRGLRPLNPKLEVEGV
            KEDPRHKLVDPRYLYOEXKLAFTSYSSACGLKNTAPDICTPODDPLRQWETHL
            ETRSRATPPTDVPFTFLRPPDFFPNLKSLTSGPFLAMKDLISYVKLPKLEVLQ
            SHNAEFGEEVEEYEPHLKELFLDSITIRWRASDHPYLERLFLSDCFYLSIP
            RDPADITTLALIDIFRCQDSVGSARQI00DIODNDSISIEVTRVLYRNGAEVY"
BASE COUNT 3150 a 1542 c 1924 g 3714 t 1 others
ORIGIN
Query Match 8.8%; Score 272.8; DB 8; Length 10331;
Best Local Similarity 54.7%; Pred. No. 1,2e-51;
Matches 738; Conservative 0; Mismatches 567; Indels 45; Gaps 8;

```

OY	472	aaagatcaaaagatcaatctgttcacatgattttcaagttccaagttcaaatctgttga	531
OY	472	aaagatcaaaagatcaatctgttcacatgattttcaagttccaagttcaaatctgttga	531
Db	5228	AAGATCTRAAACCCAAACTAGCTACTCTTCTGATTACTGTAAC---ATGATGTTGAC	5286
OY	532	aggttaagaacaataatggtttgagcgtgatgatcaaaagaacagttgtttaagaatctga	591
Db	5285	AGCCCGAATAATATATGTTGGCGCGTGAATAATTAATTAAGATGATGCGTGAATCACTTG	5344
OY	592	ctagaagctactctgggaaacccaagtaaccgaattctgggattgggaagctagatga	651
Db	5345	CTAAGAG---AGGAAGGGAACTAGAAGTGTCTCAATCGTAGGATGGAGGACATCGGGA	5401
OY	652	aaacacacttagcaaaagaattacaatgatgatcaatctcatatgacgttttagatgttc	711
Db	5402	AAACACACTTGTGGTGCAAAACCTATAGTATCTTACATTTATAGTCCATTTGATTAATTC	5461
OY	712	atgctgtggtaccatattctccacagcacacaacaaagaatattgctgggcctctgcg	771
Db	5462	GTGCAAAAGCAACGTGTTCCAAAGAGATTTGTGTGAATAATGACTCCTAGGCCTTCTTT	5522
OY	772	attccacatcaaatatgatgacagaggttaagatgatgttgaagcagagctcagacaga	831
Db	5522	CTTTGACAAAGTAGAAGACGTGATTATC-----AGCTAAGGGAC	5566
OY	832	tgttacagaaaagtttaagaagaagaggttaattgttcttgatgatctcggagtt	891
Db	5561	AACGTCAAAACATCTAAGAGCAGGAGATCTGTTGATGCTATGATGTCATATGAGCTA	5620
OY	892	gtgagatgtggagctgagcgttagagcagatgcttccaactcaagaacaatgagagatcgaa	951
Db	5621	CAGAAAGCTGGGATGATATTAACCTATGTTCCCA---GACTGCCAATATGGAAACAGAA	5677
OY	952	tactgttgactaccggtaatgatgaagtagctgtgtatgctggtgtgtagaagatttctc	1011
Db	5678	TACTCTGACTACTCTCGGAATGTGAAGTGAGCTCAATATGCTATGCTAGCTAAGCCCTCTC	5733
OY	1012	tggagatgaagtttaagatcaagatgaaggttggagttcttccaagaagtgaagcatttt	1071
Db	5738	ATCACATGCGCCTCATATAATTTTGACAAAGTTGGAAATTTACTACCAAAAAGATCTTTG	5791
OY	1072	caagltgaag---cattacacatagttgctgagacgtttggaagcaaatcgacagatgat	1128
Db	5798	AAAAAGAAAGTGTATTATCTCTCAGCAATTTGAATAATTTGGGAACAAATTTGCATTAAAT	5857
OY	1129	gtcaaggtgtaccactaactatctgtgctgttcagagctctt---caatctaaagga	1188
Db	5858	GTGAGGGTATCCCTGTAGCAATTACTTTGATGCTGTGACTCTCTCCAAAATCACTATAAA	5917
OY	1186	caatagaagatctggaacacgtttgctaaagaatgtcaagtcattcgtccacaatgtacctg	1245
Db	5918	CATTGATGATGTGGCAAAATGTTCCGAGAGATGTACGTTGGTGTATACCAAGATCTTG	5977
OY	1246	atgaacgatgttcaogtgcgttgaggttgaagttacgatcaactgtgacaagcgatctaaaa	1305
Db	5978	AAGCAAAATGATATAGAGTGTGGCTTTGAGTTGATACATCACTTGCTTCTCAACTATAAAC	6037
OY	1306	catgctctctgcattcttgggaattttccagaagaacagtgatattccaagtgaaagaattga	1365
Db	6038	CGTGTTTTCTATTTTTCGCAATTTTTCGACAGAGATGAACGGAATTTATGTAATTAACCTG	6097
OY	1366	tgaagatcatgatatgctgtcgttgaggttgcga---agttggaanaatgtatttgaaagag	1419
Db	6098	TTGATTTATGGCGCGTGAAGGGGTTTTTGTGATGAACAAAGGCAAAAACATAGAGAGG	6157
OY	1420	aggttgaagaagtgtttgcaagagcttgttgcataagatgttgcctcgttcagcaagagaa	1479
Db	6158	TGGCAGAAACATGATTAACGAACCTTGTATGAAGTCAATTTCTATTCACAAATGTGA	6211
OY	1480	gtcagagatggaacaaaattagatcatgtlaagtttcatatcatatataatgacctgtgcg	1535
Db	6218	GTTTTTGAATGGGGAACACAGAG---ATGTGAATGATGATGATGACCCGTGAACCTGTT	6274
OY	1540	tgaagagaagttcaaaagggaacacattttaa	1569

DB	6275	TCGAGGAGCTCGAAACATGAATTTTGTA	6304
RESULT	9		
LOCUS	AF265664	187352 bp	DNA linear
DEFINITION	Solanum tuberosum resistance gene cluster, complete sequence.		
ACCESSION	AF265664		
VERSION	AF265664.1	GI:9587171	
KEYWORDS	Potato.		
SOURCE	Solanum tuberosum		
ORGANISM	Eumariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; easterids I; Solanales; Solanaceae; Solanum.		
REFERENCE	1 (bases 1 to 187352) van der Vossen, E.A.G., Roupe van der Voort, J., Kanyka, K., Bendahmane, A., Sandbrink, J.M., Baulcombe, D., Bakker, J., Slekema, W.J., and Kleh-Lankhorst, R.		
AUTHORS	Homologs of a single resistance gene cluster of potato confer resistance to distinct pathogens: a virus and a nematode		
TITLE	Plant J. (2000) In press		
JOURNAL	2 (bases 1 to 187352) van der Vossen, E.A.G., Roupe van der Voort, J., Kanyka, K., Bendahmane, A., Sandbrink, J.M., Baulcombe, D., Bakker, J., Slekema, W.J., and Kleh-Lankhorst, R.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (10-MAY-2000) Genomics, Plant Res. Int., Droeveendaalsesteeg 1, Wageningen, Gld 6708PB, Netherlands		
FEATURES	Location/Qualifiers		
SOURCE	1..187352 /organism="Solanum tuberosum" /db_xref="taxon:4113"		
misc_feature	1..187352 /note="resistance gene cluster"		
BASE COUNT	62100 a	30871 c	30984 g 63397 t
ORIGIN			
Query Match	8.8%;	Score 212.8;	DB 8; Length 187352;
Best Local Similarity	54.7%;	Pred. No. 9.2e-52;	
Matches 738;	Conservative	0; Mismatches 567;	Indels 45; Gaps 8;
QY	232	ttgtcaagaactttagaanaacaatgttttggggaaatgacggaattttagaagag	291
Db	151394	ttgagagaaatccgcgaatataaaggcgcgacatcagagggcttaacaattcttgagaa	151335
QY	292	taagaagaattgcgaagtgcctgatacacaaattcaacttgagactaacaggaactgtac	351
Db	151334	tcattatgaggttacatnacacacagaaagatgatgtgactcggaaatcaamaatgttttt	151275
QY	352	ttggagaaaataaagccagaaaagaagcgctgcgaaggtttcgtaaacctcgcaac	411
Db	151274	ttgacacggagatgtgggaaamaaacagggcctatgtggggatTTTTTTTCGCTTGGAAC	151215
QY	412	aagtcagaggaactgtgcatcatctatctgaaaagatcgacaagaatccaagaataaagaa	471
Db	151214	aaagcactagaatgcaattgatttccaccgctgaamaacagtgcatgacacatcgacacatga	151155
QY	472	aacaagatcaagaagaatcatgtgttcatalgtatttccaagttccaacaagaatatttga	531
Db	151154	aagatcttaaaacacaaactacactcctcttgcattttaccctaacac--atgattgttgac	151098
QY	532	aggttaagaacaatagtgttgcagctgtagatccaaggaacagttgttagaagatctga	591
Db	151097	agcccgagaaatattatgtgttgccctgaaataatgattttgacatgattcgtgatacttg	151038
QY	592	ctagaagaactactctggtggaacccaagaatcatccgatttgcgatttgggaagcatagta	651
Db	151037	cttagag--aggaagcgcaactagaagattgtctcatctagcgaatggagcgatcgcgga	150981
QY	652	aaacaaccttagcaaaagaagtttcaaatgatgaatcaatctcatgacgcttttgatgttc	711

```

Db 150980 AAAAACTTGGCTGCAAACTCTATAGTATCCTTACATATATGTCGATTTGATATTC 150921
QY 712 atgcttggtgacatattcaacagacaacaagaatttctggtccttcgc 771
Db 150920 GTGGAAAAAGCAAGCTTTCACAAAGATTTGTGTGAGAAATGTAAGCTTCTTCTTT 150861
QY 772 attcacaatcaaatgatgacaggggtlaagatgattggtgaagcagagtagacagaca 831
Db 150860 CTTTGACAAAGTATGATGAACCTGATATC-----AGCTACCGGACCC 150822
QY 832 tgttaagaaagttlaagagaagaggtactaattgttcttgatgatatctggaagt 891
Db 150821 AACTGCAAAAGCATCTGAAAGGAGAGATCTGTAGTATGATGATGACATATGACTA 150762
QY 892 gtgagagtgtgagaggtgagagaggttccaaactgaaagaacaagcagagagtgagaa 951
Db 150761 CAGAAAGCTTGGGATGATATTAATACTATGTTCCCA---GACTGCGATATATGGAAGCAGAA 150705
QY 952 tactgtgactaccgtaatgatgatgaagtagctgttatgctggtgtagagaatttctt 1011
Db 150704 TACTCCGACTACTCGGAATATGTGAAGTGGCTGAATATGCTACAGTAAAGCTCTCTC 150645
QY 1012 tgcggatgaagctcaatgagatgaagatgagagtgagagcttcaaaaagtgacagattt 1071
Db 150644 ATCAATGCGCGCTCATGAATTTTGACGAAAGTTGGAATTTACTACACAAAAGATCTTTG 150585
QY 1072 caagtgaag---caatacaatgatgagtagactgttgaagaagaacatgacagatgaat 1128
Db 150584 AAAAAAGAGGTTCTTATTTCTCTCAATTTGAAATTTGGAAATTTGGAAATTTGAAAT 150525
QY 1129 gtcaaggttaccactactatgctggtgtgagagagcttct---caactcaaaagga 1185
Db 150524 GTGAGAGGTTACCTCTTGACATTTACTTTGATGCTGAGCTTCTCTCAAAATCAGTAA 150465
QY 1186 caataagaagattggaagaacgtgtgctaaagatgcaagtaactgctacaagaatgctg 1245
Db 150464 CATTGATGAGTGCGCAAAATGTTGCGGAGATGATGATGCTGCTGAGAGCAGATCTTG 150405
QY 1246 atgaagatgttcaagctgtgctgtgagtgtagacgatactgtgacaagagatcaaaa 1305
Db 150404 AAGCAAAATGATGAGAGTGTGGCTTTGAGTTTCCATCTACTCTCTTCCACCTTAAC 150345
QY 1306 catgtcttcgtcatcttggaattttccagaagaacagtgatatccagtgagaagattga 1365
Db 150344 CGGCTTTCTGATTTTGTGCAATTTTCCAGAGAGATGAACGATTTATGTAATAACTTG 150285
QY 1366 tgaatcatgagatgagctgagaggttctctga-----agttggaatgattggaagag 1419
Db 150284 TTGAGTTATGCGCGTAGAGGGGTTTGTGATGAAGAAGAGGAAAAAGCATGAAAGAG 150225
QY 1420 aggttgaagaggtgttcaagagagctgtgtagatgtagtctgagctgctgcaagaagaa 1479
Db 150224 TGGCAGAAATGATGATTAAGCAACTTTAGTATGAGATCTTAATTTCTATCCACATGTGA 150165
QY 1480 gtgcagatggaacaaaattagatcagtgtaaggttcaatgataatagacctgtgcg 1539
Db 150164 GTTTTGTGAGGGAACACAGAG---ATGTGAATGATGATGATGACCCGTAACCTGTT 150108
QY 1540 tgaagagaagttcaagaggaagacatttta 1569
Db 150107 TGAAGGAAGCTCGAAACATGATTTTGTGA 150078

```

```

RESULT 10
LOCUS AX012617 3229 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 12 from Patent WO954490.
ACCESSION AX012617
VERSION AX012617.1 GI:9998601
KEYWORDS
SOURCE potato.
ORGANISM Solanum tuberosum

```

```

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; easterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 3229)
REFERENCE
AUTHORS Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.
TITLE Plant-derived resistance gene
JOURNAL Patent: WO 9954490-A 12 28-OCT-1999;
BAILCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA
KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)
FEATURES
SOURCE location/Qualifiers
1..3229
/organism="Solanum tuberosum"
/db_xref="taxon:4113"
BASE COUNT 952 a 571 c 686 g 1020 t
ORIGIN

```

```

Query Match 8.8%; Score 272.4; DB 6; Length 3229;
Best Local Similarity 55.0%; Pred. No. 1.7e-51;
Matches 728; Conservative 0; Mismatches 551; Indels 45; Gaps 8;

```

```

QY 258 gttttggygaatgagagatttgaagtagaagtaagaagttgcaagtgtcgtgaa 317
Db 176 GATCATGAGAGGTTAAACAATCTTGGAAGTTGAGAGTACATACACACAGAA 235
QY 318 tacaacttcaactgagactacagagagctgtactggtggaataataaagccagaaanaa 377
Db 236 GATATGCTGCTCGGAATCAAGAAAGTCTTTTATGACACAGAAATTTGAGAGAAAGAAC 295
QY 378 aagcgcgctgaaggttctgcataaagcctgcaacaagtagaagagagatgatactac 437
Db 296 AGGCTATGTTGGAGATTTTCTGCTTGGAAACAGCACTAAGATGATGATTCACAC 355
QY 438 tgaagaagtgtaacaagaatccaagataaagaagaagratcaagaagatcattggt 497
Db 356 GTGAACAGTGATGAGCAACATCGACGATGAAGATCTTAACCAACAACATGACTCA 415
QY 498 catgattttcaagttcaacaacagatatttgaagtgtaagaacaataatgattggaagt 557
Db 416 CTTTCAAGTTTACCTGAGACC---ATGCTTTTGAAGCAGCCTGAGAAATATATGTTGGCGCT 472
QY 558 gatgatcaagaagaacaggtgtgtagaatctgactagaagctactctggygaacccaaa 617
Db 473 GAAATGAAATTTGAGATGATGCTGAGATCACTTTTAAAGAGAGAA---GGGAACTAGAA 529
QY 618 gtactccagatgtcggagatgagagatagtgtaaaacacttagaagaagaagttac 677
Db 530 GTTGTCTCAATCGTAGGAGATGGAGATTCGGAAGAAACAACTTTGGCTTAAACTCTAT 589
QY 678 aatgatcaatcaattcactatgctgttgaatttcatgctcgtgctacatattcaacag 737
Db 590 AGTATCTCTTCAATTAATGATCGATTTGATTTGTGTGCAAAAAGCAACGTTTCCACAGAG 649
QY 738 cacaacaaaagaagaatttgcgtggtccttctgattccacaatcaaaatgatgacag 797
Db 650 TATGTGTGAGAAATGATCTCTAGGCTTCTTTTGAACAAGTATGAAACCTGAT--- 706
QY 798 gttaaagtattgttgaagcagagctagcacacatgttcaagaagaagtttaagaagaag 857
Db 707 -----GATCAACTAGCGGAGACGACTGCAAAAGCATCTTAAGAGGACGG 748
QY 858 aggtacttaattgtcttgatgatatcgaggtgtgtaaggtgtggaatgagcgtgagagaa 917
Db 749 AGATACCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 808
QY 918 tgccttcaactgaagaacatgacagagagtgtaactgttgcactaccgtaatgatgaa 977
Db 809 TGTTCCTCA---GACTGTTATTAAGGGAAGCAATATCTCGATCTCGGAAATGATGAT 865
QY 978 gtgactgttatgtgtgtgtagaagaattttcttggatgagacttcaatgatgacagat 1037
Db 866 GTGCTGAATATGCTAGTCAAGTACGCTCTCATCAACATGCGCTCATGATGATTTTGAC 925

```

QY 1038 gagagttgagctcttcaaaaagtcagcatttccaaagtaag---cataccataatag 1094  
 |||||  
 Db 926 GAAAGTTGGAATTTACTACACAAAAGATCTTTGAAAAGAGGTTCTTATTCTCCGAA 985  
 QY 1095 ttccgagactgttggaaagcaaatcgcagatgaatgcaaggttaccactaatattgct 1154  
 |||||  
 Db 986 TTGGAATAATATGGAACAAATTCATTAATATGAGAGATTCCTCTGACAAATTAAT 1045  
 QY 1155 gtggtgtcagagctctc---caatctaaaggaataagaatgtggaataacgttgc 1211  
 |||||  
 Db 1046 GTGATTCGTCGACCTCTCTCCAAAATCAGTAAACATTGATGAGTGGCAAAATGTTGCG 1105  
 QY 1212 aaagatgtcaagcttcgtccaaatgatccctgaatgaatgttccagtgctgctg 1271  
 |||||  
 Db 1106 GAGAAATGTAAGTTCGGTGTGTAAGCACAATCTTGAAGCAAAATGATAGAGTGTGCT 1165  
 QY 1272 ttgaatgacatcacttgcagaaagcatctaaacatgcttctgcatlctcggaatltt 1331  
 |||||  
 Db 1166 TTGAGTTACCATCTGCTCTCTCACCMAAACCGTGTTCATTTGCAATTTTC 1225  
 QY 1332 ccagaagaagtgatattccagtggaagatttgatgataatgcatgagtgctgaggggtc 1391  
 |||||  
 Db 1226 GCAGAGAGTGAACGGATTTCTGTAACTTTGATGAGGCTGTAGAGGGGCTT 1285  
 QY 1392 ctga-----agttgaaatgatttggaaagagagtgctggaagtgcttcaagaact 1445  
 |||||  
 Db 1286 TTGAATGGAAGAGAGGAAAAAGCATAGAGGTGGCAGAAACATGATTAACGACGCTT 1345  
 QY 1446 gtccagatgactgactgctcgtcgcagaaagagtgagatggaacaaatagatca 1505  
 |||||  
 Db 1346 GTAGATTAGAGATCTAATTTCTATCCACAATTTGAGTTGATGTC---GAAATAGAAAGT 1402  
 QY 1506 tctaaagttcactatataatatactgtgcgtgagaagatgcaagggaagactt 1565  
 |||||  
 Db 1403 TGTGGAATGATGATGTGACCCGTGACCTGTTTGAAGGAGCTCGAACAATGATTTT 1462  
 QY 1566 ttta 1569  
 |||||  
 Db 1463 GTAA 1466  
 |||||

RESULT 11  
 AX012618 3229 bp DNA linear PAT 06-SEP-2000  
 LOCUS AX012618  
 DEFINITION Sequence 13 from Patent WO9544490.  
 ACCESSION AX012618  
 VERSION AX012618.1 GI:9998602  
 KEYWORDS  
 SOURCE  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 1 (bases 1 to 3229)  
 Baulcombe, D.C., Bendahmane, A. and Kanyuka, K.V.  
 Plant-derived resistance gene  
 Patent: WO 9544490-A 13 28-OCT-1999;  
 BAUDCOMBE DAVID CHARLES (GB); BENDAHMANE ABDELHAFID (GB); KANYUKA  
 KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)  
 FEATURES  
 source location/Qualifiers  
 1..3229  
 /organism="Solanum tuberosum"  
 /db\_xref="taxon:4113"  
 BASE COUNT 951 a 570 c 687 g 1021 t  
 ORIGIN

Query Match 8.8%; Score 272.4; DB 6; Length 3229;  
 Best Local Similarity 55.0%; Pred. No. 1,76-51;  
 Matches 728; Conservative 0; Mismatches 551; Indels 45; Gaps 8;  
 QY 258 gttttggggaatagcagattttgaagtagaggaagatgcaagtgctgctgaa 317  
 |||||

Db 176 GATCATGACGAGTTAAACATCTTGAAGTTGAATCTTAGAGGTACATACACACGAA 235  
 QY 318 taccaattcaactgagactcaacaggaactgctcgtgggaaataaagccgaagaaaaa 377  
 |||||  
 Db 236 GATATGCTTACCTCGGATCAGAAAGGTTTATTTTGTAGCACAGATTTGGAGCAAAAC 295  
 QY 378 aagcgcgctgaaggttctgcaaacctcgcacaaagtagcagaggaacatgacatc 437  
 |||||  
 Db 296 AGGCTTATGAGGAGATTTTTCGCTTGGAACCAAGCACTAGAAATGATGATTCACAC 355  
 QY 438 tggaaagatgcgaagaagatccaaagataaagaaacaaagatcaagaagatcattgct 497  
 |||||  
 Db 356 GTGAACAGTGGATGGCAGCATCGACAGCATMAAAGATCTAAACACAACTAGCTCA 415  
 QY 498 catgatttccaagttcaacaacgaatatttgaaggttaagacaataatggttgaagt 557  
 |||||  
 Db 416 CTGTGCTTTTACCTGAC---ATGCTTTTGACACCTGAGAAATTAATGTTGGCCCT 472  
 QY 558 gatgatcaagaagaacagttgttagaagatctgactagaagctactcgtgggaacccaa 617  
 |||||  
 Db 473 GAAATGATTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529  
 QY 618 gtcatccgattgtcgggagtggaagcagatgtaaaacaaacttgaagaaagatttcc 677  
 |||||  
 Db 530 GTTGTCTCAATCGTAGGAGTGGAGGATTCGGGAAAAACAATTTGGCTACAAAACCTAT 589  
 QY 678 aatgatgaatcaatcttcagtcgctttagatgctcagcccggtccacatccaaag 737  
 |||||  
 Db 590 AGTGAATCTTACATTTATGCTCTCATTTTGAATTCGTGCAAAACAACTGTTTACAAAG 649  
 QY 738 cacaacaaaaggaanaatttgcctggtccttgcattccacaacaaatgagtgacag 797  
 |||||  
 Db 650 TATGTGTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 706  
 QY 798 gttaagatgattgtgaagcagagctagcagacatgttaccagaagaagtttaagaagaag 857  
 |||||  
 Db 707 -----GATCACTAGCGGACGAGCTCGCAAAAGCATCTGAAAGGCGAG 748  
 QY 858 aggtacttaattgtctgtgatactgatactgagtgtaagtgctggaagtgctggaagcga 917  
 |||||  
 Db 749 AGATACCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 808  
 QY 918 tgccttcaactgaagaacatgcaaggaagtcgaatcctgttgcatacccgtaatgaa 977  
 |||||  
 Db 809 TGTTCCTCA---GACTGTATTAAGGGAGGAGCAATCTCTGCTACTCGGAATGCGAA 865  
 QY 978 gtacgtgtatctgctggtgagagaatttctcttgcggaagagctcagtgatcaagat 1037  
 |||||  
 Db 866 GTGCTGATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 925  
 QY 1038 gagagttgagctcttcaaaaagtcagcatttccaaagtaag---cataccataatag 1094  
 |||||  
 Db 926 GAAAGTTGGAATTTACTACACAAAAGATCTTTGAAAAGAGGTTCTTATTCTCCGAA 985  
 QY 1095 ttccgagactgttggaaagcaaatcgcagatgaatgcaaggttaccactaatattgct 1154  
 |||||  
 Db 986 TTGGAATAATATGGAACAAATTCATTAATATGAGAGATTCCTCTGACAAATTAAT 1045  
 QY 1155 gtggtgtcagagctctc---caatctaaaggaataagaatgtggaataacgttgc 1211  
 |||||  
 Db 1046 GTGATTCGTCGACCTCTCTCCAAAATCAGTAAACATTGATGAGTGGCAAAATGTTGCG 1105  
 QY 1212 aaagatgtcaagcttcgtccaaatgatccctgaatgaatgttccagtgctgctg 1271  
 |||||  
 Db 1106 GAGAAATGTAAGTTCGGTGTGTAAGCACAATCTTGAAGCAAAATGATAGAGTGTGCT 1165  
 QY 1272 ttgaatgacatcacttgcagaaagcatctaaacatgcttctgcatlctcggaatltt 1331  
 |||||  
 Db 1166 TTGAGTTACCATCTGCTCTCTCACCMAAACCGTGTTCATTTGCAATTTTC 1225  
 QY 1332 ccagaagaagtgatattccagtggaagatttgatgataatgcatgagtgctgaggggtc 1391  
 |||||  
 Db 1226 GCAGAGATGACGAGATTTCTGTAACATAAATGATGAGTATGAGGCTGTAGAGGGGCTT 1285









QY 232 ttgtcaagactttagaanaacaatgcttttggggaattgacggaatttgaatgaagg 291  
 Db 2361 tggagaaatccctgcataatattggcggaatcagaagggtttacaaatttggaagttgaaa 2420  
 QY 292 taagaagaattgcaagtgctgctgaatacacaaattcaactgaactgaactgaactgtac 351  
 Db 2421 tggtagaggttagcatnaccacagaagaatngttagctcggaatcagaatgaaatgtttttt 2480  
 QY 352 tgggagaataataaagccagaanaaagcgctcggaagtttcogtcaagcctgcaac 411  
 Db 2481 ttagcagcagaaatttggaggaamaacagcgctgtagtggagaaatttttttgcctcggaac 2540  
 QY 412 aagtagcaggaagacatgcatatcctggaagagtcgacaagaatcccaagaataaggaa 471  
 Db 2541 aagcactgaatagcatgtatttccaccgtgaaacagtgatggcaacatcggaacacagca 2600  
 QY 472 aacaagatcaaaaagaatcattgtgtcatgattttcaagttcaacaagaacgatatltga 531  
 Db 2601 aagatcttataaacacaaactagctgcgtgtagttagttagctg--aacatgattgttagac 2657  
 QY 532 aagtttaagaacataatgtgttagcgtagatgataagaagaacagttgttagaagtttga 591  
 Db 2658 aagccgagaaatattatgtgtgctggaataatgaaatttggagatgattgctggaacttg 2717  
 QY 592 ctagaagctactctggggaacccaagatcaccgattgctggggaatgggagacatagta 651  
 Db 2718 ctagaagc--aggaagggaactagaagttgtctcaatgtaggaatggagacacatcgga 2774  
 QY 652 aacaacacttagcaaaaagaatttacaatgataatcaatcattgcgctttagatgttc 711  
 Db 2775 aacacaaatttggctcacaamaactctatagatccctgcatatgctgattgtgatttgc 2834  
 QY 712 atgacctggctacacatctacacagcaacaagaagaatttgcctggcctctgcgc 771  
 Db 2835 gtgcacaaacacactgttttcacaaagatattgtgtgagaatgttactccttagccttcttt 2894  
 QY 772 attccacaatcaaaaatgtagaaggttaagaatgattgtagaagcagagtcagacaga 831  
 Db 2895 ctttgacagatgtagtgaactgt-----gattcagctagcggagc 2933  
 QY 832 tgttacagaagaatttaagaagaagaagtagtaattgtcttgaatgatatctggaatt 891  
 Db 2934 gactgcacaaagcattggaagcagagatctgtgtgattgttattatgacatnattgactga 2993  
 QY 892 gtagaattgtggagatgtaggaagcattcttccaaactgaagacatgcaaggagtcgaa 951  
 Db 2994 cagaagccttgggaatgataaaactatgtttccca--gactgttattatggaagcagaaa 3050  
 QY 952 tactgttgactaccgtaataatgaatgaatgattgttattgtgtgtagagaattttctt 1011  
 Db 3051 tactcctgactactcgaatgtggaatgtagaagtggaattgtgtagttagtgaagcctctc 3110  
 QY 1012 tgcgagatgagcttcatgataagaatgagatgtgagtttcaaaagtccagacattt 1071  
 Db 3111 atcacattggcctcctgaaatgaaatttggaaatttctacacaaaaaagatcttttg 3170  
 QY 1072 caagtgaag--cattacataatgagtcgagacgttggaaagaacatgcagatgat 1128  
 Db 3171 aaaaagaagcttcttattctcctgaatttggaaatatttgggaacaaatttgcattttaaatt 3230  
 QY 1129 gtaacggtttaccacttaacttgcgtgtgtgtgtagaggtctct--caaatcaaaagga 1185  
 Db 3231 gtagagagatttactctgacaaatttactgtgtagttagttagttagttagttagttagt 3290  
 QY 1186 caatagaagaattggaagaactgttgcataagaatgtagatcattgtcacaatgtagctg 1245  
 Db 3291 gatttagatagtggaacaaatatttggggaataatgtagttagttagttagttagttagt 3350  
 QY 1246 atgaagaatgtagcgt 1305  
 Db 3351 aagcacaatgcatgagagattgt 3410

QY 1306 catgtcttgcattcttcggaatttccagaagacagtgatattccagtgaaagtattga 1365  
 Db 3411 cgttttttctgtatttttgcataattttcacagagatgacaagattttctgtaaaatgaacttg 3470  
 QY 1366 tgaatcaatgtagtgcgtgaagggttccga-----agttgaaatgatttggaaagag 1419  
 Db 3471 ttgatttatgtgctgttagagagatttttgaaatgaaagcaggaagaaacaaatgaaagag 3530  
 QY 1420 aggtttagaagttgttgcagaagctgtgtgataatgtagttagttagttagttagttagt 1479  
 Db 3531 tggcacaacacatgatttataagaaactttagatgaaagctttaaatttttcatccacaaattt 3590  
 QY 1480 gtcgagaatggaacaaatataatgataagttgataatgataatgataatgataatgata 1539  
 Db 3591 gttttgttggaacaaatgaaag--ttgtgaaatgcatgattggaacccgtgaaactctgtt 3647  
 QY 1540 tggagaagtttcaaaagggaacattttta-----tctgaagcagcattgtcttgaagtt 1596  
 Db 3648 tgaaggagagctcgaaacataatgtttagaattgtttagaaggaaggaaggaaggaagga 3707  
 QY 1597 catatccagaatgttcaatctctgataatgataaataatgacagccttgaagcgtgtgact 1656  
 Db 3708 catgtgcacaaatccatgacacagcttccctttagaagtggaagtggaatcagaatcagaat 3767  
 QY 1657 gtagaagaatlaattatgttccctgaatgttcttaagagcttcttctta----- 1704  
 Db 3768 tggaaagaatttggctgt 3827  
 QY 1705 -----ccctgtaaatgctgagttgagtagatcatgaaacacaa--atctttga 1752  
 Db 3828 tgcgaatcgtgcacactggaattgttcttcaagcttagtaagacttagatcttggatttga 3887  
 QY 1753 aacgaacccaattctgttcttcttcaatcttgaagccttataatgatttctcaatcag 1812  
 Db 3888 ataatagccaaatttttccagtgagatgacttcttcaatattttagatattactattctt 3947  
 QY 1813 aggttgcatttcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 1863  
 Db 3948 tgcgtttttaaatttctgt 4007  
 QY 1864 ttgattgttccctcgagagataactaagctcatctgagttg-----agttacc 1911  
 Db 4008 taatagacatttctttagatgataatgaaagcctttagatgaaactttaaactttaaact 4067  
 QY 1912 tatcatgttgcataatggaatttgcattgtagttagttagttagttagttagttagttagt 1971  
 Db 4068 ttccattttccagatttatttatttatttatttatttatttatttatttatttatttattt 4127  
 QY 1972 tgcagacattcatgttcaagcgttccatgacataataaatttgcctgaggaattt 2031  
 Db 4128 tgaagagagctgt 4187  
 QY 2032 gtagaactaagcaatt--aagcattcttaactgcccagatttatttgcagagattgcgc 2088  
 Db 4188 tggatttgaataattttcaatgcttcaatgaaatgaaacccctgattgtgacagggcttt 4247  
 QY 2089 caagttagatctgttgcacaaagaagcacttggatttccaactta--caaatctattct 2147  
 Db 4248 ttttttagacatttttcccaattttaaagaagttgcaagattttgagcagagacatttgc 4307  
 QY 2148 tactgtctcacaagttgttgcacagaagaggtatataatgaggaattcaagaattcaca 2207  
 Db 4308 gcaattaccagagacagctgtaagatttttgcatttataatgacgtgaaagatttgcattt 4367  
 QY 2208 tttaggaatcagttgaaataagatgactataaagaatttgcagagcctgagccttcccaac 2267  
 Db 4368 gttttattatttccatattgcttgccttcttctttaaataaacctgacacttcaagtttacc 4427  
 QY 2268 aatctgtcatctgcagcagcacttgaataatgagcttataatgagcttataatgagctt 2322  
 Db 4428 aagattccttgcagagtttcaacagcaaaatatttgcacaaagagatttggggggaactg 4487  
 QY 2323 gcttttgcagtagatcatttcaagtgcaaaagcttccagcaagcgtcgaagaattga 2382



Db 4488 CACCTCCAACTTACTCTTACCTCCCTCCGATGCTTTTCCACAAAACCTTAAGACTTTAA 4547  
 Qy 2383 agt---gaaagaactatcatgaactgatactatgagatcatgactgagccta 2439  
 Db 4548 CTTTAGGGGGAATTTCTCTGCGATGGAAGATTGAGCATGTTGTAATTAATCCCA 4607  
 Qy 2440 acctgaagtgctgaagctgatagaactgctgtgtgtgaaagaatgacatccaatg 2499  
 Db 4608 AACGCGAGCTCTTATATCATCATGAGATGCCTTCATAGGCAAGAGTGGGAAGTGTG 4667  
 Qy 2500 ttatggacttaacatgactgaaactttgtcaatataatagtttctcaagtctgca 2559  
 Db 4668 AGGAAGGCTTCCCTCAGCTTGAAGTGTGTTGATGATGATATACATTCGATCTGGA 4727  
 Qy 2560 aagccacaatgacaaatttctctgtctgtgagccctcatgattagaaagtgcacaaat 2619  
 Db 4728 GAGCTAGTAGTACACTTCTCGTACCTTGAACGAGTATCTTGAAGATTGCCGTAAAT 4787  
 Qy 2620 tgaagaagatacccatgagtttgcagatatacaacacatacagctgattgagtaagag 2679  
 Db 4788 TGGATTCATCCCTCGAGATTTTGCAGATATACACACATGACTTATTGATATAGATT 4847  
 Qy 2680 agtgcctcccaacttggggaactctgctgacgaatcagaagaagaagaagacactcg 2739  
 Db 4848 ACTGTCAACAATCTGTGTGATTCGCCCAAGCAATTCACAGACATTCACAGCAACT 4907  
 Qy 2740 gaacaacccctgtgagtgctgtatctcaatcattgaagaagagatgattctgattag 2799  
 Db 4908 ATGGAAGCTATCATGAGTGCATCTCGTCATCTTTGTAAGACATCTTCTCTGCTT 4967  
 Qy 2800 aagaacattagaaga 2814  
 Db 4968 TACAACAATATATA 4982

RESULT 15  
 STU011801 18284 bp DNA linear PLN 20-JUL-1999  
 LOCUS Solanum tuberosum rx gene.  
 DEFINITION A011801.1 GI:5524753  
 VERSION A011801.1  
 KEYWORDS LRR domain; NBS domain; potato virus X resistance gene; rx gene.  
 SOURCE potato.  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; easterids I; Solanales; Solanaceae; Solanum.  
 REFERENCE 1 (bases 1 to 18284)  
 Bendañmane,A., Kanyuka,K. and Baulcombe,D.C.  
 TITLE The Rx gene from potato controls separate virus resistance and cell  
 death responses  
 JOURNAL Plant Cell 11 (5), 781-792 (1999)  
 MEDLINE 99264301  
 REFERENCE 2 (bases 1 to 18284)  
 Bendañmane,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-AUG-1998) Bendañmane A., The Sainsbury Laboratory,  
 John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk  
 NR4 7UH, United Kingdom  
 FEATURES  
 source  
 1. 18284  
 /organism="Solanum tuberosum"  
 /cultivar="Cara"  
 /db\_xref="taxon:4113"  
 /chromosome="12"  
 /clone="BAC77"  
 /sub\_clone="BAC9"  
 /clone\_1id="Solanum tuberosum genomic library in  
 pBelOBAC11"  
 /note="introduced from Solanum tuberosum ssp. andigena"  
 join(11849..14544,14779..14889,15001..15007)  
 /gene="rx"

CDS  
 join(11849..14544,14779..14889,15001..15007)  
 /gene="rx"  
 /function="confers disease resistance against potato virus  
 X (PVX)"  
 /note="contains NBS and LRR domains"  
 /codon\_start=1  
 /product="Rx protein"  
 /protein\_id="CAB50786.1"  
 /db\_xref="GI:5524754"  
 /translation="MAYAAVYSLMRTIHOSMELTNGCDLPYERKLSIRATLESCNI  
 MGDEHGLTILEVEVAAYTTEDWDSDSRVFLAQNLEERSRMWELFFYLEQALBC  
 IDSTVKQMWATSDSKDKLPQTSLSVSLPEHDVQPEINIVGRNEFMIDLAGG  
 RELVSVISVMGIGIKTTAKLYSDCIPISIRFPI RAKATVSOEYCAVNLGLSLR  
 SDEPDQDLADLHKGRLVLYIDWTPEAMDDILCPDQNGSRILITIRNVE  
 VAERYASGKPPHNRKLNKDESMWLNHKKIFEKGSYSPEENIGKQALCKGGLPLA  
 ITVYAGLSKKGQRLDEMQRIGENVSSVSDPPRACQRYVALSYHHHPSLKCEFL  
 FAITEDQLSVNELVEPVEGLNEEGSGSIEVATCTINELIDSLITINSEFR  
 GTIISCGMHDVTRLECLREARNMNFVNI RKSQNSQNSQMSRPSRSRI RHKYE  
 ELAMCRNSEASHIIMLGFEVLELSFKILRVLDLNPWPISPGVLSLIRLYLS  
 LRPNCLOOYOGSKSAVSSIIDIPLSISCIOTPEKLNLPSPYFPIIPSEILTM  
 POLRTICGMWYLSRSHPTENRILYIKNLQCLNOLNPRYCSGSPRLPNLKKLVGCV  
 PEDRRNSODLIDFERILVQLELITRLIYPRACFLKNTAPSGSTQDPLRPTETLHK  
 IDEGTAPEPTILLPPDAFPQNLKSLTFRGFSVAMKDLSTGKLPKLEVLILSNAR  
 IGMEEVVEBEPHLPKFLIDVYIRWRASDHPYLERVILKDCRMLDSIPDFAD  
 ITTALALIDYCCQSVNSAKIODIODIODNCGSSIEVHTRLFLPKSVTVEDDDDSV  
 TTDEDDDDDEFEKVCARNVE"  
 BASE COUNT 5967 a 3022 c 3120 g 6175 t  
 ORIGIN

Query Match 8.8%; Score 271.8; DB 8; Length 18284;  
 Best Local Similarity 48.9%; Pred. No. 1.9e-51;  
 Matches 1298; Conservative 0; Mismatches 1252; Indels 105; Gaps 17;

Qy 232 ttgtcaagaacttgaagaacaactgttttggggaatgacgagatttgaagtaagag 291  
 Db 11961 TGGACAAATCCCTGCAATATTAAGGGCGCATGAGGGGTAAACAATCTGGAGTGA 12020  
 Qy 292 taagaagaattgcaagtgctgtgatacaactcaactgacatgacagaaactgtac 351  
 Db 12021 TGTAGAGGTGACATACACACAGAGATATGTTGACTCGGAATCAAGAAATGTTT 12080  
 Qy 352 tggggaataaagaacagaacaaagcgctgcgaagtttgcgtaaacctgcgaac 411  
 Db 12081 TAGCACAAATTTGGAGGAAGAAGAACAGGCGCATGTGGAGATTTTTCGTCGGAAC 12140  
 Qy 412 aagtagcagaagacatgatacatctggaagaagtcgacaaagatccaagaataagaa 471  
 Db 12141 AAGCACTGAAATGCAATGATTCACCGTGAAACAGTGATGGCAATCGGACACATGA 12200  
 Qy 472 aacaagttacaagaagatcatgtgttcatttccaagtccaacaagatatttga 531  
 Db 12201 AAGATCTAAACCCACAACTAGCTGCTTGTCAGATTACCTG---AACATGATGTTGAC 12257  
 Qy 532 agttaagaacaatatgttggacgtgatagtcaagaagaacagttgttagaagatctga 591  
 Db 12258 AGCCCGAATATATATGTTGGCCGTGAATAATGATTTGAGATGATGCTGATCAACTTG 12317  
 Qy 592 ctagaagctactctggggaacccaagatcccgatgtgggagtggaagacatagta 651  
 Db 12318 CTAGAGG---AGGAAGGAGACCTAGAAAGTGTCTCAATGTAGGGATGGGAGCAACG 12374  
 Qy 652 aacacacttagcaaaagaagtttcaatgataatcaactatagcgcgtttgactgtc 711  
 Db 12375 AAACAACCTTTGGCTACAAACTCTATAGTATCCGTGATTTATGCTGATTTGATATTC 12434  
 Qy 712 atgctggctacacatctcaacagcaacaaagaagaatttggctggcctctgc 771  
 Db 12435 GTGCAAAAGCAACTGTTTCCACAAGATATGTGTGGAAGAAAGTACTCTTAGGCCCTTCT 12494  
 Qy 772 attcacacataaataatgatacagaggttaagatgattgttgaagcagaagctagcagca 831  
 Db 12495 CTTTGACAAAGTATGATCAACTGAT-----GATCAGCTAGCGGAC 12533

-QY 832 tgttaagaagaagttaagaagaaggtacttaattgtcttgatgatcgtgaatt 891  
 Db 12534 GACTGCAAAAAGCATCTGAAAGAGCAGAGATCTTGTGTCTTATGATGATATGACTA 12533  
 QY 892 gtgaagtgctggagatgctgagacagatgcttcccaactggaagacaatgcaggagtcgaa 951  
 Db 12594 CAGAACTTGGGATGATTAATAAATATGTTCCCA---GACTGTATATGGAAGACAGAA 12650  
 QY 952 tactgtgtactaccgttaattgataagtgatgctgttatgctgtgtatagaatttttctt 1011  
 Db 12651 TACTCTGTACTCTGGAATGGAAGTGGGAATGGAATATGCTATGCTAGCTAAGCCTCTC 12710  
 QY 1012 tgcgagtgagcttcaatgataagatgagatgagatgagcttcttcaaaagtgcagattt 1071  
 Db 12711 ATCACATGCGCTCATGAAATTTTGAGCAAGATTTGGAATTTACTAACACAAAAGATCTTTG 12770  
 QY 1072 caagtgaaag---caatacatagagtcgagactgctgtggaagaacatcgagatgaat 1128  
 Db 12771 AAAAAGAGGTTCTTATCTCTGAAATTTGAAATATGGAACAAAATTTGATTTAAAT 12830  
 QY 1129 gtcaaggttaccactaactatgtcgtgtgtgtcagggctctt---caatctaaagaa 1185  
 Db 12831 GTGAGAGATTACCTTAGCAATTTACTGTGATTTGCTGGACTTCTCCAAAATGGCTCAA 12890  
 QY 1186 caataagaattggaagaactgtgtctaagatgtaagtcagtcacgtcacaatgtacctg 1245  
 Db 12891 GATTATATAGTGGCAAAATTTGGGAAATGTAAGTTGCTGCTTACACAGATCTCTG 12950  
 QY 1246 atgaacagatgtaacgt 1305  
 Db 12951 AAGCAAAATGCAATGAGAGGTGGCTTTGAGTTTACCATCTACTTGGCTTCTCTCACTTAAAC 13010  
 QY 1306 catgttcttgatcttgcgaatttttccagaagaacagatgatactccagtgaagaatttga 1365  
 Db 13011 CGGTTTCTGTATTTTGCATTTTTCACAGAGATGAAACAGATTTCTGTAAATGTAACTTG 13070  
 QY 1366 tgaatcatgagatgctgctgagaggtctccta-----agttgaaatgatttgaagag 1419  
 Db 13071 TTGAGTTATGGCTGTAGAGGGATTTTTCATGAAAGAGAGGAAAGACATGAAAGAG 13130  
 QY 1420 aggttgaagaagtgttgcagaagctgtgcagatagatgtctagtcctcgtcagaagagaa 1479  
 Db 13131 TGGCAACAACATGTATTAACGAACCTATGATGAAAGCTTAATTTTCAATCCCAATTTTGA 13190  
 QY 1480 gtgcgaattggaacaaatatacatcatgtaagttcatatcatatataatagccgtgcg 1539  
 Db 13191 GTTTTCTGTGACCAATGAAAG---TTGTGGAATGATGATGTGACCCGTGAATCTGTT 13247  
 QY 1540 tgaagaagtccaagaaggaacaatttta---tcatagaacacattgttcttgcgtat 1596  
 Db 13248 TGAAGGAGACTCGAAACATGAAATTTTGTGATGTATTCAGAGAAAGAGTGTATCAAAAT 13397  
 QY 1597 catatccagaatgttcatatctctgtatgataataatgacgccctttaaagcgtgactg 1656  
 Db 13308 CATGTCAACAATCCATGACGCTTCTCTTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 13367  
 QY 1657 gtgataaataataattatcttccatagtcgttataaggtcttctta----- 1704  
 Db 13368 TGAAGAATTTGGCTGTGTCTGTACAGTGAAGCTCATTTCTATATCAATTTGGTGGAT 13427  
 QY 1705 -----ccctgtlaactcgtcagttgagagatcatalgacaacaaca---atctttga 1752  
 Db 13428 TCGAATGCGTCACTACGTAATTTGTCTTTCACACTGTAGTAAGATCTGTGTTTGA 13487  
 QY 1753 aacgaaccatctcgttcttcttcttcatccttgagccttataatagttctcaaatga 1812  
 Db 13488 ATACATGGCCAAATTTTCCCATGAGAGTGTCTTCTATTCATTTGAGATACCTATCTT 13547  
 QY 1813 aggttgttatttcaattacccaagttcttgagctgaga-----cacagaacga 1863  
 Db 13548 TGGGTTTATCTCTGCTTACAGCAGATCAAGAGATCGAAAGACCTGTTCCCTCATCA 13607

QY 1864 ttgatgttccctcagagatactaagccctcatctgtgt-----aggtaacc 1911  
 Db 13608 TAAATAGCATTTCCCTATGATATCAAGGCTATGCTATGCAAACTTTAACTTAAC 13667  
 QY 1912 tatcatgttccagctatggaatttgcagtacccagaaatttgcaggttatggaacc 1971  
 Db 13668 TTCCATTTCCCAAGTATTAATTCCTTCAATTAATACATCGAAATTTGACATCCCAAT 13727  
 QY 1972 tgcagacatcatgttctcaacggttctgcagatataataatttcttgcagaagaatt 2031  
 Db 13728 TGAGAGCCCTGTATGAGGCTGGAATTTACTTGGGAGATCAATGACCTACAGAACAGAT 13787  
 QY 2032 gggactaatgcaatt---aaggatcttaactgcagcagatttatcttgcagattgc 2088  
 Db 13788 TGGTTTGAATAAATTTGCAATGCTCAATCAATGAACTTCAAGCCTCGTATTTGACAGGCTT 13847  
 QY 2089 caagtgatctgttgcagaagaagagcaattgtatttcaaaacta---caactattctc 2147  
 Db 13848 TTTTATAGACTATTTCCCAATTTAAAGAGTTCGAAGATTTTGGCTGCCGAAAGACTTTC 13907  
 QY 2148 tactgtctccagctgttgcagaagaaggttatataatgggagattcagaatgcagaanaa 2207  
 Db 13908 GCAATAGCCAGAGACTGTATGATTTTGTGCTACTTATATCAAGCTCGAAGATTCATTTTC 13967  
 QY 2208 ttaaggaatcagtggaataaagatgactataaagaatttccggacttgcagcttcccaac 2267  
 Db 13968 GTTATATATTTATGCAATGCTGCTTCTTAAACAACTGACCTTCAAGTTCTTACCG 14027  
 QY 2268 aatctgtctatctgcagcaacttgaatatgtagttctatctgt-----gattata 2322  
 Db 14028 AAGATCTCTGAGGTTTTCAGACGGAATTTTGCACAAAGAGATTTTGGGGGAAC 14087  
 QY 2323 gctcttgcagatgactatcttcaagtcaaaagcttcttccagaacagctcaagaattga 2382  
 Db 14088 CACCTCCAACTTATCTTACTTACTTCTCTCCGATGCTTTTCCACAAACCTTAAGAAGTTTAA 14147  
 QY 2383 agt---ggaagaactatctaaagctgtcatatcttgcagatcatagctgagttccta 2439  
 Db 14148 CTTTATAGGGGAGAAATTTCTGTGATGAGAAAGATTTTGAACCAATTTGATTAATCCCA 14207  
 QY 2440 accttgaggtgtgaacatgataagatgacgtgtgtgtgtgtgaagaatgacccaattg 2499  
 Db 14208 AACTCGAGGCTTATCTATCATGGAATGCTTTCATAGCAAGAGAGTGGAGATGATG 14267  
 QY 2500 ttatggatttaactcgaattgaagcttctgcaataataatagtttctcaagtctcga 2559  
 Db 14268 AGGAAGGTTTCCCTCACTTGAAGTCTTGTGTTTGTGATGATGATGATGATGATGATG 14327  
 QY 2560 aagccacaatgacaatttctcgttcttgcagcgcctcatgattgaagaatgccaanaatt 2619  
 Db 14328 GAGCTAGAGATGATCATTCTTCCGATGACGAGTATTTTGTAGATTTGCGCTTAAT 14387  
 QY 2620 tgaagaagatcccatgtgattgtgcagataatacaacacacagcgtgattgagttgaag 2679  
 Db 14388 TGAATTCATTCCTCGAGATTTTTCAGATTAATCAACACATGACCTTATGATTAATG 14447  
 QY 2680 agttcccccacaacttggggaatctgtcagaacatctgagaagaacaagaagactcgcg 2739  
 Db 14448 ACTGTCAACAATCTGTTGTGATTTCCGCCCAAGCAAAATTCACAGAGATTCACAGACACT 14507  
 QY 2740 gaacaacccctgtgagatgtcgtatctcaaaatccatgtgaagaagagatgattcgtacg 2799  
 Db 14508 ATGGAACCTCATGAGAGTGCATATCTGATCTTTTGTGAAGCAATCTTCTCTGCTT 14567  
 QY 2800 aagaacattggaana 2814  
 Db 14568 TACACAATATATTAA 14582

Search completed: September 11, 2002, 22:23:56  
 Job time: 38507 sec







Db 301 ttctgtcaaaagcctgcgaacagtagcagaggacatggaatcatatctgtgaaagatcgaca 360  
Qy 361 aagatccaaagaataaaggaaacaagatcatcaagaatcatcgtgtctgtatcttccaagt 420  
Db 361 aagatccaaagaataaaggaaacaagatcatcaagaatcatcgtgtctgtatcttccaagt 420  
Qy 421 tcaacaacagatatttgaaggttaagaacaataatgtgtgagcgtgtatgtatcaagaagaa 480  
Db 421 tcaacaacagatatttgaaggttaagaacaataatgtgtgagcgtgtatgtatcaagaagaa 480  
Qy 481 cagttgttaagaagatctgactagaagaagctactctgtgggaaccccaagatcccgattgtc 540  
Db 481 cagttgttaagaagatctgactagaagaagctactctgtgggaaccccaagatcccgattgtc 540  
Qy 541 gggatgaggagcctagatgaacaaacaccttagcaagaagatttcaaatgtatgaatcaatt 600  
Db 541 gggatgaggagcctagatgaacaaacaccttagcaagaagatttcaaatgtatgaatcaatt 600  
Qy 601 ctatgacgctttgtatgtctatgcctgtgggtacacatctcaacagacaaacaaagaa 660  
Db 601 ctatgacgctttgtatgtctatgcctgtgggtacacatctcaacagacaaacaaagaa 660  
Qy 661 atttgcctggcctcttgcacatccacaatacaaatgtgacaggggttaagatgtgt 720  
Db 661 atttgcctggcctcttgcacatccacaatacaaatgtgacaggggttaagatgtgt 720  
Qy 721 gaagcagagctagcagacatggttacagaagaatttaagaaggaaggttaattatgtc 780  
Db 721 gaagcagagctagcagacatggttacagaagaatttaagaaggaaggttaattatgtc 780  
Qy 781 ttggaatgatatctggaatgtgtgaagtgctggagatggcgtgagacgatcttccaaactgaa 840  
Db 781 ttggaatgatatctggaatgtgtgaagtgctggagatggcgtgagacgatcttccaaactgaa 840  
Qy 841 gacaaatgcagggatgcgaatactgttgaactaccgtaataatgaatgattgtctgtc 900  
Db 841 gacaaatgcagggatgcgaatactgttgaactaccgtaataatgaatgattgtctgtc 900  
Qy 901 ggtatagaagaatttctctgcgagatgagcttcaatgagatcaagatgtgaaatct 960  
Db 901 ggtatagaagaatttctctgcgagatgagcttcaatgagatcaagatgtgaaatct 960  
Qy 961 ttcaaaagtcagacatttccaagtgaagcatctacatagatctgagactgttggaaag 1020  
Db 961 ttcaaaagtcagacatttccaagtgaagcatctacatagatctgagactgttggaaag 1020  
Qy 1021 caaatgcagatgaatttccacgggttaaccaatactatgttgcgtgttgcagagctcttc 1080  
Db 1021 caaatgcagatgaatttccacgggttaaccaatactatgttgcgtgttgcagagctcttc 1080  
Qy 1081 aaatctaaagagcaatagaagaattgaaacagctgtgctaaagaatgtcaagctatctgc 1140  
Db 1081 aaatctaaagagcaatagaagaattgaaacagctgtgctaaagaatgtcaagctatctgc 1140  
Qy 1141 acaaatgtatccctgtatgaacgaatgttcaacgtgtgtgtgtgtgaatgaatcaacttgaca 1200  
Db 1141 acaaatgtatccctgtatgaacgaatgttcaacgtgtgtgtgtgtgaatgaatcaacttgaca 1200  
Qy 1201 agcgaatcaaaacatgctctcgcacatttcggaatttccagaagaacagtgatattcca 1260  
Db 1201 agcgaatcaaaacatgctctcgcacatttcggaatttccagaagaacagtgatattcca 1260  
Qy 1261 gtgaagaattgtatgagatcatgagatgctgctgaggggttccctgaagtgtgaaatgatctg 1320  
Db 1261 gtgaagaattgtatgagatcatgagatgctgctgaggggttccctgaagtgtgaaatgatctg 1320  
Qy 1321 gaagggagaggtgtgaagaggtgttgcagaagcctgtctgataagatgtctcctgcagc 1380  
Db 1321 gaagggagaggtgtgaagaggtgttgcagaagcctgtctgataagatgtctcctgcagc 1380  
Qy 1381 aagagaagctcgagatggaacaaatattagatcatgttaaggttcacatgatatatgac 1440  
Db 1381 aagagaagctcgagatggaacaaatattagatcatgttaaggttcacatgatatatgac 1440

Qy 1441 ctgtgcgtgaagaagttcaaaagggaacattttatcatgaacgacattgttctgac 1500  
Db 1441 ctgtgcgtgaagaagttcaaaagggaacattttatcatgaacgacattgttctgac 1500  
Qy 1501 gtaataatccgaagatgttccatctctgtatgataaaatgcaagcctttaaagcgtg 1560  
Db 1501 gtaataatccgaagatgttccatctctgtatgataaaatgcaagcctttaaagcgtg 1560  
Qy 1561 actgtgtatgaataatattatgttccctatggttctttaaaggccttcttaaccctgtta 1620  
Db 1561 actgtgtatgaataatattatgttccctatggttctttaaaggccttcttaaccctgtta 1620  
Qy 1621 aatgcctgattgagagatatacaacaacacatttcttgaacaggaacccattctgttc 1680  
Db 1621 aatgcctgattgagagatatacaacaacacatttcttgaacaggaacccattctgttc 1680  
Qy 1681 tctttcatcttgagccttataatattatgttctcaaatccagaggtgttcaattcaaat 1740  
Db 1681 tctttcatcttgagccttataatattatgttctcaaatccagaggtgttcaattcaaat 1740  
Qy 1741 ctcaaatgtcttgagatctgagacacagacagatgtgttccctcagagataactaagc 1800  
Db 1741 ctcaaatgtcttgagatctgagacacagacagatgtgttccctcagagataactaagc 1800  
Qy 1801 cccatctgtgtgaagttaccatcatgttcaagctatgggaatttgcagatcttcccaaga 1860  
Db 1801 cccatctgtgtgaagttaccatcatgttcaagctatgggaatttgcagatcttcccaaga 1860  
Qy 1861 atttgcaggttataatgaatcagacacatcatgttctcaacaggttctcgaatcaataa 1920  
Db 1861 atttgcaggttataatgaatcagacacatcatgttctcaacaggttctcgaatcaataa 1920  
Qy 1921 atttgcctgaggaatttgggaactaatgcaattaaaggcatcttaaacctgccaagatt 1980  
Db 1921 atttgcctgaggaatttgggaactaatgcaattaaaggcatcttaaacctgccaagatt 1980  
Qy 1981 taattgcagatcttgcgaagtgatctgttgaacaaaggaagcatttgaatttccaac 2040  
Db 1981 taattgcagatcttgcgaagtgatctgttgaacaaaggaagcatttgaatttccaac 2040  
Qy 2041 ttacaactatttcttactgtctccacgtgtgttgcagaaaggagttatattaggagatt 2100  
Db 2041 ttacaactatttcttactgtctccacgtgtgttgcagaaaggagttatattaggagatt 2100  
Qy 2101 caggaatgtccaaaatttgggaatcagtggaataaagggttctataaagtcttcggagc 2160  
Db 2101 caggaatgtccaaaatttgggaatcagtggaataaagggttctataaagtcttcggagc 2160  
Qy 2161 tctgggcttcccaacacattgtctatctgcagcaacttgaataatgtagcttatatct 2220  
Db 2161 tctgggcttcccaacacattgtctatctgcagcaacttgaataatgtagcttatatct 2220  
Qy 2221 gttgattatagccttctgcagtgatcaattcaagtgcaaaagccttccagcaagctc 2280  
Db 2221 gttgattatagccttctgcagtgatcaattcaagtgcaaaagccttccagcaagctc 2280  
Qy 2281 aagaaggtgaaggttggaaagaactatcgaacgtgtgatacttggacatcatgctggag 2340  
Db 2281 aagaaggtgaaggttggaaagaactatcgaacgtgtgatacttggacatcatgctggag 2340  
Qy 2341 ttgcctaaaccttgagtgctgaagcctgataatgacgtgtgtgtgtgaagaatgagc 2400  
Db 2341 ttgcctaaaccttgagtgctgaagcctgataatgacgtgtgtgtgtgaagaatgagc 2400  
Qy 2401 ccaattgtatggatataatcgaatgaagccttctgttaataataatgaatcttctcaag 2460  
Db 2401 ccaattgtatggatataatcgaatgaagccttctgttaataataatgaatcttctcaag 2460  
Qy 2461 ttctggaaagccacaatgacaatttctcgtcttcttgaagcctcacaatgataaagtgtc 2520  
Db 2461 ttctggaaagccacaatgacaatttctcgtcttcttgaagcctcacaatgataaagtgtc 2520

QY 2521 aaaaattgaaagatgataccatgtgatttgacagataatacaacactacagctgtatgag 2580  
| | | | |  
Db 2521 aaaaattgaaagatgataccatgtgatttgacagataatacaacactacagctgtatgag 2580  
QY 2581 ttaaaagatgtctccccaacttggagatctgtcgccagatcaattagaagaagaagaaga 2640  
| | | | |  
Db 2581 ttaaaagatgtctccccaacttggagatctgtcgccagatcaattagaagaagaagaaga 2640  
QY 2641 gacctcgaaacacacctgtgtgattgtcgtatctcaatccatctgaaggagatgtatct 2700  
| | | | |  
Db 2641 gacctcgaaacacacctgtgtgattgtcgtatctcaatccatctgaaggagatgtatct 2700  
QY 2701 gattcaagaagaacattag 2718  
| | | | |  
Db 2701 gattcaagaagaacattag 2718

RESULT 2  
US-09-360-186-2  
; Sequence 2, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; EARLIER FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: 60/093,957  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 3099  
; TYPE: DNA  
; ORGANISM: Capsicum annuum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (93)..(2810)  
US-09-360-186-2

Query Match 100.0%; Score 2718; DB 4; Length 3099;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 abggtccatgcaagctgtgcttctctttagagaacatagaaatctcttgcattcaat 60  
| | | | |  
Db 93 atggtccatgcaagctgtgcttctctttagagaacatagaaatctcttgcattcaat 152  
QY 61 tcgcatgcaatctctatctctgtatcacagagaagaacttcgcgtcttcgtgaaaaa 120  
| | | | |  
Db 153 tcgcatgcaatctctatctctgtatcacagagaagaacttcgcgtcttcgtgaaaaa 212  
QY 121 gttagtccctgtgaaglatattgttcaagaactttgagaanaaacaatgttttggggaatg 180  
| | | | |  
Db 213 gttagtccctgtgaaglatattgttcaagaactttgagaanaaacaatgttttggggaatg 272  
QY 181 acggattttgaagtagaggaagaagaattgcaagtgctgtcaatatcaaatcaactg 240  
| | | | |  
Db 273 acggattttgaagtagaggaagaagaattgcaagtgctgtcaatatcaaatcaactg 332  
QY 241 agactcaagaactgtactcgggagagaatacaaaagccagaanaaaagcgctcgaaag 300  
| | | | |  
Db 333 agactcaagaactgtactcgggagagaatacaaaagccagaanaaaagcgctcgaaag 392  
QY 301 ttctgtcaaaagcctgcacaagaatagcagagagacatgataatctgtgaaagagtcgaca 360  
| | | | |  
Db 393 ttctgtcaaaagcctgcacaagaatagcagagagacatgataatctgtgaaagagtcgaca 452  
QY 361 aagatccaagaataaagaanaaagatatacaagaagatcatgtgttcattgttttcaagt 420  
| | | | |  
Db 453 aagatccaagaataaagaanaaagatatacaagaagatcatgtgttcattgttttcaagt 512

QY 421 tcaacaacagatatttgaaggttaagaacaatatgttgacatgatacgataaaggaaa 480  
| | | | |  
Db 513 tcaacaacagatatttgaaggttaagaacaatatgttgacatgatacgataaaggaaa 572  
QY 481 caatttgaagaatctgtcagtaagaactactctgtgggaaccacaagltcatccgatgtgc 540  
| | | | |  
Db 573 caatttgaagaatctgtcagtaagaactactctgtgggaaccacaagltcatccgatgtgc 632  
QY 541 gggatgggagagcataggttaaaaacaaccttgcagaagaagtattacaatgtatgaat 600  
| | | | |  
Db 633 gggatgggagagcataggttaaaaacaaccttgcagaagaagtattacaatgtatgaat 692  
QY 601 ctatgcgcttttgaattgtcatctgtcgtggtacacatcttcaacaagcacaacaagaagaa 660  
| | | | |  
Db 693 ctatgcgcttttgaattgtcatctgtcgtggtacacatcttcaacaagcacaacaagaagaa 752  
QY 661 atttgcgtggcctctcgtcatctccacaatcaaaaatgtagacagaggttaagatgtgt 720  
| | | | |  
Db 753 atttgcgtggcctctcgtcatctccacaatcaaaaatgtagacagaggttaagatgtgt 812  
QY 721 gaagcagagctagcagacatgttacaagaagaagttaagaagaaggttaactatgtc 780  
| | | | |  
Db 813 gaagcagagctagcagacatgttacaagaagaagttaagaagaaggttaactatgtc 872  
QY 781 ttgatatatactcgtgagcttgtagagtgtagagtcgtgagacatgcttccaactgaa 840  
| | | | |  
Db 873 ttgatatatactcgtgagcttgtagagtgtagagtcgtgagacatgcttccaactgaa 932  
QY 841 gacaatgcaaggagctcgaaatctgttgactaacccgttaagtatgaagtgtttatgtc 900  
| | | | |  
Db 933 gacaatgcaaggagctcgaaatctgttgactaacccgttaagtatgaagtgtttatgtc 992  
QY 901 ggtgtgagagatttttcttgcgagatgcttcaatgatacagaatgttagagcttc 960  
| | | | |  
Db 993 ggtgtgagagatttttcttgcgagatgcttcaatgatacagaatgttagagcttc 1052  
QY 961 ttcaaaagtgcagacatttcaagtgaagcatctacataatgattcgaactgttgaag 1020  
| | | | |  
Db 1053 ttcaaaagtgcagacatttcaagtgaagcatctacataatgattcgaactgttgaag 1112  
QY 1021 caaatcgcaatgtaatttcaacgggttcaacatacttgcgtgttgaaggctctc 1080  
| | | | |  
Db 1113 caaatcgcaatgtaatttcaacgggttcaacatacttgcgtgttgaaggctctc 1172  
QY 1081 aaatctaaagagacaatagagaatgtgaaaactgttctaaagaatgtcgaatctcgtc 1140  
| | | | |  
Db 1173 aaatctaaagagacaatagagaatgtgaaaactgttctaaagaatgtcgaatctcgtc 1232  
QY 1141 acaaatgacatctgataagagatgttcaagtgctgtggtgtgattcagatcatgaca 1200  
| | | | |  
Db 1233 acaaatgacatctgataagagatgttcaagtgctgtggtgtgattcagatcatgaca 1292  
QY 1201 agcagatcaaaaacatctctctcgtcatttcggaattttccagaagaacatgatacca 1260  
| | | | |  
Db 1293 agcagatcaaaaacatctctcgtcatttcggaattttccagaagaacatgatacca 1352  
QY 1261 gtgagaatttgatgacatgatactgtcgtgaagggttccctgaagtgtgaaaatgattg 1320  
| | | | |  
Db 1353 gtgagaatttgatgacatgatactgtcgtgaagggttccctgaagtgtgaaaatgattg 1412  
QY 1321 gaaggaaggttgaagaagtgttgcagaagctgtcgtatagatgtcagtcctgtcagc 1380  
| | | | |  
Db 1413 gaaggaaggttgaagaagtgttgcagaagctgtcgtatagatgtcagtcctgtcagc 1472  
QY 1381 aaggaaggttgaagtggaacaaaatagatcatgataaggttcatgataatataagac 1440  
| | | | |  
Db 1473 aaggaaggttgaagtggaacaaaatagatcatgataaggttcatgataatataagac 1532  
QY 1441 ctgtgcgtgagaagaagctcaaaaggagagacaattttcatcatgaacagcatgtcttgac 1500  
| | | | |  
Db 1533 ctgtgcgtgagaagaagctcaaaaggagagacaattttcatcatgaacagcatgtcttgac 1592  
QY 1501 gtatcatataccagaatgttcatatctctgtatgtataaagtgcagccctttaagcggtg 1560

Db 1593 gtaacacacagatgtacatctctgtagtataaagacagcccttaagcgcgtg 1652  
 Qy 1561 actggtgataaataattgttccctatgagctttataggctcttcttacccttga 1620  
 Db 1653 actggtgataaataattgttccctatgagctttataggctcttcttacccttga 1712  
 Qy 1621 aatcgtcagttgagatgatacagacaacacatcttctgaaacgaaacccatctgtttc 1680  
 Db 1713 aatcgtcagttgagatgatacagacaacacatcttctgaaacgaaacccatctgtttc 1772  
 Qy 1681 tcttttcaatctgagccttataatattgttctcaaatcagaggttgttcaatctta 1740  
 Db 1773 tcttttcaatctgagccttataatattgttctcaaatcagaggttgttcaatctta 1832  
 Qy 1741 ctcaaaagcttggagcctgagacacagacagatgattgttccctcagagatacctaag 1800  
 Db 1833 ctcaaaagcttggagcctgagacacagacagatgattgttccctcagagatacctaag 1892  
 Qy 1801 ctcaatctggttgaagtaacctatcatgttcaagctatgagaaattcgatgactccagaa 1860  
 Db 1893 ctcaatctggttgaagtaacctatcatgttcaagctatgagaaattcgatgactccagaa 1952  
 Qy 1861 attgacaggttatggaatctgcagacattcatgttcaacaggtttcgatcagataaata 1920  
 Db 1953 attgacaggttatggaatctgcagacattcatgttcaacaggtttcgatcagataaata 2012  
 Qy 1921 atttgcgtgagaaatttggaaactatgcaatlaagcatttcaacgcccagatt 1980  
 Db 2013 atttgcgtgagaaatttggaaactatgcaatlaagcatttcaacgcccagatt 2072  
 Qy 1981 tattgcacagatttgcacagatggaatctgttgacaagaagagcaacttgaatttccaac 2040  
 Db 2073 tattgcacagatttgcacagatggaatctgttgacaagaagagcaacttgaatttccaac 2132  
 Qy 2041 ttacaacatttcttactgttccacagcttgttgcacagagaggttataggggatt 2100  
 Db 2133 ttacaacatttcttactgttccacagcttgttgcacagagaggttataggggatt 2192  
 Qy 2101 cagaatgtlcaaaaaaataatagaaatcagtggaataaagatgacataaagtcttcggagc 2160  
 Db 2193 cagaatgtlcaaaaaaataatagaaatcagtggaataaagatgacataaagtcttcggagc 2252  
 Qy 2161 tctggtgctcccaacaactctgtctatctgcagacacttgaataattgagcttatact 2220  
 Db 2253 tctggtgctcccaacaactctgtctatctgcagacacttgaataattgagcttatact 2312  
 Qy 2221 gtgattataagccttctgacagatcatcttcaagtgcacaaagcttctcagcaacgctc 2280  
 Db 2313 gtgattataagccttctgacagatcatcttcaagtgcacaaagcttctcagcaacgctc 2372  
 Qy 2281 aagaagtgtgaagttggaagaacctatctaaagctgtgcatacttggacatcatagctgag 2340  
 Db 2373 aagaagtgtgaagttggaagaacctatctaaagctgtgcatacttggacatcatagctgag 2432  
 Qy 2341 ttggtcctaacttggaggtgctggaagctatgatacagctgtgttggtagaagaatgcat 2400  
 Db 2433 ttggtcctaacttggaggtgctggaagctatgatacagctgtgttggtagaagaatgcat 2492  
 Qy 2401 ccaattgttataagatttaatactgatacttgaagcttctgtaataataataatttctcgaag 2460  
 Db 2493 ccaattgttataagatttaatactgatacttgaagcttctgtaataataataatttctcgaag 2552  
 Qy 2461 ttctggaagcccaacaatgacaatttctcgtctccttgaagcctcatgattagaagtgc 2520  
 Db 2553 ttctggaagcccaacaatgacaatttctcgtctccttgaagcctcatgattagaagtgc 2612  
 Qy 2521 aaaaatttgaagaagatacccatgagtttgcagataatacaacacacagcgtattgag 2580  
 Db 2613 aaaaatttgaagaagatacccatgagtttgcagataatacaacacacagcgtattgag 2672  
 Qy 2581 ttaagagagtgctccccaacttggagatctgtcagcaatctcgaagaagaagaaga 2640

Db 2673 ttaagaagtgctccccaacttggggaatctgtcgaagaattcagaagaagaaga 2732  
 Qy 2641 gacctcggaacaacacctgtgtgattgttactcaaatccattggaagagatgattct 2700  
 Db 2733 gacctcggaacaacacctgtgtgattgttactcaaatccattggaagagatgattct 2792  
 Qy 2701 gattcagaagaacattag 2718  
 Db 2793 gattcagaagaacattag 2810  
 RESULT 3  
 US-09-360-186-1  
 ; Sequence 1, Application US/09360186  
 ; Patent No. 6262343  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Staskawicz, et al.  
 ; TITLE OF INVENTION: B82 Resistance Gene  
 ; FILE REFERENCE: 50687  
 ; CURRENT APPLICATION NUMBER: US/09/360,186  
 ; CURRENT FILING DATE: 1999-07-23  
 ; EARLIER APPLICATION NUMBER: 60/093,957  
 ; EARLIER FILING DATE: 1998-07-23  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 31491  
 ; TYPE: DNA  
 ; ORGANISM: Capsicum annuum  
 US-09-360-186-1  
 Query Match 98.8%; Score 2685.6; DB 4; Length 31491;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2688; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 atggtcctatgcaagtggtgctctctcttattgagaacaatagaaatctcttgcacat 60  
 Db 1480 atggtcctatgcaagtggtgctctctcttattgagaacaatagaaatctcttgcacat 1539  
 Qy 61 tcgacgattgaatctctatctatctctgtgatacagagagaagaacttgcgtctctcgtgaa 120  
 Db 1540 tcgacgattgaatctctatctatctctgtgatacagagagaagaacttgcgtctctcgtgaa 1599  
 Qy 121 gttagtctccctggaagtatttgcagaacttggaaacaaatggttttgggggaaatg 180  
 Db 1600 gttagtctccctggaagtatttgcagaacttggaaacaaatggttttgggggaaatg 1659  
 Qy 181 acggaatttgaagtgaagtaagagaagctgcaagtgtcgtctgaaatacaaatctcaactg 240  
 Db 1660 acggaatttgaagtgaagtaagagaagctgcaagtgtcgtctgaaatacaaatctcaactg 1719  
 Qy 241 agactaacaagaaactgtactgtgagagaaataaagccagaaataaagccgtctgaag 300  
 Db 1720 agactaacaagaaactgtactgtgagagaaataaagccagaaataaagccgtctgaag 1779  
 Qy 301 ttctgtcaagcctgcaacaagttagcagagacatggaatcatatctggaagagtcgaca 360  
 Db 1780 ttctgtcaagcctgcaacaagttagcagagacatggaatcatatctggaagagtcgaca 1839  
 Qy 361 aagatccaagataaagaaacaaaglatcaagaagaatcattgttcatgattttcaagt 420  
 Db 1840 aagatccaagataaagaaacaaaglatcaagaagaatcattgttcatgattttcaagt 1899  
 Qy 421 tcaacaacaagataatttgaaggttgaagaacaatagtgttgcgcgtgagatcaagaagaa 480  
 Db 1900 tcaacaacaagataatttgaaggttgaagaacaatagtgttgcgcgtgagatcaagaagaa 1959  
 Qy 481 cagtgttgaagatctgactgaagcctactctggtggaacccaaggtcatcccgattgc 540  
 Db 1960 cagtgttgaagatctgactgaagcctactctggtggaacccaaggtcatcccgattgc 2019  
 Qy 541 gggatggaagcctaagtaaaacaaccttagcaaaagaagtttaacatgatgaatcaat 600



Db 2020 gggatgggagcatagtgaaacaacattagcaaaagaagtttaacatgatgatcaatt 2079  
QY 601 ctatgcgcttttgatgttcatatgcctgggtaccatacttcaacagcacaaaaagaa 660  
Db 2080 ctatgcgcttttgatgttcatatgcctgggtaccatacttcaacagcacaaaaagaa 2139  
QY 661 atttgctgggcttctgcattccacaatcaaatgatgatcgaggttaagatgtgt 720  
Db 2140 atttgctgggcttctgcattccacaatcaaatgatgatcgaggttaagatgtgt 2199  
QY 721 gaagcagagctagcagacactgttacagaagaagttlaaagagaagaaggtacttaattgc 780  
Db 2200 gaagcagagctagcagacactgttacagaagaagaaggtacttaattatgtc 2259  
QY 781 ttggatgatatacttgagctgtgaaagtgtggatgctgtgagacgactgtcttccaaactgaa 840  
Db 2260 ttggatgatatacttgagctgtgaaagtgtggatgctgtgagacgactgtcttccaaactgaa 2319  
QY 841 ggaatgcagagagctgagtaactgtgtgacttaaccgttaacgtatgaatgtttatgtct 900  
Db 2320 ggaatgcagagagagctgagtaactgtgtgacttaaccgttaacgtatgaatgtttatgtct 2379  
QY 901 ggtgtgagaatatttcttctgcgagctgagcttcaatgatcaagatlgagaagttgagctt 960  
Db 2380 ggtgtgagaatatttcttctgcgagctgagcttcaatgatcaagatlgagaagttgagctt 2439  
QY 961 ttcaaaagtgcagcacttttcaagtgaaagcattacacatagatgtcgagactgttggaaag 1020  
Db 2440 ttcaaaagtgcagcacttttcaagtgaaagcattacacatagatgtcgagactgttggaaag 2499  
QY 1021 caaatgcagatgaatgtacaggggttacacactaactgttgcgttgcagaggtcttc 1080  
Db 2500 caaatgcagatgaatgtacaggggttacacactaactgttgcgttgcagaggtcttc 2559  
QY 1081 aaatctaaaggagcaatlaagaagatlgaaaactgttgcctaaagatltcaagttactgtc 1140  
Db 2560 aaatctaaaggagcaatlaagaagatlgaaaactgttgcctaaagatltcaagttactgtc 2619  
QY 1141 acaaatgatccctgatgaacagatgttcaagtgctgtggttgagtgatcgatcaacttgaa 1200  
Db 2620 acaaatgatccctgatgaacagatgttcaagtgctgtggttgagtgatcgatcaacttgaa 2679  
QY 1201 agcgatctaaaaacatgtcttctgcacttccggaattttccaaagaacagtgatcca 1260  
Db 2680 agcgatctaaaaacatgtcttctgcacttccggaattttccaaagaacagtgatcca 2739  
QY 1261 gtgaagaatttgatgagatcatgagctgaggggttccctgagagtgtgaaatgtattg 1320  
Db 2740 gtgaagaatttgatgagatcatgagctgaggggttccctgagagtgtgaaatgtattg 2799  
QY 1321 gaagagagagttgagaagtgcttgcaagagctgttcgatatagatgttcagtcctgcagc 1380  
Db 2800 gaagagagagttgagaagtgcttgcaagagctgttcgatatagatgttcagtcctgcagc 2859  
QY 1381 aagagagaatcgagatggaaacaaatltagatcatgtgaagttcatatcatatgatgc 1440  
Db 2860 aagagagaatcgagatggaaacaaatltagatcatgtgaagttcatatcatatgatgc 2919  
QY 1441 ctgtgctgtagagaagttcaaaaggagaaacattttatcatgaaagacattgttcttgac 1500  
Db 2920 ctgtgctgtagagaagttcaaaaggagaaacattttatcatgaaagacattgttcttgac 2979  
QY 1501 gtatcatatccagaaatgttcatatactctgtatgtatataaatagcagccctttaaagcgctg 1560  
Db 2980 gtatcatatccagaaatgttcatatactctgtatgtatataaatagcagccctttaaagcgctg 3039  
QY 1561 actgtgagaaataatattatgttcctatgtcttataagggcttcttaacccctgtga 1620  
Db 3040 actgtgagaaataatattatgttcctatgtcttataagggcttcttaacccctgtga 3099  
QY 1621 aactgtcagttgagagatcatgacaacaacatcttltgaagaagaccatctgttttc 1680

Db 3100 aactgtcagttgagagatcatgacaacaacatcttltgaagaagaccatctgttttc 3159  
QY 1681 tctttcatctttagagcttattatattgttctaaatcaaggttgcatttccaattga 1740  
Db 3160 tctttcatctttagagcttattatattgttctaaatcaaggttgcatttccaattga 3219  
QY 1741 ctcaaaagctttagagctgagacacagacagatgatgttcttccctcgagagatactaac 1800  
Db 3220 ctcaaaagctttagagctgagacacagacagatgatgttcttccctcgagagatactaac 3279  
QY 1801 ctcaatctgtttagagctgagacacatcatgttgcagatagagaaatltcgatccagaa 1860  
Db 3280 ctcaatctgtttagagctgagacacatcatgttgcagatagagaaatltcgatccagaa 3339  
QY 1861 atttgaggttatgaaatcgagacacatcatgttgcagatagagaaatltcgatccagaa 1920  
Db 3340 atttgaggttatgaaatcgagacacatcatgttgcagatagagaaatltcgatccagaa 3399  
QY 1921 attttgtgaggaatatttggaactaatgcaatlaaagcacttaactgcccagatt 1980  
Db 3400 attttgtgaggaatatttggaactaatgcaatlaaagcacttaactgcccagatt 3459  
QY 1981 taattgcagaatgcccagaatgagctgtgtgacaaagaagcacttgatlttccaac 2040  
Db 3460 taattgcagaatgcccagaatgagctgtgtgacaaagaagcacttgatlttccaac 3519  
QY 2041 ttacaactatttcttactgttctcaagtttgcagggagaggttatatgggatt 2100  
Db 3520 ttacaactatttcttactgttctcaagtttgcagggagaggttatatgggatt 3579  
QY 2101 cagaatgtcaaaaaatlagaaatcagtgagaaatlaagaagatctataaaagtttccggag 2160  
Db 3580 cagaatgtcaaaaaatlagaaatcagtgagaaatlaagaagatctataaaagtttccggag 3639  
QY 2161 tctgtgcttcccaacaacttgcctatctgcagcaactgtgaaatlatgtatatact 2220  
Db 3640 tctgtgcttcccaacaacttgcctatctgcagcaactgtgaaatlatgtatatact 3699  
QY 2221 gttgatataagcttttgcagtgatcatattcaagtgcaaaagctttccagaagctc 2280  
Db 3700 gttgatataagcttttgcagtgatcatattcaagtgcaaaagctttccagaagctc 3759  
QY 2281 aagaagtttgagcttggaaaacttactaaagctgtgcatacttgagacataagctgag 2340  
Db 3760 aagaagtttgagcttggaaaacttactaaagctgtgcatacttgagacataagctgag 3819  
QY 2341 ttgcctaaacttgaggtgtcgaagctgagatgagacgctgtgtgtgagaaatgagat 2400  
Db 3820 ttgcctaaacttgaggtgtcgaagctgagatgagacgctgtgtgtgagaaatgagat 3879  
QY 2401 ccaattgtttaggtattatcgatgtgaagcttttgcataatataagttttccaag 2460  
Db 3880 ccaattgtttaggtattatcgatgtgaagcttttgcataatataagttttccaag 3939  
QY 2461 ttctggaaaagccaaatgacaatttccgtctctgagagcctcatgataagaagtgc 2520  
Db 3940 ttctggaaaagccaaatgacaatttccgtctctgagagcctcatgataagaagtgc 3999  
QY 2521 aaaaatttgaagaagataccatltgagttgcagatatcacacaactacagctgatgag 2580  
Db 4000 aaaaatttgaagaagataccatltgagttgcagatatcacacaactacagctgatgag 4059  
QY 2581 ttaagagagtgcttcccaacttgggaatctgcctgacagaatlaagaagaagaagaa 2640  
Db 4060 ttaagagagtgcttcccaacttgggaatctgcctgacagaatltcgaagaagaagaagaa 4119  
QY 2641 gacctggaaaacacccctgagatgttcgatatccaatccatggaagga 2692  
Db 4120 gacctggaaaacacccctgagatgttcgatatccaatccatggaagga 4171

RESULT 4  
US-08-680-327-1



```

:
: EARLIER APPLICATION NUMBER: 08/227,360
:
: EARLIER FILING DATE: 1994-04-13
:
: NUMBER OF SEQ ID NOS: 5
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 3
:
: LENGTH: 5475
:
: TYPE: DNA
:
: ORGANISM: Lycopersicon esculentum
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (1)..(5475)
:
: OS-09-228-246-3

```

Query Match	6.3%	Score 172.2	DB 4	Length 5475
Best Local Similarity	50.6%	Pred. No. 2e-39		
Matches 554	Conservative 0	Mismatches 523	Indels 18	Gaps 5

QY	416	caagttccaacaaacgataattttgaaggttgaagacaatacttggttgacgtgacgtgaacaa	475
Db	3242	catcttttcagcttaaccataccaagaagcaaacgaagaataatgaaaggttttcagatacaa	3301
QY	476	ggaacaagcttgttagaagatctgaactagaagctactctggtgggaaccacaagtcaccga	535
Db	3302	tagatgataatlaaaggataaactactcttggaagatcaact--gagcttgatgtcatctcoa	3358
QY	536	ttgcgggagtgaggagcatatgtaaaaaaacctcttgcaaaaagaatttacaatgttgat	595
Db	3359	tcgtttgcacatgcagaagatcttggaagaactacactatgacaagaagatltcaaatgtccag	3418
QY	596	caattctatgcgtttttgatatgttcagctctggtgtcccaatactcaacagcgacaacaaa	655
Db	3419	aagtcacctctgccttcogatagtccatgcgtccaatgtgttggtgctcaattataattga	3478
QY	656	aggaaaattgtcgtggtcctctgcattccacaatcaaaaatgaaatgacaggttaagatga	715
Db	3479	gagaggtgtgtgcaccacattttaatgatgctcttgagctcttcgatccgaatgaaa--	3536
QY	716	ttgttgagagcagagctcagcagacattgttccagaaaagtttaagugaaagtgtaacttaa	775
Db	3537	-agagaagctggatgaaatagcctgagatgttcgcgcgaattttgttgccaagaaatctctga	3595
QY	776	ttgtctctggaatgatactcgtgaagtttggaagctgtgagatgctgtgagacagatcttccaa	835
Db	3596	ttctcatctgtgtgtgtggtgagactataaagttgtggacaactcatgatatgtgtc--ca	3652
QY	836	ctgaagaacaaatgcaggtatgcataactcgttgaactaccgttaaaatgaatgaatcgtgt	895
Db	3653	gtgatgtttccaatagaagatagaattatacttaaccaaacccgcttgatgatgtccgcgaat	3712
QY	896	atctcgtgtgtagaagaattttctcttgccgatagtacttaagatacgaatgagatgtga	955
Db	3713	atgtccaatgtgaaatgtatccccaatcattctcgttattcaagagatgacaggaatttga	3772
QY	956	gtctttccaagaatgtgacgattttccaagtgaaagcattcaacatgatgttcgagactgttg	1015
Db	3773	catattacagaagaagaagctttccaaggttcaaggtgagagctgtccacactgaactgaagaatggtg	3832
QY	1016	gaaagcaaatcgcagatgtatgtacacggttatccacataactatgttcgtgttgcaagtc	1075
Db	3833	gatttgaatatatacaaaaagtgttagagggttgcctctccagtttgttgaatgactgtgtg	3892
QY	1076	ttctccaatctaaagaagacaatagaagaatttgaaaacgtgtgtcaagaatgtccaagtcatt	1135
Db	3893	ttctgaaaacagaaaagaagacactagatctcatatgtgaaaatgtatgaaacaagaatctaagt	3932
QY	1136	tcgttccaatgtatccctgaatgaacgtatgttcacgtgtcgtgtgtgtgtgttcatgatacact	1195
Db	3953	cccagaggaattgcagcttggaagagagatactataatgtgattcatgaaatgaagaatt	4012
QY	1196	tgaacaagcgatctaaaacaatgtctcttcgtacatttcoggaattttccagaagaacatgtata	1255
Db	4013	taccacaactacttaagcctgttctctcattttttgttggtggagatttttgcagaaggaagata	4072

QY	1256	ttccagtgaaagaaatttgaatgaagtcctgaatgcctgaagggttcc-----gaagttgg	1309
Db	4073	ttctatcctcaaaaaatgaaaccaagtcttgggtacgtgaagggttttgaacaagcaacaacag	4133
QY	1310	aaaatgatttgaaaggaaggaaggtttgagaagtgtttgtaagaagcttgcatagaatgctag	1369
Db	4133	aaaaagacaaagaaagatacgcgaagaagttcttcgtgaacatcttattgtagaatgtag	4192
QY	1370	tccctcgtcagcaagaagagaagtcgagatgagacaaaaattgatcatgaagtgtatgctc	1422
Db	4193	tgaagcgcaatgaggaagaagaccctaatt--accagaatgtaaaacggtgcgaatcctatgatt	4249
QY	1430	taataatatgacctgtgtgtgtagaagaattccaaggaaggagaacattttatcatgaaacgaca	1488
Db	4250	tgttgataataattctgatgatgtaaaagccaacaagaagattttctctccaatcata	4309
QY	1490	ttgtctctgacgtat	1504
Db	4310	gtcggagaagtggtat	4324

RESULT 6  
US-08-680-327-2

## GENERAL INFORMATION

;;	Staskawicz, Brian S., Oldroyd, Giles Edward
APPLICANT:	
;;	Salmeron, John M., Rommens, Calus
APPLICANT:	

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT  
; TITLE OF INVENTION: PATHOGEN RESISTANCE
```

```

; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESS: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston

```

STREET: One World Trade Center  
STREET: 121 S.W. Salmon Street  
STREET: 1500

STREET: Suite 1600  
CITY: Portland  
STATE: Oregon

STATE: OLE  
COUNTRY: U  
719: 97304

DATE: 5/20/4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk 3-1/2 inch

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS DOS

```
SOFTWARE: wordperfect 5.1
CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/680,327  
FILING DATE: July 11, 1996

```

; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
;

```

APPLICATION NUMBER: 08/310,912  
FILING DATE: September 22, 1994

CLASSIFICATION: 800  
APPLICATION NUMBER: 08/227,360

FILING DATE: April 13, 1994  
 CLASSIFICATION: 800  
 PRODUCT / AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:  
NAME: DOW, Alan. E.  
REGISTRATION NUMBER: 35 133

REGISTRATION NUMBER: 33,123  
REFERENCE/DOCKET NUMBER: 5151-450  
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 10968 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: double stranded
; TOPOLOGY: linear

```

US-08-680-327-2



```

QY 896 atgctgtgtgagaaatttcttcttcgagatgagcttcatcagatcaagaatgagattgga 955
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7591 atgtcaaatgtgaagaatgagatcccatcattctgttattcagaagatgagagagattgga 7650
QY 956 gtcttttcaaaatgacagattttcaagtgaagcattacacataagtttcgagagattg 1015
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7651 cattatcagaagaagagcttccaagagagagagctgcacactgacttgaagatgtg 7710
QY 1016 gaaagcaatcgagatgagatgacaggttaccactaatctatgtcggtgtgagagc 1075
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7711 gatctgaatatacaaaaagtctgagaggttgcctctcctcctcagttgttagtagctg 7770
QY 1076 ttctcaaatctaaagaacatagaagattggaactgttgcgttaagatgataatgcat 1135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7771 ttctgaaacagaagaagaagacactagattcattcagaagatgagaaagctaaagt 7830
QY 1136 tgcgcacaatgactctgtagaagcagatgtcagctgtgctgtgtgagttacagatcact 1195
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7831 ccagagagattgagcagcttggaagagagcatatctataattgattcagttacagaatt 7890
QY 1196 tgacaagcagatctaaacatgtctctgcatcttgcgaattttccagaagacagtgata 1255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7891 taccacacatcttaagccttgccttctcatttctgagagattttgcagggaaagagata 7950
QY 1256 ttccaatgagaatttgatgagatcagatgagctgagaggttctcct-----gaagttg 1309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7951 ttcatgtctcaaaaatgaccagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8010
QY 1310 aaaaatgattggaagagagaggtgtgagaatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8011 aaaaagacaagaagaatgacgcacaggttcttgcagcagatcttattgttagaagatgag 8070
QY 1370 tctctgtcgaagaagagatgagatgagaaacaaatgatcatgttaagttcagatc 1429
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8071 tgatgcccattgagagaagacctaact--acaaagtgaaaacgtgcccattcagatc 8127
QY 1430 taatatgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8128 tgttgataaatctgtcagtgagaagaagccaaagaagagatttctctcccaaatcaata 8187

```

```

RESULT 8
US-08-310-912A-157
; Sequence 157, Application US/08310912A
; Patent No. 5981730
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas F.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,912A
; FILING DATE: September 22, 1994
; CLASSIFICATION: 536

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5134 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-310-912A-157

```

```

Query Match 6.0%; Score 164.2; DB 2; Length 5134;
Best Local Similarity 50.3%; Pred. No. 4e-37;
Matches 544; Conservative 0; Mismatches 518; Indels 19; Gaps 5;

```

```

QY 416 caagttcaacaaacagatatttgaagtttaagaacaataatggttgagcgtgatgataaa 475
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1196 CATCTTTTACGCTTATACCAAGACGACCAAGAAATGAGAGGTTTTCAGAGATCAAA 1255
QY 476 ggaacacgtgtttagaagatcagtagaagctactctgagggaacccaagatcccca 535
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1256 TAGATGATTAAGGATTAACCTACTTGAGAGATCACT--GAGCTTGATGTCATCTCA 1312
QY 536 ttgtcggatggagagatagtgtaaaacacacttagcaaaagaagtttaaatgagat 595
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1313 TCGTTGGCAGCCAGATGGGCAAGACTACACTAGCAAGAAAGATTACAAATGATCCAG 1372
QY 596 caattctatgcgcttctgagatcagctcagctgagctcaccatctcaacagcacaca 655
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1373 AAGTCACTCTCCCTTCGATGATGCTCAATGCTCAATGCTGATGCTCAATTTATTCATGCA 1432
QY 656 aggaatttctgctggcctctgcatctccacaataatgataagaggttaagatga 715
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1433 GAGAGTTGTTGCTCACCATTTTGAATGATGTGCTTGAGCTTCTGATCCGCAATGAA 1491
QY 716 ttgttgaagcagagctagcagacatgtttacagaagaagtttaagagagaagttactaa 775
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1492 --GAAGATGAGAAATAGCTGATGATCTACGCCGATTTTGTGACCAAGAGATTCTTGA 1549
QY 776 ttgtcttgatgatctgagagttgtgaagtgtggagatggcgtgagacgattgttccaa 835
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1550 TTCTCATTTGATGTGTGTGGGACTATTAAGTGTGGGCAATCTATGATATGCTT--CA 1606
QY 836 ctgaagacaatgagagagtcgaatactgttgaactcccgtaalgtagaatgagctgt 895
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1607 GTGATGTTCAATAGAGAGATTAATCTTACCAACCCCTTGAAATGATGTCGCCGAT 1666
QY 896 atgctgtgtgagaaatttcttcttcgagatgagctcagatcagatcagaatgagattgga 955
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1667 AAGTCAAAATGTGAAGTGAATGCCCATCATCTTGTATTATCAGAGATGAGAAAGTTTGA 1726
QY 956 gtcttcaaaatgagcagcttctcaagtgaagcattacataatgagttgagagctgt 1015
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1727 CATTTATTACAGAAAGAGCTTTTCAAGGAGAGAGCTGTCCACTGCAACTTGAAGATGTG 1786
QY 1016 gaaagcaaatcgacagatgagatgacaggttaccactaatctatgtcgtgtgtgcagggc 1075
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1787 GATTTGAAATATCAAAAAGGTTGAGAGGGTGTGCTCTCAGTGTGTGTGTGTGTGTGTGT 1846
QY 1076 ttctcaaatcaaaagacaatgagatgtgaaactgtgtcgttaagaatgataatcatt 1135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1847 TTCTGAAACGAAAAAAGAGACACTAGATTTCATGGAAGTATGAAACAAAGTCTAAGTT 1906

```



```

APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
APPLICANT: Katagiri, Fumitaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 5134 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-04589-157

```

```

Query Match 6.0%; Score 164.2; DB 5; Length 5134;
Best Local Similarity 50.3%; Pred. No. 4e-37;
Matches 544; Conservative 0; Mismatches 518; Indels 19; Gaps 5;

```

```

QY 416 caattcacacaacgaatatttgaaaggttaagaacaatatgtgtgacgtgatgacaaa 475
DB 1196 CATCTTTTACAGCTTATCTCAAGAGCAAGCAAGAAATGGAGGTTTTCAGGATACAA 1255
QY 476 ggaacaagttgttagaagaatctgactagaagctactctggggaacccaagtcaccca 535
DB 1256 TAGATGAATTAAGGATAAAGTAACTACTGAGAGATCACT---GAGCTTGATGTCATCTCA 1312
QY 536 ttgtcgaggtgggagggacataagtaaaacaaccttagcaaaagaagtttcaatgatgaat 595
DB 1313 TCGTTGGCGTGCAGAGATGGGCAAGACTACACTAGCAAAAGAAAGATTTCAAATGATCCAG 1372
QY 596 caattcctagcgcgtttgttgctgctgctggctgctacccatcctacacagcacaacaaaa 655
DB 1373 AAGTACCTCTGCTTCATGCTCAATGCTCAATGCTTGTGACTCAATTATTCATGGA 1432
QY 656 aggaattttgctgggacctctgcatctccacaatcaaaatggatgacaaggtttaagatga 715
DB 1433 GAGAGTGTGCTGCACCAATTTGAATGATGTGCTTGAGGCTTCTGATTCGCAATGAAAAA- 1491
QY 716 ttggtgaaagcaagactagacacatgctacagaaaaagtttaagagaaaaagtgacttaa 775
DB 1492 --GAAGATGAGAAATAGCTGATGATCTACGCCGATTTTGTGTTGACCAAGAGATCTTGA 1549

```

```

QY 776 ttgtcttgatgatcatctggaagtgtgaagtgtggagatggcgtgagacagatgcttccaa 835
DB 1550 TTCTCATTTGATGATGTTGGGACTATTAAGTGTGGCAATCTATGATGTCCTT---CA 1606
QY 836 ctgaagacaatgcagagagtcgaatactgttgactaccctgaatgaagatgaagctgtt 895
DB 1607 GTGATGTTTCAATPAGAGATGAGATTTTCTTACACACCCCTTCAATGATGTCCCAAT 1666
QY 896 atcgtggttagagaatttcttcttgcgagatgagcttcattgatacaagatgagatgtga 955
DB 1667 ATGTCAATGTGAAGATGATCCCATCATCTGTTTATTCAGAGATGAGAGAGTGTGA 1726
QY 956 gtcttttcaaaagtgcagcatttcaagtgaagcattacatatgaattgagatgttg 1015
DB 1727 CATTTATTCAGAAAGAGTCTTTCAGAGAGAGACTGTCCACCTGAACCTTGAAGATGG 1786
QY 1016 gaaagcaaatcgagatgaatgtcaacggttaccactaatatgtgtgtgcaaggc 1075
DB 1787 GATTTGAATATCAAAAGTTGTAGAGGTTGCTCTCTCAGTTGTGTAGTACCTGTG 1846
QY 1076 ttctcaaatctaaaggaacaatagaagattgaaaactgttgctaaagatgtcaagtc 1135
DB 1847 TTCTGAAACAGAAAAGAAAGAACACTAGATTCAATGAGAAAGTAGAACAAAGTCTAAGT 1906
QY 1136 tgcacaaatgatccctgataagcagatgttcaacgtgtgtgtgtgagatgatact 1195
DB 1907 CCCAGAGATTTGGCAGCTTGGAAGAGACATATCTTAATGATTTGATTCAGTAAGAT 1966
QY 1196 tgacaagcgaatctcaaaacatgctcttctgatttcggaatttccagaagacagtata 1255
DB 1967 TACCACACTATCTTAAGCCCTGTTTCTCTATTTTGGAGAGATTTTTCAGAGAAAGATA 2026
QY 1256 ttccagtgaaagatttgatgatacatgatagtgctgaggggttccctgaagttggaagt 1315
DB 2027 TTCTATGCTCAAAAATGACCAAGTTGTGGGTACTGTGAAGGTTGTACCAAGCAACACG 2086
QY 1316 attggaagagaggtt-----gagaagtgttgcagaagctgtgcagatgata 1368
DB 2087 AAAAAGACAAAGAGATACCCGCACAAAGTTTCTTGGACATCTTATTTGGATGAAATCTG 2146
QY 1369 gtccctgcagcaaggaagtcagatgagacaaaattagatcatgtlaagttcatgat 1428
DB 2147 GTGATGGCCATGGAAGAGACCTAATG---CCAAGGTGAAAAGTCCCATTCATGAT 2203
QY 1429 ctaatatagacctgtgcgtgagagaagttcaaaagggagacattttcatcatgacgac 1488
DB 2204 TTGTTGCATTAATTTCTGCATGAAAAAGGCCAAACAGAGAGATTCTTCTCCAGATCAAT 2263
QY 1489 a 1489
DB 2264 A 2264

```

```

RESULT 11
US-08-947-823-2
Sequence 2, Application US/08947823
Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Confering
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

```



ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/947,823

FILING DATE: 09-OCT-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/18802

FILING DATE: 09-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/028,191

FILING DATE: 10-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 023070-070210US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3997 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 85..3852

OTHER INFORMATION: /note="Copy 1 cDNA for M1 nematode"

OTHER INFORMATION: resistance gene of tomato"

US-08-947-823-2

Query Match 5.5% Score 149.2; DB 3; Length 3997;

Best Local Similarity 49.5%; Pred. No. 7.1e-33;

Matches 512; Conservative 0; Mismatches 498; Indels 24; Gaps 4;

QY 449 acaatagtggtgagcgtgatgatcaagaagaaacagtggttagaagatctgtagaagct 508

DB 1637 ATAAATATACGTGATGTTTGAGAGAGAAACAACTTGATTAAGAAAGCTCACCGTG 1696

QY 509 actctggggaacccaagatcccgatgtcgagatggagagatgataaataaacct 568

DB 1697 GATCGGCGATCTGATGTCATTTTCGACCTGGATGCGGGTTCAGGTAAACTACTT 1756

QY 569 tagcaaaagaggttacaatgatcatctatgcggtttagatgctcattgctcgtg 628

DB 1757 TGGCATACAAAGTATACATATATAGTCAGTTCAGCCGTTTGACCTCGTGCATAGT 1816

QY 629 ctacatatctcaacagcaacaacaaagaaatttgctgggctcttcgcatccaca 688

DB 1817 GCACGCTGACCAAGGATGTGATGAGAAAGATTGTGATTAATTTTCACTCAACTTA 1876

QY 689 tcaaatgatgacaaggttaagtattgttgaagacagagctagacagatgtaaga 748

DB 1877 GTGACTCAGAT-----TCAAAATTTGAGTGAGAAATTTGATTTGCTGATTAATTAACGA 1930

QY 749 aaagttaaaagaaagagacttaattgtctgtgtagatcatctggaagtgat 808

DB 1931 AAACAACGTTTGAAGAGGATATCTTAATTTCTAGATGAGCTGGGATTAATTAATTA 1990

QY 809 gggatgagcgtgagacgatttccaaactgaagaacatgcaaggagctgaactgttga 868

DB 1991 GGGATGAGTTAAACAAGACCTTTTC---CTGAATCTAAGAAAGGAGTAAAGATTTTGA 2047

QY 869 ctaccggaatgatgaagtagctgtttagtctgtgtgtagaagaatttctcttgagatga 928

DB 2048 CAACCTGGGAAAAGAGATGGCTTTGCAATGGAAGCTGAACACTGATCTCTTGACCTTC 2107

QY 929 gcttcatgatcaagaatgagatgtagagctctttccaagaatgcaagcatcttcaagtgaag 988

DB 2108 GATTGCTTAAGACACAGATGAAGTTGGGAACATTTAGAAAAAGGCAATTTGGGATATGA 2167

QY 989 catcacatgatgctgagacgtgttgaagaacaaatgcagatgaatgtaacaggttacc 1048

DB 2168 GTTGCCCGTATGACTAATTAATGATGTCGGTAAAGAAATAGCCGAAATGTGAAGGGCTTC 2227

QY 1049 caactaatgtcgtgtgttgcagagcttccaatctcaaaagagcaatgaagaattgga 1108

DB 2228 CTTTGGTGCTATCTGATTTGCTGAGTCATTCGTGGAAGGAAAAAGAGAGTGTGT 2287

QY 1109 aaactgttctaagatgcaagtcattcgttcacaatgatccatgaatgaagatgtcac 1168

DB 2288 GCCTTGAAGTTCAAGTACTTTGACTTCTTTATTTTGAACAGTGAAGTGAAGTGAAGCA 2347

QY 1169 gctgcttggttggttgaatgcaatcctgacaagcgatcctaaacatgcttctgcatc 1228

DB 2348 AAGTTATAGAAATTAAGTTATGACATTTACCAATCACCTCAAGCCATGCTTGTCTGTAT 2407

QY 1229 tgggaattttccagaagacagtgatattccagtgtagaagaatttgaatgtagatgagatg 1288

DB 2408 TTGCAAGTTTTCGAAGGACCTTCATTCACATCTATGAGTTGAATGTTATTTTCGCTG 2467

QY 1289 ctgaggggttctct-----gaagttgaaatgatgttgaaaggaggttgtagaagtgct 1342

DB 2468 CTGAAGATTTTGTGGAAAGACGAGATGAACAGTATGGAAGAGTGAAGATTTATTA 2527

QY 1343 tgcnaagactgtcgatagatgctagtcctcgtcgaagcaagaagatgtagatgtagaaca 1402

DB 2528 TGATGATTTTAATTAACATGACTTGTGAATTTGTTTCAATGAGTAAAGTATGACATGA 2587

QY 1403 aaatgatcatgtagatgctgaatgaataatgatgacctgtgtgtagaagaatgtaaca 1462

DB 2588 A-----TTTCCAAATTCATGATCTTGTGCATGACTTTTGTGATTAAGCAAGAA 2638

QY 1463 gggagacaatttt 1476

DB 2639 AGCAAAATTTGTTT 2652

RESULT 12

US-08-947-823-1

Sequence 1, Application US/08947823

Patent No. 6114605

GENERAL INFORMATION:

APPLICANT: Williamson, Valerie M.

APPLICANT: Kaloshian, Isouhi

APPLICANT: Yaghoobi, Jafar

APPLICANT: Bodeau, John

APPLICANT: Milligan, Stephen

TITLE OF INVENTION: Procedures and Materials for Confering

NUMBER OF INVENTION: Pest Resistance in Plants

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/947,823

FILING DATE: 09-OCT-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/18802



FILING DATE: 09-OCT-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/028,191  
 FILING DATE: 10-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bastian, Kevin L.  
 REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 023070-070210US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 51952 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-947-823-1

Query Match 5.5%; Score 149.2; DB 3; Length 51952;  
 Best Local Similarity 49.3%; Fred. No. 3e-32;  
 Matches 512; Conservative 0; Mismatches 498; Indels 24; Gaps 4;

QY 449 acaatattgtgacgtgatgaatgaagaacagttgttagaagatcgtgacatagaagct 508  
 DB 46729 ATAAATTAAGTACTAGTGTGAGGAGGAGAACTTGTACTTGAAGAGCTCACCAGTG 46788  
 QY 509 actctgggaacccaaagatcaccgcatgtcggagatgggaagcatalagtaaacacct 568  
 DB 46789 GATCGGAGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 46848  
 QY 569 tagcaagaagtttacaatgtatgaatcattctatgcggttttgatgttctatgcctgg 628  
 DB 46849 TGGCATACAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 46908  
 QY 629 ctacatatctcaacagcaacaaagaatcttgcggcctctgcattccacaa 688  
 DB 46909 GCACGCTGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 46968  
 QY 689 tcaaaatgatgacaggggttaagatgtgtgaagcagagctagacagatgtatcaga 748  
 DB 46969 GTGACTCAGAT-----TCAAAATGAGAGGAGATGATGATGATGATGATGATGATGATGAT 47022  
 QY 749 aagatttaagagaagaggtcttaattgtcttggatgatctcggagttgtgaagtg 808  
 DB 47023 AACAACTGTTGGAAAGAGGTATCTTATGCTTAGATGACGCTGGGATTAATTAATTAAT 47082  
 QY 809 gggatggcgtgagagatgcttcaactgaagacatgacagagagctgaatcagttga 868  
 DB 47083 GGGATGAGTAAACAGACCTTTTCTGAAATCTAAGAAAGAGGATGATGATGATGATGAT 47139  
 QY 869 ctaccgtaatatgaaatgactgttctgtgtgtagaagaatttcttgcgagatga 928  
 DB 47140 CAATCGGAAAGAGAGGCTTTCATGAAAGCTGAACCTGATCTCTTGAACCTTC 47199  
 QY 929 gcttcaatgataagatgagagttgagttcttcaaaaagtcagacatcttcaagtga 988  
 DB 47200 GATTTCTAAGACCAAGATGAACTTGGAACTATTAGAGAAAGGCGATTTGGGAATGAGA 47259  
 QY 989 cattaccatagatgagactgttgaagaacaatgcagatgaatgacaggtttac 1048  
 DB 47260 GTTGCCCTGATGAATATTAGATGTCGGTAAAGAAATAGCCAAAATTTTAAAGGGCTTC 47319  
 QY 1049 caataactatgtcgtgttgcaaggtcttcaaatctaaagaacatagaagaattgga 1108  
 DB 47320 CTTTGTGCTGATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 47379  
 QY 1109 aaacgttgctaaagatgtcaagatcgtacacaaatgatcgtatgaagatgtttcac 1168  
 DB 47380 GCGTTGAAGTCAAAAGTGTGAGTCTTTTATTTTGAACAGTGAAGTGAAGTGAAGTGA 47439

QY 1169 gttgtgtgtgtgactgacatcacttgacaagcgatctaaacatgtcttctgact 1228  
 DB 47440 AAGTTATGAATTAAGTATGACATTTTACACATGATGATGATGATGATGATGATGATGATGAT 47499  
 QY 1229 tcggaatttccagaagacagtgatattccagtgagaagattgatgatgatgatgat 1288  
 DB 47500 TTGCAAGTTTCCGAAGACACTTCAATGACATCTATGAGTGAATGTTTATTTGGTGTG 47559  
 QY 1289 ctgaggggttcc-----gaagttgaaatgatattggaagaagaggtttgagaatgt 1342  
 DB 47560 CTGAAGATTTTGGGAAAGACGAGATGAACGATGATGAAAGAGTGTGAAGATTTATA 47619  
 QY 1343 tcaagaagctgtcgaatagatgtctatgcctgcgcagaagaagtcagatgagacaa 1402  
 DB 47620 TGATGATTTAATTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 47679  
 QY 1403 aaatagatcatgtaagttcatatcatatataatgaacctgtgctgagagaagttcaa 1462  
 DB 47680 A-----TTTCCAAATTCATGATCTTGTGATGATGATGATGATGATGATGATGATGAT 47730  
 QY 1463 gggagacatttt 1476  
 DB 47731 AGGAAATTTGTTT 47744

RESULT 13  
 US-08-947-823-4  
 Sequence 4, Application US/08947823  
 Patent No. 6114605  
 GENERAL INFORMATION:  
 APPLICANT: Williamson, Valerie M.  
 APPLICANT: Kaloshian, Isouhl  
 APPLICANT: Vaghoobi, Jafar  
 APPLICANT: Bodeau, John  
 APPLICANT: Milligan, Stephen  
 TITLE OF INVENTION: Procedures and Materials for Confering  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/947,823  
 FILING DATE: 09-OCT-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US97/18802  
 FILING DATE: 09-OCT-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/028,191  
 FILING DATE: 10-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bastian, Kevin L.  
 REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 023070-070210US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0300  
 TELEFAX: (415) 576-0200  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3982 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear





